

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 6, 2002, 20:59:53 ; Search time 2365.28 seconds  
(without alignments)  
2790.372 Million updates/sec

Title: US-09-724-841-4

Perfect score: 489

Sequence: 1 ATGAGATTTCGAACACCA.....TGTTTCATCAACACTTCTGA 489

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 674877542 residues

Word size : 12

Total number of hits satisfying chosen parameters: 616261

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

EST:\*

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estnu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_htc:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_htc:\*
- 12: gb\_gss:\*
- 13: em\_gss\_hum:\*
- 14: em\_gss\_inv:\*
- 15: em\_gss\_pln:\*
- 16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	107	21.9	509	9	AA463370
2	107	21.9	800	10	BG184658
3	107	21.9	982	9	AL548180
4	72	14.7	483	9	AW804165
5	72	14.7	494	9	AW804168
6	72	14.7	637	9	AL860008
7	72	14.7	994	10	AL572832
8	63	12.9	301	10	BF088290
9	62	12.7	872	10	BI758686
10	55	11.2	474	10	N49734
11	54	11.0	471	10	N76741
12	51	10.4	756	10	BI832895
13	48	9.8	278	9	BE177883
14	48	9.8	718	10	BI766231
15	46	9.4	309	10	BF095213
16	37	7.6	817	10	BI756810
17	35	7.2	550	10	BE698667

91	18	3.7	209	10	BE938076	BE938076 MRI-TN004	18	3.7	564	10	BM087942	BM087942 501279 MA
92	18	3.7	240	9	AU072894	AU072894 AU072894	18	3.7	568	9	AV608082	AV608082 AV608082
93	18	3.7	240	9	AU073785	AU073785 AU073785	18	3.7	570	12	AZ105435	AZ105435 RPT-23-2
94	18	3.7	246	9	A1216676	A1216676 q96604.x	18	3.7	572	12	AQ480604	AQ480604 RPT-11-2
95	18	3.7	252	9	A16162341	A16162341 ms28h11.r	18	3.7	578	12	AQ434059	AQ434059 RPT-11-12
96	18	3.7	255	12	AQ266553	AQ266553 RPT-11-75	18	3.7	582	9	AV601815	AV601815 AV601815
97	18	3.7	271	9	A1425144	A1425144 v13a08.y	18	3.7	586	10	BG713068	BG713068 p11n.pk0
98	18	3.7	277	9	AV091358	AV091358 AV091358	18	3.7	586	10	AZ523793	AZ523793 223PbE09
99	18	3.7	281	9	B8227954	B8227954 B8227954	18	3.7	588	10	BJ084067	BJ084067 RPT-24-3
100	18	3.7	287	9	B8479348	B8479348 B8479348	18	3.7	591	12	AQ268847	AQ268847 RPT-11-74
101	18	3.7	301	12	AZ893931	AZ893931 RPT-24-1	18	3.7	595	12	AQ278117	AQ278117 2M0033E03
102	18	3.7	303	12	AQ571160	AQ571160 HS_5375_B	18	3.7	600	10	BG805303	BG805303 0691-05 M
103	18	3.7	311	9	B8121198	B8121198 B8121198	18	3.7	602	9	AJ396846	AJ396846 AJ396846
104	18	3.7	316	10	BF894555	BF894555 CMO-MT015	18	3.7	606	12	BH050025	BH050025 RPT-24-3
105	18	3.7	321	10	BE956674	BE956674 P11_55_B1	18	3.7	613	12	AZ453878	AZ453878 1M0255L04
106	18	3.7	328	10	BM166474	BM166474 EST568997	18	3.7	616	10	BJ085968	BJ085968 BJO85968
107	18	3.7	333	10	T53024	T53024 ya82h10.s1	18	3.7	619	12	BH301289	BH301289 CH230-36K
108	18	3.7	348	9	A1922279	A1922279 wn9c03.x	18	3.7	620	12	BH430568	BH430568 BOHNG2TR
109	18	3.7	359	12	AQ097232	AQ097232 HS_3038_B	18	3.7	621	12	AQ240058	AQ240058 CIT-HSP-2
110	18	3.7	360	12	BH286458	BH286458 CH230-76L	18	3.7	624	12	BH615724	BH615724 BMAC304B
111	18	3.7	361	10	BM234783	BM234783 K0406E03-	18	3.7	627	10	BG274900	BG274900 WHE2118.F
112	18	3.7	367	9	A1471341	A1471341 cm10g12.x	18	3.7	629	10	BG641951	BG641951 p911c.pk0
113	18	3.7	368	12	AZ841111	AZ841111 2M0138M23	18	3.7	636	9	A1084738	A1084738 oz79f02.x
114	18	3.7	372	12	AQ243976	AQ243976 HS_2058_B	18	3.7	640	10	BF296518	BF296518 03BPBC02
115	18	3.7	374	9	AA884912	AA884912 am29c07.s	18	3.7	644	10	BF295663	BF295663 02PBG04
116	18	3.7	400	9	AV435067	AV435067 AV435067	18	3.7	655	12	AZ939870	AZ939870 2M0199J06
117	18	3.7	401	10	B1813883	B1813883 PfESToaal	18	3.7	659	10	BT619393	BT619393 RH50424_5
118	18	3.7	405	10	R08563	R08563 yf20c05.s1	18	3.7	660	12	BH366449	BH366449 CH230-60M
119	18	3.7	408	10	W88449	W88449 zh69h03.r1	18	3.7	661	9	AL558400	AL558400
120	18	3.7	415	9	AQ038028	AQ038028 AU038028	18	3.7	679	12	BH028386	BH028386 RPT-24-3
121	18	3.7	415	10	C90402	C90402 C90402 Dict	18	3.7	684	12	AZ148608	AZ148608 Pan trogl
122	18	3.7	418	12	AQ314939	AQ314939 RPT-11-95	18	3.7	684	12	AG256768	AG256768 238PvA08
123	18	3.7	419	10	C92187	C92187 Dict	18	3.7	687	9	BB245993	BB245993 BH245993
124	18	3.7	428	10	C91313	C91313 C91313 Dict	18	3.7	689	10	BE672442	BE672442 7a60h04.x
125	18	3.7	429	12	AZ376171	AZ376171 1M0129J19	18	3.7	689	12	AZ047778	AZ047778 nbe00094M
126	18	3.7	433	9	B8814995	B8814995 BB814995	18	3.7	739	9	BE055345	BE055345 GA_Ea000
127	18	3.7	447	12	AZ376943	AZ376943 1M0130J19	18	3.7	739	9	AL558401	AL558401
128	18	3.7	448	9	AG655185	AG655185 v13a08.r	18	3.7	750	10	BI520192	BI520192 603071440
129	18	3.7	453	12	B95318	B95318 CIT-HSP-217	18	3.7	751	12	BH573707	BH573707 BOHCU72TF
130	18	3.7	458	10	BM087956	BM087956 501285 MA	18	3.7	757	12	BH560224	BH560224 ROGZW11TF
131	18	3.7	459	9	AW291764	AW291764 UI-H-B12-	18	3.7	759	12	CNS02C9N	CNS02C9N Tetraodon
132	18	3.7	470	10	BF426717	BF426717 da823b09.	18	3.7	767	12	BH556210	BH556210 BOHUV48TF
133	18	3.7	472	10	BM108956	BM108956 EST556492	18	3.7	769	12	B21922	B21922 F4P15-T7 IG
134	18	3.7	475	12	AQ480622	AQ480622 RPT-11-2	18	3.7	778	12	AQ796876	AQ796876 nbx0071G
135	18	3.7	477	10	BF250356	BF250356 pa98b08.y	18	3.7	797	12	BH203201	BH203201 Sm1-58L11
136	18	3.7	480	12	AQ839796	AQ839796 RG558.F.D	18	3.7	800	10	BG410034	BG410034 S10-7-A5
137	18	3.7	485	12	AQ129107	AQ129107 HS_3032_B	18	3.7	808	12	BH097232	BH097232 RPT-24-3
138	18	3.7	486	12	A2151908	A2151908 SP_0033_A	18	3.7	813	12	BH537808	BH537808 BOHPB08TR
139	18	3.7	492	10	BG511261	BG511261 sad15f03.	18	3.7	819	12	AG112337	AG112337 Pan trogl
140	18	3.7	492	10	BF707238	BF707238 282765 MA	18	3.7	828	10	BG975177	BG975177 602843271
141	18	3.7	494	12	AZ896962	AZ896962 RPT-24-1	18	3.7	835	12	AQ746923	AQ746923 HS_5538_A
142	18	3.7	500	9	AU086794	AU086794 AU086794	18	3.7	861	12	AQ750054	AQ750054 HS_5574_A
143	18	3.7	502	10	BG156404	BG156404 sa974c11.	18	3.7	863	10	BG622794	BG622794 602647582
144	18	3.7	504	12	AQ188512	AQ188512 HS_3229_B	18	3.7	874	12	CNS01XDI	CNS01XDI Tetraodon
145	18	3.7	506	12	AZ214069	AZ214069 Sheared D	18	3.7	885	12	AQ878812	AQ878812 HS_5135_A
146	18	3.7	510	10	BF565107	BF565107 RH62779.5	18	3.7	886	12	BH181333	BH181333 018_M_10
147	18	3.7	513	9	AA779991	AA779991 zj24c04.s	18	3.7	886	12	CNS07M2D	CNS07M2D T7 end of
148	18	3.7	513	10	BG711644	BG711644 p911n.pk0	18	3.7	940	9	AW729338	AW729338 GA_Ea002
149	18	3.7	514	12	AQ279658	AQ279658 CITBI-E1-	18	3.7	954	12	AG056800	AG056800 Pan trogl
150	18	3.7	519	12	AQ599545	AQ599545 HS_5353_A	18	3.7	954	12	CNS05JDB	CNS05JDB Tetraodon
151	18	3.7	527	9	AV667301	AV667301 AV667301	18	3.7	954	12	CNS05JDB	CNS05JDB Tetraodon
152	18	3.7	528	10	BM419388	BM419388 R013B02 O	18	3.7	996	12	CNS04RLI	CNS04RLI Tetraodon
153	18	3.7	531	12	BH594729	BH594729 BORJU30TF	18	3.7	1017	12	CNS07CEW	CNS07CEW T3 end of
154	18	3.7	537	10	BJ077949	BJ077949 BJO77949	18	3.7	1075	12	CNS0269P	CNS0269P Tetraodon
155	18	3.7	538	12	AQ0883720	AQ0883720 HS_5480_B	18	3.7	1092	12	CNS05RNI	CNS05RNI Tetraodon
156	18	3.7	538	12	BH070952	BH070952 RPT-24-3	18	3.7	1092	12	CNS05RNI	CNS05RNI Tetraodon
157	18	3.7	545	10	BH273689	BH273689 PfESToaas	18	3.7	1272	10	BG848826	BG848826 1024022H0
158	18	3.7	545	12	AZ816255	AZ816255 2M0084122	18	3.7	1390	10	BG696442	BG696442 602659550
159	18	3.7	549	10	BM275035	BM275035 PfESToaas	18	3.7	1481	10	BG618683	BG618683 601462889
160	18	3.7	552	10	BG602945	BG602945 EST502035	18	3.7	1511	10	BG995101	BG995101 CMO-HT129
161	18	3.7	552	12	AQ238897	AQ238897 HS_3234_B	18	3.7	1511	10	BG995098	BG995098 CMO-HT129
162	18	3.7	554	12	A2159078	A2159078 SP_0062_A	18	3.7	1525	9	AV411597	AV411597 AV411597
163	18	3.7	558	12	B65439	B65439 CIT-HSP-202	18	3.7	163	9	AV752429	AV752429 AV752429

c 237	17	3.5	168	9	AA140688	AA140688 CK00399.3	c 310	17	3.5	346	12	AQ042979	AQ042979 CIT-HSP-2
238	17	3.5	170	9	AW020780	AW020780 dfl14c12.y	c 311	17	3.5	346	12	AQ097137	AQ097137 HS_3036.A
239	17	3.5	172	12	AZ560996	AZ560996 RPCI-23-2	c 312	17	3.5	346	12	CNS01047	AL153048 ANoheles
240	17	3.5	173	12	AQ285804	AQ285804 RPCI11-88	c 313	17	3.5	347	9	AV660392	AV660392 AV660392
c 241	17	3.5	176	10	B1795077	B1795077 H007H01.E	c 314	17	3.5	347	9	AA343755	AA343755 EST49584
c 242	17	3.5	185	9	BB028532	BB028532 BB028532	c 315	17	3.5	347	10	BM068576	BM068576 WHE3459.C
c 243	17	3.5	191	12	AZ259959	AZ259959 RPCI-23-1	c 316	17	3.5	348	10	BF881504	BF881504 QV1-ET018
c 244	17	3.5	196	9	AF114083	AF114083 AF114083	c 317	17	3.5	350	9	AV653496	AV653496 AV653496
c 245	17	3.5	203	9	BE186072	BE186072 946005A04	c 318	17	3.5	350	9	AV688898	AV688898 AV688898
c 246	17	3.5	204	9	AW998631	AW998631 PM0-BM006	c 319	17	3.5	354	9	AV689018	AV689018 AV689018
c 247	17	3.5	209	10	BF652679	BF652679 276322.MA	c 320	17	3.5	354	9	AV692243	AV692243 AV692243
c 248	17	3.5	212	9	BB587929	BB587929 BB587929	c 321	17	3.5	354	9	AV694127	AV694127 AV694127
c 249	17	3.5	214	9	BB084087	BB084087 BB084087	c 322	17	3.5	356	9	AA790941	AA790941 VW21E02.F
c 250	17	3.5	221	9	AV359601	AV359601 AV359601	c 323	17	3.5	356	9	AV696331	AV696331 AV696331
c 251	17	3.5	221	9	BB049492	BB049492 BB049492	c 324	17	3.5	357	9	AV693324	AV693324 AV693324
c 252	17	3.5	225	9	BB478631	BB478631 BB478631	c 325	17	3.5	358	9	AV694137	AV694137 AV694137
c 253	17	3.5	231	9	BB084185	BB084185 BB084185	c 326	17	3.5	360	6	BE363609	BE363609 WSL_64.A0
c 254	17	3.5	233	10	BE580514	BE580514 K411F01.Y	c 327	17	3.5	360	9	AV193274	AV193274 AV193274
c 255	17	3.5	237	9	AW429683	AW429683 68069.MAR	c 328	17	3.5	360	9	AV651138	AV651138 AV651138
c 256	17	3.5	238	9	BB084088	BB084088 BB084088	c 329	17	3.5	360	10	BM317751	BM317751 WSL_63.A0
c 257	17	3.5	240	9	AV253405	AV253405 AV253405	c 330	17	3.5	360	10	C68513	C68513 C68513 YU1
c 258	17	3.5	242	9	BE073782	BE073782 RC0-BT056	c 331	17	3.5	360	10	C71328	C71328 C71328 YU1
c 259	17	3.5	244	10	R29531	R29531 FI-1045D.22	c 332	17	3.5	360	10	D36775	D36775 CELK036H8F
c 260	17	3.5	252	9	BB177561	BB177561 BB177561	c 333	17	3.5	360	10	D74735	D74735 CELK084GYF
c 261	17	3.5	255	9	AA562271	AA562271 V134d11.r	c 334	17	3.5	361	9	AV651947	AV651947 AV651947
c 262	17	3.5	258	9	BB216124	BB216124 BB216124	c 335	17	3.5	362	10	BF881502	BF881502 QV1-ET018
c 263	17	3.5	260	9	BB595324	BB595324 BB595324	c 336	17	3.5	363	9	AV646229	AV646229 AV646229
c 264	17	3.5	263	9	AV235753	AV235753 AV235753	c 337	17	3.5	363	9	AV662110	AV662110 AV662110
c 265	17	3.5	271	12	BH143445	BH143445 TDGEA14TH	c 338	17	3.5	363	9	AV692799	AV692799 AV692799
c 266	17	3.5	273	9	AV040912	AV040912 AV040912	c 339	17	3.5	365	9	AV662130	AV662130 AV662130
c 267	17	3.5	273	9	AA344119	AA344119 EST49991	c 340	17	3.5	366	9	AV654237	AV654237 AV654237
c 268	17	3.5	276	9	AV252434	AV252434 AV252434	c 341	17	3.5	366	9	AV657329	AV657329 AV657329
c 269	17	3.5	281	9	AW798655	AW798655 RC2-UM005	c 342	17	3.5	366	12	B66283	B66283 CIT-HSP-202
c 270	17	3.5	282	9	AA226442	AA226442 nc18406.S	c 343	17	3.5	367	9	AV522656	AV522656 AV522656
c 271	17	3.5	283	9	BB065754	BB065754 BB065754	c 344	17	3.5	367	12	AZ125692	AZ125692 OSJNB009
c 272	17	3.5	283	10	B1155083	B1155083 60290223-2	c 345	17	3.5	368	9	AV646054	AV646054 AV646054
c 273	17	3.5	283	12	AQ986268	AQ986268 RPCI-29-32	c 346	17	3.5	368	12	AQ033736	AQ033736 HS_2237.A
c 274	17	3.5	284	9	AA343616	AA343616 EST49426	c 347	17	3.5	369	9	AV651137	AV651137 AV651137
c 275	17	3.5	284	12	AQ527922	AQ527922 RPCI-11-3	c 348	17	3.5	369	12	AQ056164	AQ056164 CIT-HSP-2
c 276	17	3.5	285	9	BB091976	BB091976 BB091976	c 349	17	3.5	369	12	AQ074480	AQ074480 CIT-HSP-2
c 277	17	3.5	288	9	BB249039	BB249039 BB249039	c 350	17	3.5	370	9	AV660075	AV660075 AV660075
c 278	17	3.5	289	9	AV016164	AV016164 AV016164	c 351	17	3.5	370	9	AV653049	AV653049 AV653049
c 279	17	3.5	291	10	B1026450	B1026450 CM4-MT028	c 352	17	3.5	371	9	AV689132	AV689132 AV689132
c 280	17	3.5	291	10	B1594660	B1594660 As_nc_195E	c 353	17	3.5	371	10	R08023	R08023 YF17C04.s1
c 281	17	3.5	294	12	AQ789234	AQ789234 HS_3113.B	c 354	17	3.5	372	10	T08118	T08118 EST06009.1n
c 282	17	3.5	296	10	BF545081	BF545081 UI-R-C2P-	c 355	17	3.5	374	10	B1346759	B1346759 376089.MA
c 283	17	3.5	298	9	AV134103	AV134103 AV134103	c 356	17	3.5	374	10	B1346760	B1346760 376070.MA
c 284	17	3.5	299	9	AV047271	AV047271 AV047271	c 357	17	3.5	376	9	AA141116	AA141116 CK01216.5
c 285	17	3.5	300	9	AA343501	AA343501 EST49372	c 358	17	3.5	376	9	AV661412	AV661412 AV661412
c 286	17	3.5	302	10	M77939	M77939 EST01523.Fe	c 359	17	3.5	377	9	AW238376	AW238376 XP24d07.x
c 287	17	3.5	307	9	AV710185	AV710185 AV710185	c 360	17	3.5	377	10	BM162969	BM162969 EST565492
c 288	17	3.5	308	9	AV100794	AV100794 AV100794	c 361	17	3.5	377	10	BF391552	BF391552 UI-R-CAL-
c 289	17	3.5	311	12	BH584386	BH584386 BORHX20FF	c 362	17	3.5	377	12	AZ852217	AZ852217 2M0154A22
c 290	17	3.5	313	9	AA343884	AA343884 EST49753	c 363	17	3.5	378	9	AA141117	AA141117 CK01216.3
c 291	17	3.5	315	9	BE102135	BE102135 UI-R-BT1-	c 364	17	3.5	378	9	AV203654	AV203654 AV203654
c 292	17	3.5	315	10	T50936	T50936 Yb88e11.r1	c 365	17	3.5	378	9	AV646315	AV646315 AV646315
c 293	17	3.5	319	9	BB162079	BB162079 BB162079	c 366	17	3.5	378	9	AV646338	AV646338 AV646338
c 294	17	3.5	321	9	AA343796	AA343796 EST49629	c 367	17	3.5	378	9	AV660277	AV660277 AV660277
c 295	17	3.5	323	9	AI615495	AI615495 V134d11.y	c 368	17	3.5	380	9	AV649851	AV649851 AV649851
c 296	17	3.5	324	12	BB279820	BB279820 CH230-178	c 369	17	3.5	382	9	AV649811	AV649811 AV649811
c 297	17	3.5	325	9	AW292244	AW292244 UI-H-B12-	c 370	17	3.5	382	9	AV649899	AV649899 AV649899
c 298	17	3.5	328	9	BB314867	BB314867 BB314867	c 371	17	3.5	382	10	BE287207	BE287207 601093903
c 299	17	3.5	328	10	T53903	T53903 Yb83f02.r1	c 372	17	3.5	382	12	BH049792	BH049792 RPCI-24-2
c 300	17	3.5	331	10	F07852	F07852 HSC2JH051.n	c 373	17	3.5	383	12	AQ462501	AQ462501 HS_5213.A
c 301	17	3.5	334	10	BF366203	BF366203 IL2-TN009	c 374	17	3.5	384	10	BI302090	BI302090 UI-R-DLO-
c 302	17	3.5	335	9	AV657252	AV657252 AV657252	c 375	17	3.5	386	10	BF392836	BF392836 UI-R-CAO-
c 303	17	3.5	336	10	BG316932	BG316932 947024B11	c 376	17	3.5	388	10	T86348	T86348 Yd84f10.r1
c 304	17	3.5	338	12	AZ709836	AZ709836 RPCI-24-1	c 377	17	3.5	388	10	W58451	W58451 zd25q05.s1
c 305	17	3.5	339	10	BE716123	BE716123 MR2-HT075	c 378	17	3.5	389	12	AZ036778	AZ036778 RPCI-23-3
c 306	17	3.5	341	9	AV656936	AV656936 AV656936	c 379	17	3.5	390	9	AV654777	AV654777 AV654777
c 307	17	3.5	341	9	BB236349	BB236349 BB236349	c 380	17	3.5	390	9	AA475487	AA475487 VHL5E05.F
c 308	17	3.5	345	10	BE510715	BE510715 946055A02	c 381	17	3.5	393	12	AQ990526	AQ990526 RFC01314
c 309	17	3.5	345	12	AQ546315	AQ546315 CITBI-EI-	c 382	17	3.5	394	10	BF818509	BF818509 CM2-CI017

c 383	17	3.5	394	12	AZ653452	AZ653452 1M0527E09	c 456	17	3.5	460	10	BE674314	BE674314 7d78D03.x
c 384	17	3.5	396	9	AA247631	AA247631 CSq4706.s	c 457	17	3.5	462	10	R43029	R43029 Yg09e03.s1
c 385	17	3.5	397	12	AZ119077	AZ119077 RPCI-23-1	c 458	17	3.5	462	12	B57426	B57426 CIT-HSP-200
c 386	17	3.5	397	12	AQ363379	AQ363379 ndx60060A	c 459	17	3.5	464	9	BB690102	BB690102 BB690102
c 387	17	3.5	401	9	AV654903	AV654903 AV654903	c 460	17	3.5	464	10	BF826997	BF826997 RCI-IN003
c 388	17	3.5	401	9	AV655411	AV655411 AV655411	c 461	17	3.5	465	12	AQ972596	AQ972596 RPCI-23-3
c 389	17	3.5	401	9	AW306258	AW306258 s848D01.Y	c 462	17	3.5	466	10	BF388495	BF388495 UI-R-CA1-
c 390	17	3.5	402	12	AZ118679	AZ118679 RPCI-23-1	c 463	17	3.5	466	12	B44971	B44971 HS-1060-A2-
c 391	17	3.5	405	10	T18997	T18997 e02038t.Tes	c 464	17	3.5	466	12	AQ517286	AQ517286 HS_5130.B
c 392	17	3.5	405	10	BE946773	BE946773 UI-M-B20-	c 465	17	3.5	467	10	BF963910	BF963910 QV2-NN004
c 393	17	3.5	405	12	AZ936279	AZ936279 Gm_UMB001	c 466	17	3.5	468	12	AZ275335	AZ275335 RPCI-23-1
c 394	17	3.5	407	9	AA141417	AA141417 CK01710.S	c 467	17	3.5	469	9	AA926738	AA926738 Om28H06.s
c 395	17	3.5	407	9	AI643100	AI643100 mm51G08.Y	c 468	17	3.5	469	10	HS3231	HS3231 Yg84f02.r1
c 396	17	3.5	407	9	BE081810	BE081810 QV2-BT063	c 469	17	3.5	472	10	B1512000	B1512000 BB160007B
c 397	17	3.5	408	10	T74630	T74630 YC57B09.r1	c 470	17	3.5	472	10	BE368620	BE368620 601220230
c 398	17	3.5	410	10	H06581	H06581 Y178H03.r1	c 471	17	3.5	472	12	AQ706678	AQ706678 HS_554.M_B
c 399	17	3.5	411	10	F14049	F14049 ATTS4971.Ve	c 472	17	3.5	472	12	AQ237497	AQ237497 RPCI-11-61
c 400	17	3.5	411	12	AQ127177	AQ127177 HS_3042.B	c 473	17	3.5	472	12	AQ457917	AQ457917 HS_5189.B
c 401	17	3.5	412	10	BF440274	BF440274 BS2900020	c 474	17	3.5	473	9	AW632188	AW632188 91826.MAR
c 402	17	3.5	414	10	BI749372	BI749372 ro77C12.Y	c 475	17	3.5	473	12	AZ231554	AZ231554 RPCI-23-6
c 403	17	3.5	414	12	AQ767359	AQ767359 HS_2269.B	c 476	17	3.5	475	9	AA773580	AA773580 ab61G02.s
c 404	17	3.5	418	10	BE669472	BE669472 7e13C08.x	c 477	17	3.5	475	10	AL120453	AL120453 DKF2P7611
c 405	17	3.5	418	12	AZ852816	AZ852816 2M0155805	c 478	17	3.5	475	10	BG893960	BG893960 kt22a03.Y
c 406	17	3.5	419	9	AW124430	AW124430 UI-M-BH2.	c 479	17	3.5	475	12	AZ805823	AZ805823 2M0067K24
c 407	17	3.5	419	9	BE219493	BE219493 hv58G08.x	c 480	17	3.5	479	9	BE186377	BE186377 946005A04
c 408	17	3.5	422	9	AA769398	AA769398 n238E04.s	c 481	17	3.5	480	12	BH011282	BH011282 qd79f01.b
c 409	17	3.5	422	9	AW288264	AW288264 SNOV3MCAM	c 482	17	3.5	483	12	AL597025	AL597025 DKF2P313A
c 410	17	3.5	422	9	AA456864	AA456864 ad38a10.r	c 483	12	TA263F02P	TA263F02P	AL483825 T. bruce1		
c 411	17	3.5	422	10	T67776	T67776 YC27B12.r1	c 484	12	AQ293225	AQ293225 HS_2239.B			
c 412	17	3.5	422	10	BF632832	BF632832 NF044B02D	c 485	12	AG653785	AG653785 sad55B04.			
c 413	17	3.5	423	9	AW020154	AW020154 df05C12.Y	c 486	9	AI005265	AI005265 ou07f02.x			
c 414	17	3.5	423	10	BG928581	BG928581 HNC8-1-B3	c 487	10	BE630696	BE630696 uu47c03.x			
c 415	17	3.5	424	12	AQ167304	AQ167304 HS_3154.A	c 488	12	BH043470	BH043470 RPCI-24-3			
c 416	17	3.5	424	12	BH586030	BH586030 BOHEU85TF	c 489	12	AZ777853	AZ777853 2M0012G12			
c 417	17	3.5	425	12	AQ835977	AQ835977 HS_3350.A	c 490	17	3.5	494	9	AW876507	AW876507 RCI-PT002
c 418	17	3.5	426	12	AQ359668	AQ359668 HS_5034.A	c 491	17	3.5	500	10	BI174448	BI174448 OSTF044F3
c 419	17	3.5	429	10	BG633645	BG633645 GM04730.3	c 492	17	3.5	500	10	BF220768	BF220768 NXCI.150
c 420	17	3.5	429	10	BE946448	BE946448 UI-M-B20-	c 493	17	3.5	504	9	AA700024	AA700024 z169d10.s
c 421	17	3.5	431	10	BE512194	BE512194 946065G10	c 494	17	3.5	504	9	AV624180	AV624180 AV624180
c 422	17	3.5	433	10	B1070984	B1070984 C050P42U	c 495	17	3.5	504	9	AW567767	AW567767 s154f03.Y
c 423	17	3.5	434	12	AQ080266	AQ080266 HS_2174.B	c 496	17	3.5	504	10	B1396920	B1396920 ro63f01.Y
c 424	17	3.5	435	9	AA416629	AA416629 CK02453.3	c 497	17	3.5	505	12	AZ259548	AZ259548 RPCI-23-4
c 425	17	3.5	435	12	AQ054234	AQ054234 RPCI-11-35	c 498	17	3.5	506	12	AB753346	AB753346 BB753346
c 426	17	3.5	436	9	AV651836	AV651836 AV651836	c 499	17	3.5	506	12	AZ035938	AZ035938 RPCI-23-2
c 427	17	3.5	436	9	AV704108	AV704108 AV704108	c 500	17	3.5	506	12	AZ633006	AZ633006 1M0487P22
c 428	17	3.5	437	9	AW773592	AW773592 EST332578	c 501	17	3.5	507	12	AV623350	AV623350 AV623550
c 429	17	3.5	437	9	BB710432	BB710432 BB710432	c 502	17	3.5	508	9	AV348865	AV348865 AV548865
c 430	17	3.5	438	12	PCR303735	PCR303735 Plaemodiu	c 503	17	3.5	508	12	B29563	B29563 T12C14TFB.T
c 431	17	3.5	439	10	BG801791	BG801791 0121-06.M	c 504	17	3.5	510	10	T60265	T60265 Yb87B11.r1
c 432	17	3.5	440	9	AA690407	AA690407 yu52C01.r	c 505	17	3.5	511	12	AA141745	AA141745 CK02431.5
c 433	17	3.5	440	12	AQ345266	AQ345266 RPCI-11-13	c 506	17	3.5	511	12	BH344697	BH344697 CH230-54A
c 434	17	3.5	441	12	AZ405427	AZ405427 1M0174C18	c 507	17	3.5	515	10	BF126565	BF126565 601650819
c 435	17	3.5	442	9	BE218404	BE218404 re65407.r	c 508	17	3.5	515	10	B1301395	B1301395 UI-R-D10-
c 436	17	3.5	442	9	BE218404	BE218404 hv38b12.x	c 509	17	3.5	516	9	AL119446	AL119446 DKF2P761K
c 437	17	3.5	444	10	H69259	H69259 Yr92H11.r1	c 510	17	3.5	516	12	BH050346	BH050346 RPCI-24-3
c 438	17	3.5	445	12	AQ493881	AQ493881 HS_5135.B	c 511	17	3.5	521	9	AV547821	AV547821 AV547821
c 439	17	3.5	446	9	AI433461	AI433461 t165G09.x	c 512	17	3.5	522	9	AW952991	AW952991 EST365061
c 440	17	3.5	446	9	AV655379	AV655379 AV655379	c 513	17	3.5	522	12	AQ211890	AQ211890 HS_3241.B
c 441	17	3.5	446	9	AW292330	AW292330 UI-H-B12-	c 514	17	3.5	524	12	AQ23123	AQ23123 RPCI-23-3
c 442	17	3.5	447	9	AV655347	AV655347 AV655347	c 515	17	3.5	525	10	AV547828	AV547828 AV547828
c 443	17	3.5	447	10	W00810	W00810 za38B11.r1	c 516	17	3.5	525	10	BI446655	BI446655 dac81C10.
c 444	17	3.5	448	9	BB678948	BB678948 BB678948	c 517	17	3.5	526	9	AV385438	AV385438 AV385438
c 445	17	3.5	451	12	AQ842456	AQ842456 CpG1109A	c 518	17	3.5	526	10	BG227108	BG227108 kp97B08.Y
c 446	17	3.5	451	12	AQ842532	AQ842532 CpG1109B	c 519	17	3.5	526	10	H58906	H58906 Yr36g12.r1
c 447	17	3.5	452	12	AQ174605	AQ174605 HS_3208.A	c 520	17	3.5	526	12	BH523687	BH523687 BOHUS94TR
c 448	17	3.5	453	10	NK3991	NK3991 Yr81908.s1	c 521	17	3.5	528	10	BI513181	BI513181 BB160011B
c 449	17	3.5	453	12	AJ099363	AJ099363 RPCI-11-47	c 522	17	3.5	529	9	AI668154	AI668154 605015E06
c 450	17	3.5	456	9	AJ402296	AJ402296 AJ402296	c 523	17	3.5	529	12	BH318883	BH318883 CH230-115
c 451	17	3.5	457	10	BE551848	BE551848 hx95B02.x	c 524	17	3.5	530	12	AQ489553	AQ489553 RPCI-11-2
c 452	17	3.5	458	10	BI446640	BI446640 dac81a10.	c 525	17	3.5	531	12	AQ341448	AQ341448 RPCI-11-1
c 453	17	3.5	458	10	AQ200495	AQ200495 RPCI-11-47	c 526	17	3.5	532	10	BI749251	BI749251 ro75g10.Y
c 454	17	3.5	459	12	AZ936250	AZ936250 Gm_UMB001	c 527	17	3.5	532	12	AZ289083	AZ289083 RPCI-23-1
c 455	17	3.5	460	10	BE579810	BE579810 kq32f10.Y	c 528	17	3.5	532	12	AQ580750	AQ580750 RPCI-11-4

c 529	17	3.5	533	10	BM030454	BM030454 494837 MA	602	17	3.5	598	9	AV653192	AV653192
530	17	3.5	533	12	AQ118780	AQ118780 HS_3013_A	603	17	3.5	600	9	AV658691	AV658691
531	17	3.5	534	10	BJ116686	BJ116686 BJI16686	604	17	3.5	600	10	BG384845	BG384845
532	17	3.5	535	9	BE030385	BE030385 128440 MA	605	17	3.5	601	10	BG617174	BG617174
c 533	17	3.5	535	12	AQ322008	AQ322008 RPCI11-10	606	17	3.5	601	12	BH368079	BH368079
534	17	3.5	536	10	BE756530	BE756530 210697 MA	c 607	17	3.5	602	10	BG565703	BG565703
535	17	3.5	537	12	AQ015111	AQ015111 HS_5067_A	608	17	3.5	602	10	BI503960	BI503960
536	17	3.5	538	10	BG714801	BG714801 602677119	609	17	3.5	602	12	AQ961739	AQ961739
537	17	3.5	538	12	AQ515161	AQ515161 HS_2208_B	c 610	17	3.5	602	12	AZ774456	AZ774456
c 538	17	3.5	540	9	A1453596	A1453596 tj57908.x	611	17	3.5	606	9	AV683471	AV683471
c 539	17	3.5	540	12	BH386119	BH386119 AG-ND-119	612	17	3.5	607	12	AQ506983	AQ506983
c 540	17	3.5	541	12	AZ259344	AZ259344 RPCI-23-4	613	17	3.5	608	10	BG572126	BG572126
c 541	17	3.5	541	12	AZ955734	AZ955734 2M0221019	614	17	3.5	609	10	BI546582	BI546582
542	17	3.5	542	9	AW289420	AW289420 2047 Lewi	615	17	3.5	610	9	AI996558	AI996558
543	17	3.5	543	9	AW895490	AW895490 QV4-NR003	616	17	3.5	610	10	BI503765	BI503765
c 544	17	3.5	544	10	BG2868071	BG2868071 1000163A1	617	17	3.5	611	10	BJ062787	BJ062787
545	17	3.5	546	9	AV662323	AV662323 AV662323	c 618	17	3.5	613	9	AL564112	AL564112
c 546	17	3.5	547	9	AV385533	AV385533 AV385533	c 619	17	3.5	617	12	AZ863096	AZ863096
c 547	17	3.5	547	12	AQ285024	AQ285024 RPCI11-72	c 620	17	3.5	618	10	BI362830	BI362830
c 548	17	3.5	548	12	AQ833454	AQ833454 HS_5296_B	c 621	17	3.5	618	10	BF520819	BF520819
c 549	17	3.5	548	12	AQ468281	AQ468281 HS_5215_B	c 622	17	3.5	619	12	AQ968300	AQ968300
c 550	17	3.5	550	9	AW039589	AW039589 ES282037	c 623	17	3.5	619	12	AZ750919	AZ750919
c 551	17	3.5	550	12	AQ385366	AQ385366 RPCI11-14	c 624	17	3.5	619	12	FR0003566	FR0003566
552	17	3.5	550	12	AQ527773	AQ527773 RPCI-11-3	c 625	17	3.5	621	9	AL657065	AL657065
553	17	3.5	553	12	AZ838152	AZ838152 2M0133B14	c 626	17	3.5	622	12	AZ655299	AZ655299
c 554	17	3.5	553	12	BH543679	BH543679 BQOD95TF	c 627	17	3.5	623	12	AQ418484	AQ418484
c 555	17	3.5	554	9	AW616844	AW616844 ES9323255	c 628	17	3.5	624	10	BG602344	BG602344
c 556	17	3.5	554	9	BM389876	BM389876 UI-R-CN1-	c 629	17	3.5	624	12	BH005698	BH005698
c 557	17	3.5	554	12	AZ044299	AZ044299 RPCI-23-3	c 630	17	3.5	626	12	AV650134	AV650134
c 558	17	3.5	555	9	AA814314	AA814314 nz07f07.s	631	17	3.5	626	12	CNS03GR9	CNS03GR9
559	17	3.5	555	9	AW624998	AW624998 ES9313827	632	17	3.5	627	9	AV646115	AV646115
560	17	3.5	555	12	AQ0800956	AQ0800956 HS_5249_B	633	17	3.5	628	9	AI174950	AI174950
c 561	17	3.5	556	9	AL531852	AL531852 AL531852	634	17	3.5	628	9	AV662100	AV662100
c 562	17	3.5	556	10	BG045876	BG045876 saa07e01.	635	17	3.5	628	12	AG096756	AG096756
c 563	17	3.5	556	10	BE749510	BE749510 200468 MA	c 636	17	3.5	629	12	BH048064	BH048064
564	17	3.5	559	10	BG384875	BG384875 304216 MA	637	17	3.5	629	12	AQ3326911	AQ3326911
565	17	3.5	561	10	BJ120946	BJ120946 BJI20946	638	17	3.5	630	9	AV655650	AV655650
566	17	3.5	562	9	A1064933	A1064933 HA0752 Hu	639	17	3.5	630	9	AV684560	AV684560
c 567	17	3.5	563	12	AZ0406937	AZ0406937 1M0176F19	c 640	17	3.5	631	9	BB661881	BB661881
c 568	17	3.5	564	9	AA142083	AA142083 CK00217.3	641	17	3.5	634	10	BJ123120	BJ123120
569	17	3.5	564	12	AQ440192	AQ440192 HS_5078_A	642	17	3.5	634	10	BM164871	BM164871
c 570	17	3.5	566	9	AA411801	AA411801 zt67e06.s	c 643	17	3.5	634	12	AQ961738	AQ961738
571	17	3.5	566	12	AQ991586	AQ991586 RFC02580	644	17	3.5	635	12	AZ567047	AZ567047
572	17	3.5	566	12	AZ714866	AZ714866 RPCI-24-1	645	17	3.5	635	12	BH459531	BH459531
c 573	17	3.5	567	12	AZ092417	AZ092417 RPCI-23-4	646	17	3.5	636	9	AI114682	AI114682
574	17	3.5	567	12	TA203E10P	TA203E10P T. Bruce1	c 647	17	3.5	637	9	AW179507	AW179507
575	17	3.5	570	9	A1068486	A1068486 HA0842 Hu	648	17	3.5	637	12	AQ968299	AQ968299
576	17	3.5	570	10	BG566912	BG566912 602589411	649	17	3.5	638	10	BG617624	BG617624
577	17	3.5	571	9	AV661175	AV661175 AV661175	650	17	3.5	638	10	BG719271	BG719271
c 578	17	3.5	571	12	AQ737677	AQ737677 HS_2194_A	651	17	3.5	638	12	AZ788082	AZ788082
579	17	3.5	571	12	AQ926378	AQ926378 RPCI-23-3	652	17	3.5	640	9	AV654313	AV654313
580	17	3.5	571	12	AZ440475	AZ440475 1M02331L01	653	17	3.5	641	9	AV652492	AV652492
c 581	17	3.5	573	10	BI213355	BI213355 1031055E0	c 654	17	3.5	642	12	AZ778927	AZ778927
c 582	17	3.5	574	9	A1552611	A1552611 vx29g11.x	655	17	3.5	643	9	BB534254	BB534254
c 583	17	3.5	575	10	W89213	W89213 zh69h03.s1	656	17	3.5	643	10	BG432269	BG432269
c 584	17	3.5	577	9	AW465894	AW465894 Bp230020B	657	17	3.5	644	9	AV650917	AV650917
585	17	3.5	578	10	BI344380	BI344380 372844 MA	658	17	3.5	644	9	BG262420	BG262420
586	17	3.5	579	10	BI491201	BI491201 df05c12.w	659	17	3.5	644	10	BG402120	BG402120
587	17	3.5	579	10	BI477062	BI477062 rm35q08.y	660	17	3.5	644	10	BJ148385	BJ148385
c 588	17	3.5	579	12	AQ468501	AQ468501 HS_5216_B	661	17	3.5	646	9	AV650847	AV650847
c 589	17	3.5	580	9	AW215944	AW215944 687046G02	662	17	3.5	646	12	BH037567	BH037567
c 590	17	3.5	581	9	AA443428	AA443428 2w94a06.r	663	17	3.5	647	9	AV661847	AV661847
c 591	17	3.5	583	10	BG982047	BG982047 MR3-CN014	664	17	3.5	647	12	BH616378	BH616378
c 592	17	3.5	588	12	AZ742279	AZ742279 RPCI-24-6	665	17	3.5	648	10	BG562568	BG562568
593	17	3.5	589	9	AI692054	AI692054 606011A08	666	17	3.5	648	10	BG875327	BG875327
594	17	3.5	589	9	AV697847	AV697847 AV697847	c 667	17	3.5	650	12	AG041671	AG041671
595	17	3.5	590	10	W95079	W95079 zh46e11.r1	c 668	17	3.5	651	10	BG854199	BG854199
596	17	3.5	592	10	BM164803	BM164803 ES7567326	669	17	3.5	652	9	AL630646	AL630646
c 597	17	3.5	593	12	AZ717676	AZ717676 RPCI-24-1	c 670	17	3.5	652	12	AQ281546	AQ281546
c 598	17	3.5	595	9	AI958662	AI958662 fc94g08.y	c 671	17	3.5	653	10	BJ013222	BJ013222
599	17	3.5	596	12	BH565759	BH565759 BQGB58TR	672	17	3.5	655	9	AI065122	AI065122
c 600	17	3.5	597	9	AW749617	AW749617 RC3-BT050	673	17	3.5	655	9	AV649667	AV649667
c 601	17	3.5	597	12	AQ047492	AQ047492 CLM-1d5-t	c 674	17	3.5	655	10	BJ144340	BJ144340

675	17	3.5	656	9	AV684570	AV684570 AV684570	c 748	17	3.5	748	10	BG786758	BG786758 SEAUWC006
c 676	17	3.5	656	10	BI528620	BI528620 1024092B1	749	17	3.5	750	10	BG566692	BG566692 602585751
c 677	17	3.5	656	12	AG158612	AG158612 Pan trogl	750	17	3.5	751	10	BG430480	BG430480 602502050
678	17	3.5	657	9	BB227300	BB227300 BB227300	751	17	3.5	752	10	BG567647	BG567647 602586418
679	17	3.5	658	12	BH041889	BH041889 RPCI-24-2	c 752	17	3.5	752	12	CNS009GX	AL053359 Drosoph11
680	17	3.5	662	12	AG131319	AG131319 Pan trogl	753	17	3.5	755	10	BG567658	BG567658 602586430
c 681	17	3.5	663	10	AU244327	AU244327 AU244327	754	17	3.5	759	9	AL532113	AL532113 AL532113
682	17	3.5	663	10	BI513372	BI513372 BI160012B	755	17	3.5	761	12	AQ935048	AQ935048 CPG2305A
683	17	3.5	664	9	AA696412	AA696412 GM07634.5	756	17	3.5	764	10	BG569186	BG569186 602588455
c 684	17	3.5	664	10	BM440524	BM440524 pgr1n.pk0	c 757	17	3.5	766	12	AQ573502	AQ573502 nbxb0081H
c 685	17	3.5	665	9	AW950626	AW950626 EST362696	758	17	3.5	768	12	BH586940	BH586940 BCGK890TR
c 686	17	3.5	667	12	AZ554187	AZ554187 RPCI-23-2	759	17	3.5	769	12	AZ692670	AZ692670 ENTW21TF
687	17	3.5	668	12	CNS04KBE	AL294611 Tetraodon	760	17	3.5	773	10	BG401810	BG401810 602466502
688	17	3.5	669	12	AQ840180	AQ840180 nbxb0052I	761	17	3.5	775	10	BE780760	BE780760 601489638
c 689	17	3.5	670	12	AG070350	AG070350 Pan trogl	c 762	17	3.5	778	12	AQ050390	AQ050390 nbxb0003D
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693	17	3.5	675	12	AQ279923	AQ279923 C1TBI-E1-	c 766	17	3.5	783	12	BH560773	BH560773 HOGD012TR
694	17	3.5	675	12	AG101462	AG101462 Pan trogl	767	17	3.5	782	12	BH564279	BH564279 602586081
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696	17	3.5	680	10	BG568168	BG568168 602587060	c 769	17	3.5	788	9	AL639423	AL639423 AL639423
c 697	17	3.5	680	12	AZ940067	AZ940067 2M0199L16	c 770	17	3.5	788	9	AU125721	AU125721 AU125721
c 698	17	3.5	681	9	AG144985	AG144985 Pan trogl	c 771	17	3.5	788	12	BH102503	BH102503 RPCI-24-3
c 699	17	3.5	681	9	BB278082	BB278082 BB278082	c 772	17	3.5	790	3	BI644836	BI644836 OP2603 M1
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c 701	17	3.5	682	12	AZ088581	AZ088581 RPCI-23-4	c 774	17	3.5	794	2	BI645356	BI645356 OP2608 M1
c 702	17	3.5	683	9	AL652871	AL652871 AL652871	c 775	17	3.5	794	12	AQ287647	AQ287647 nbxb0031A
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c 704	17	3.5	686	12	AZ429071	AZ429071 IM0212015	c 777	17	3.5	797	12	AZ973175	AZ973175 2M0247K16
705	17	3.5	687	10	AV651014	AV651014 AV651014	778	17	3.5	797	12	AG031716	AG031716 Pan trogl
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707	17	3.5	688	9	AV681533	AV681533 AV681533	c 780	17	3.5	798	10	BG531760	BG531760 602560324
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c 710	17	3.5	689	12	AQ990859	AQ990859 Rfc01695	783	17	3.5	799	10	BG433875	BG433875 602497613
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c 718	17	3.5	700	12	BH367437	BH367437 AG-ND-123	791	17	3.5	810	12	BG783372	BG783372 SPAUMC003
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731	17	3.5	716	9	AL046422	AL046422 DKEZp434N	804	17	3.5	839	12	AQ250308	AQ250308 T17L21-T7
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737	17	3.5	729	10	BG917245	BG917245 602816521	c 810	17	3.5	845	9	AL531722	AL531722 AL531722
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745	17	3.5	745	9	AV653786	AV653786 AV653786	818	17	3.5	857	10	BG569260	BG569260 602588549
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824	17	3.5	867	12	AZ531216	AZ531216	ENTBX40TR	897	17	3.5	965	9	AL531544	AL531544
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828	17	3.5	871	9	AL531522	AL531522	AL531522	901	17	3.5	969	9	AL558072	AL558072
829	17	3.5	872	9	AL531522	AL531522	AL531522	c 902	17	3.5	969	10	BF980381	BF980381
830	17	3.5	873	10	B1462209	B1462209	603205524	903	17	3.5	970	9	AL557823	AL557823
831	17	3.5	874	9	AL532104	AL532104	AL532104	c 904	17	3.5	971	12	CNS00KY2	AL078379
832	17	3.5	875	12	AZ532411	AZ532411	ENTDC01TF	905	17	3.5	972	9	AL531363	AL531363
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835	17	3.5	878	9	AL564232	AL564232	AL564232	c 908	17	3.5	972	9	AL532094	AL532094
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837	17	3.5	880	12	AZ533797	AZ533797	ENTDY22TR	c 910	17	3.5	974	10	BG674384	BG674384
838	17	3.5	881	12	AZ533797	AZ533797	ENTDY22TR	c 911	17	3.5	974	10	BG674384	BG674384
839	17	3.5	882	12	AZ682963	AZ682963	ENTLQ11TR	c 912	17	3.5	976	9	AL557863	AL557863
840	17	3.5	883	12	AZ682963	AZ682963	ENTLQ11TR	c 913	17	3.5	977	12	CNS04D22	AL286391
841	17	3.5	884	10	B1771436	B1771436	603059477	914	17	3.5	977	12	CNS04D22	AL286391
842	17	3.5	885	12	AZ538128	AZ538128	ENTGE92TF	915	17	3.5	978	12	CNS03LAG	AL249217
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844	17	3.5	887	10	BG674149	BG674149	602619966	917	17	3.5	984	9	AL557815	AL557815
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847	17	3.5	890	9	AL531650	AL531650	AL531650	c 920	17	3.5	988	10	BM470264	BM470264
848	17	3.5	891	9	AL531650	AL531650	AL531650	921	17	3.5	988	10	BM470264	BM470264
849	17	3.5	892	9	AL564432	AL564432	AL564432	c 922	17	3.5	989	12	CNS014R4	AL104506
850	17	3.5	893	9	AL564432	AL564432	AL564432	923	17	3.5	991	9	AL579784	AL579784
851	17	3.5	894	10	BM360144	BM360144	GA_Ea002	c 924	17	3.5	992	9	AL531306	AL531306
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854	17	3.5	897	9	AL564100	AL564100	AL564100	c 927	17	3.5	1002	9	AL557890	AL557890
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858	17	3.5	901	9	AL564100	AL564100	AL564100	c 931	17	3.5	1008	12	CNS04R3W	AL303413
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863	17	3.5	906	9	AL531962	AL531962	AL531962	936	17	3.5	1014	9	AL564531	AL564531
864	17	3.5	907	9	AL531962	AL531962	AL531962	c 937	17	3.5	1014	9	AL564531	AL564531
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870	17	3.5	913	9	AL579861	AL579861	AL579861	c 943	17	3.5	1022	9	AL044551	AL044551
871	17	3.5	914	9	AL579861	AL579861	AL579861	944	17	3.5	1036	9	AL557942	AL557942
872	17	3.5	915	12	AZ673956	AZ673956	ENTK036TR	c 945	17	3.5	1036	9	AL557942	AL557942
873	17	3.5	916	12	AZ673956	AZ673956	ENTK036TR	946	17	3.5	1036	9	AL557942	AL557942
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877	17	3.5	920	9	AL531231	AL531231	AL531231	950	17	3.5	1071	9	AV698579	AV698579
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883	17	3.5	926	9	AL531231	AL531231	AL531231	956	17	3.5	1071	9	AV698579	AV698579
884	17	3.5	927	9	AL531231	AL531231	AL531231	c 957	17	3.5	1071	9	AV698579	AV698579
885	17	3.5	928	9	AL531231	AL531231	AL531231	958	17	3.5	1071	9	AV698579	AV698579
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888	17	3.5	931	9	AL531231	AL531231	AL531231	c 961	17	3.5	1071	9	AV698579	AV698579
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891	17	3.5	934	9	AL531231	AL531231	AL531231	964	17	3.5	1071	9	AV698579	AV698579
892	17	3.5	935	9	AL531231	AL531231	AL531231	c 965	17	3.5	1071	9	AV698579	AV698579
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c 979 16 3.3 183 9 BF397498
c 980 16 3.3 186 10 BF397498
c 981 16 3.3 191 10 BF397498
c 982 16 3.3 191 10 BF397498
c 983 16 3.3 192 9 BV236985
c 984 16 3.3 192 10 D84330
c 985 16 3.3 194 9 AV092423
c 986 16 3.3 200 9 AV017205
c 987 16 3.3 200 9 AV017205
c 988 16 3.3 200 9 AV017205
c 989 16 3.3 200 9 AV017205
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c 991 16 3.3 202 9 BE177310
c 992 16 3.3 203 9 AI583377
c 993 16 3.3 203 9 BB015268
c 994 16 3.3 203 9 BE085089
c 995 16 3.3 204 9 AV237473
c 996 16 3.3 204 12 AV287474
c 997 16 3.3 205 9 AV287474
c 998 16 3.3 205 12 AV287474
c 999 16 3.3 206 10 BH599905
c1000 16 3.3 206 10 BF091821
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## ALIGNMENTS

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RESULT 1
AA463370 509 bp mRNA linear EST 10-JUN-1997
LOCUS zx97d12.r1 Soares_NhHMPu.S1 Homo sapiens cDNA clone IMAGE:811703 5
DEFINITION similar to SW:IL15_HUMAN P40933 INTERLEUKIN-15 PRECURSOR ; mRNA
sequence.
ACCESSION AA463370.1 GI:2188254
VERSION AA463370.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie,
T., Waterston, R., and Wilson, R.
WashU-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 416.
Location/Qualifiers
source
1..509
/organism="Homo sapiens"
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/db_xref="GDB:6042614"
/db_xref="taxon:9606"
/clone="IMAGE:811703"
/clone_lib="Soares_NhHMPu.S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/Note="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NBH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
BASE COUNT 149 a 91 c 108 g 161 t
ORIGIN
Query Match 21.9%; Score 107; DB 9; Length 509;
Best Local Similarity 99.4%; Pred. No. 6.4e-44;
Matches 157; Conservative 1; Indels 0; Gaps 0;
QY 67 AGTCATTTCTAACTGAAGCTGGCATTCATGCTTCATTTGGGCTGTTTCAGTCAGGG 126
|||||
Db 171 AGTCATTTCTAACTGAAGCTGGCATTCATGCTTCATTTGGGCTGTTTCAGTCAGGG 230
QY 127 CTCCTTAAACAGACCACTGGGTGAATGTAATGAAGTATTTGAAATTTCAAGAT 186
|||||
Db 231 CTCCTTAAACAGACCACTGGGTGAATGTAATGAAGTATTTGAAATTTCAAGAT 290
QY 187 CTTATTCATTCATCATATTGATGCTACTTTATATAC 224
|||||
Db 291 CTTATTCATTCATCATATTGATGCTACTTTATATAC 328
RESULT 2
BG184658 800 bp mRNA linear EST 21-APR-2001
LOCUS RST3720 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
DEFINITION BG184658
ACCESSION BG184658.1 GI:13706473
VERSION BG184658.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.,
Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith,
E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher,
J., Danzig, J., and Ducar, M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
JOURNAL MEDLINE
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scai@atersys.com
High quality sequence stop: 444.
Location/Qualifiers
source
1..800
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
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/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is H1080, since a random activation method was used, these sequence tags are not necessarily expressed in H1080 under normal circumstances."

BASE COUNT 235 a 151 c 165 g 247 t 2 others  
ORIGIN

Query Match 21.9%; Score 107; DB 10; Length 800;  
Best Local Similarity 99.4%; Pred. No. 6.2e-44;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCAATTTGGCGCTTTTCAGTGCAGGG 126

Db 331 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCAATTTGGCGCTTTTCAGTGCAGGG 390

QY 127 CTCCTAAAACAGAGCCAACTGGTGAATGTAATAGTGAATTTGAAAAAATTTGAAGAT 186

Db 391 CTTCTTAAACAGAGCCAACTGGTGAATGTAATAGTGAATTTGAAAAAATTTGAAGAT 450

QY 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224

Db 451 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 488

RESULT 3  
AL548180  
LOCUS  
DEFINITION AL548180 LTI\_NFL006\_PL2 Homo sapiens cDNA clone CS0DI034Y009 5 prime, mRNA sequence.  
ACCESSION AL548180  
VERSION AL548180.1 GI:12882943  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 982)  
Li, W.B., Gruber, C., Jesse, J., and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
CONTACT: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES  
1. .982  
Location/Qualifiers  
source  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="CS0DI034Y009"  
/clone\_lib="LTI\_NFL006\_PL2"  
/tissue\_type="placenta"  
/notes="Vector: pCMVSPORT 6; Site\_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 275 a 208 c 214 g 284 t 1 others  
ORIGIN

Query Match 21.9%; Score 107; DB 9; Length 982;  
Best Local Similarity 99.4%; Pred. No. 6.1e-44;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCAATTTGGCGCTTTTCAGTGCAGGG 126

Db 424 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCAATTTGGCGCTTTTCAGTGCAGGG 483

QY 127 CTCCTAAAACAGAGCCAACTGGTGAATGTAATAGTGAATTTGAAAAAATTTGAAGAT 186

Db 484 CTTCTTAAACAGAGCCAACTGGTGAATGTAATAGTGAATTTGAAAAAATTTGAAGAT 543

QY 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224

Db 544 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 581

RESULT 4  
AW804165/c  
LOCUS  
DEFINITION AW804165 483 bp mRNA linear EST 16-MAY-2000 PM4-UM0088-050400-001-cll UM0088 Homo sapiens cDNA, mRNA sequence.  
ACCESSION AW804165  
VERSION AW804165.1 GI:7856035  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 483)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F., Goldmann, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
CONTACT: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-pm4-UM0088-050400-001-cll&t3=2000-04-05&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 483.  
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1. .483  
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/clone\_lib="UM0088"  
/dev\_stage="Adult"  
/notes="Organ: uterus; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 /716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 175 a 87 c 67 g 154 t  
ORIGIN

Query Match 14.7%; Score 72; DB 9; Length 483;  
Best Local Similarity 100.0%; Pred. No. 5.7e-26;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 418 GAGGAAAAAATATAAAGAAATTTTGCAGAGTTTGTGACATATTGTCCAATGTTTCATC 477

Db 483 GAGGAAAAAATATAAAGAAATTTTGCAGAGTTTGTGACATATTGTCCAATGTTTCATC 424

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QY 478 AACACTTCTTGA 489
|||||
Db 423 AACACTTCTTGA 412

RESULT 5
AW804168/c
LOCUS
DEFINITION PM4-UM0088-050400-001-d12 UM0088 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW804168
VERSION AW804168.1 GI:7856038
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 494)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PM4-UM0088-050400-001-d12&t3=2000-04-05&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 494.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="UM0088"
/dev_stage="Adult"
/notes="Organ: uterus; Vector: puc18; Site.1: SmaI; Site.2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 ,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 174 a 91 c 69 g 160 t
ORIGIN

Query Match 14.7%; Score 72; DB 9; Length 494;
Best Local Similarity 100.0%; Pred. No. 5.7e-26;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 418 GAGGAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTGTCCAAATGTTTCATC 477
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Db 484 GAGGAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTGTCCAAATGTTTCATC 425
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QY 478 AACACTTCTTGA 489
|||||
Db 424 AACACTTCTTGA 413
|||||

RESULT 6
AI860008/c
LOCUS
DEFINITION AI860008-1 GI:5513624
ACCESSION AI860008
VERSION AI860008.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 637)
AUTHORS Contact: Robert Strausberg, Ph.D.
Email: cgapsb@email.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert length: 3944 Std Error: 0.00
Seq primer: -400P from GIBCO
High quality sequence stop: 410.
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source
1..637
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/clone_lib="NCI-CGAP_Ut4"
/tissue_type="serous papillary carcinoma, high grade, 2 pooled tumors"
/lab_host="DH10B"
/notes="Organ: uterus; Vector: pCMV-SPORT6; Site.1: SmaI; Site.2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.48 kb. Life technologies catalog #: 11542-016"
BASE COUNT 207 a 111 c 91 g 227 t 1 others
ORIGIN

Query Match 14.7%; Score 72; DB 9; Length 637;
Best Local Similarity 100.0%; Pred. No. 5.6e-26;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 418 GAGGAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTGTCCAAATGTTTCATC 477
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Db 409 GAGGAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTGTCCAAATGTTTCATC 350
|||||

QY 478 AACACTTCTTGA 489
|||||
Db 349 AACACTTCTTGA 338
|||||

RESULT 7
AL572832/c
LOCUS
DEFINITION AL572832 LTI_NFL006.PL2 Homo sapiens cDNA clone CSODI034Y009 3 prime, mRNA sequence.
ACCESSION AL572832
VERSION AL572832.1 GI:12931481
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 994)
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.

```

TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES  
source

1. 994  
/organism="Homo sapiens"  
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/note="Vector: pCMVSPORT 6; Site\_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com"

BASE COUNT 333 a 186 c 154 g 316 t 5 others  
ORIGIN

Query Match 14.7%; Score 72; DB 9; Length 994;  
Best Local Similarity 100.0%; Pred. No. 5.4e-26;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 418 GAGGAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATGTCACAAATGTTTCATC 477  
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Db 631 GAGGAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATGTCACAAATGTTTCATC 572

QY 478 AACACTTCTTGA 489  
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Db 571 AACACTTCTTGA 560

RESULT 8  
BF088290/c

LOCUS CM1-HT0875-060900-385-g04 HT0875 Homo sapiens cDNA, linear EST 19-OCT-2000  
DEFINITION BF088290  
ACCESSION BF088290  
VERSION BF088290.1 GI:10894000  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 301)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsumura, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
Contact: Simpson A.J.G.

Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tti=62t1=62t2=CM1-HT0875-060

900-385-g04t3=2000-09-06&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 52  
High quality sequence stop: 301.

FEATURES  
source

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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
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/dev\_stage="Adult"  
/note="Organ: head\_neck; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORBESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 96 a 56 c 48 g 101 t

ORIGIN

Query Match 12.9%; Score 63; DB 10; Length 301;  
Best Local Similarity 100.0%; Pred. No. 2.4e-21;  
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 427 AATATTAAAGAAATTTTGCAGAGTTTGTACATATGTCACAAATGTTTCATCAACTTCT 486  
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Db 286 AATATTAAAGAAATTTTGCAGAGTTTGTACATATGTCACAAATGTTTCATCAACTTCT 227

QY 487 TGA 489  
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Db 226 TGA 224

RESULT 9

BI758686

LOCUS 603024240F1 NIH\_MGC\_114 Homo sapiens cDNA clone IMAGE:5194977 5',  
DEFINITION mRNA sequence.

ACCESSION BI758686

VERSION BI758686.1 GI:15750264

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 872)

REFERENCE NIH-MGC http://mgc.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov

Place: LLAM1487 row: 0 column: 10  
High quality sequence start: 24  
High quality sequence stop: 859.

FEATURES  
Location/Qualifiers

1. 872  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5194977"  
/clone\_lib="NIH\_MGC\_114"  
/lab\_host="DH10B"

/note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed

upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH\_MGC Library."

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BASE COUNT      200 a      222 c      227 g      223 t
ORIGIN
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RESULT 10  
N49734/c  
LOCUS  
DEFINITION  
N49734 474 bp mRNA linear EST 14-FEB-1996  
clone IMAGE:282239 3' similar to SW:1115\_HUMAN P40933  
INTERLEUKIN-15 PRECURSOR ; mRNA sequence.  
N49734  
VERSION N49734.1 GI:1190900  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 474)  
Hillier.L., Clark.N., Dubuque.T., Elliston.K., Hawkins.M., Holman.

**TITLE**  
The WashU-Merck EST Project  
**JOURNAL**  
Unpublished (1995)  
**COMMENT**  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

```

FEATURES
source
high quality sequence stop: 263.
Location/Qualifiers
1. .474
/organism="Homo sapiens"
/db_xref="GDB:3900767"
/db_xref="taxon:9606"
/clone="IMAGE:282239"
/clone_lib="Soares_multiple_sclerosis_2NBHMS"
/sex="male"
/tissue_type="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT73D (Pharmacia) with a modified
polylinker V-YPE: phagemid; Site.1: Not I; Site.2: Eco RI
; 1st strand cDNA was primed with a Not I - oligo(4T)
primer [5',
TGTTACCAATCTGAAGTGGGAGCGCCGCAATTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento

```

BASE COUNT	160 a	81 c	67 g	161 t	5 others
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Query Match	11.2%	Score 55	DB 10	Length 474
Best Local Similarity	100.0%	Pred. No. 3e-17		
Matches	55	Conservative 0	Mismatches 0	Indels 0
			Gaps 0	
QY 435	AGAAATTTTCGAGAGTTTGTACATATTTGTCCTCAAAATGTTTCATCAACACTTCCTTGA	489		
Db 367	AGAAATTTTCGAGAGTTTGTACATATTTGTCCTCAAAATGTTTCATCAACACTTCCTTGA	313		
RESULT	11			
LOCUS	N76741			
DEFINITION	yz82g12.rl Soares_multiple_sclerosis_2NBHMSF Homo sapiens cDNA	471 bp	mRNA	linear EST 02-APR-1996
	clone IMAGE:289606 5', similar to SW:IL15_HUMAN P40933			
	INTERLEUKIN-15 PRECURSOR ; mRNA sequence.			

N76741.1 GI:1239319  
EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 471)  
REFERENCE  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman  
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,  
Rifkin, B., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston  
R., Williamson, A., Wohldmann, P. and Wilson, R.  
THE WASHU-MERCK EST Project  
TITLE

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Seq primer: reverse ET  
High quality sequence stop: 296.

```

FEATURES
source
high quality sequence stop: 29%.
location/Qualifiers
1. .471
/organism="Homo sapiens"
/db_xref="GDB:3905446"
/db_xref="taxon:9606"
/clone="IMAGE:289606"
/clone_lib="Soares_multiple_sclerosis_2NbHMS"
/sex="male"
/tissue_type="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
/notice="Vector: pT73B (Pharmacia) with a modified
polylinker V-type; phagemid; Site_1: Not I; Site_2: Eco RI
; l1st strand cDNA was primed with a Not I - o1lgo(dT)
primer [5,

```

161 a BASE COUNT  
ORIGIN  
68 c 83 g 154 t 5 others  
TGTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTTTTTT 3',  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT73 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Soares and M. Fatima Bonaldo. RNA from 4 multiple sclerosis  
lesions from one patient was kindly provided by Dr. Kevin  
G. Becker (NINDS/NIH). "

SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 278)  
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-RC3-HT0600-170300-011-e04&t3=2000-03-17&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 9  
High quality sequence stop: 278.  
High quality Location/Qualifiers  
FEATURES  
source  
1..278  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="HT0600"  
/dev\_stage="Adult"  
/note="Organ: head\_neck; Vector: puc18; Site:1: SmaI;  
Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
BASE COUNT 75 a 50 c 54 g 98 t 1 others  
ORIGIN  
Query Match 9.8%; Score 48; DB 9; Length 278;  
Best Local Similarity 100.0%; Pred. No. 1.2e-13;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGAGAAATTCGAAACACATTGAGAGTATTTCATCCAGTGCCTAC 48  
|||||  
Db 216 ATGAGAAATTCGAAACACATTGAGAGTATTTCATCCAGTGCCTAC 263  
RESULT 14  
BI766231  
LOCUS 603052877F1 NIH\_MGC\_122 Homo sapiens cDNA clone IMAGE:5202523 5',  
DEFINITION mRNA sequence.  
ACCESSION BI766231  
VERSION BI766231.1 GI:15757809  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 718)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.

Query Match 11.0%; Score 54; DB 10; Length 471;  
Best Local Similarity 100.0%; Pred. No. 9.7e-17;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 418 GAGGAAAAATATTAAGATTTTTCAGAGCTTTGTACATATTTGTCCTCAATG 471  
|||||  
Db 121 GAGGAAAAATATTAAGATTTTTCAGAGCTTTGTACATATTTGTCCTCAATG 174  
RESULT 12  
BI832895  
LOCUS 603082478F1 NIH\_MGC\_120 Homo sapiens cDNA clone IMAGE:5221771 5',  
DEFINITION mRNA sequence.  
ACCESSION BI832895  
VERSION BI832895.1 GI:15944445  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 756)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs@remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM1557 row: k column: 20  
High quality sequence stop: 756.  
High quality Location/Qualifiers  
FEATURES  
source  
1..756  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5221771"  
/clone\_lib="NIH\_MGC\_120"  
/lab\_host="DH10B"  
/note="Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH\_MGC Library."  
BASE COUNT 247 a 115 c 143 g 251 t  
ORIGIN  
Query Match 10.4%; Score 51; DB 10; Length 756;  
Best Local Similarity 100.0%; Pred. No. 3.2e-15;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 174 AAAAATTGAAGATCTTATTCATCTATGCATATTTGCTCTTATATAC 224  
|||||  
Db 1 AAAAATTGAAGATCTTATTCATCTATGCATATTTGCTCTTATATAC 51  
RESULT 13  
BE177883  
LOCUS BE177883 278 bp mRNA linear EST 22-JUN-2000  
DEFINITION RC3-HT0600-170300-011-e04 HT0600 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BE177883  
VERSION BE177883.1 GI:8657035  
KEYWORDS EST.

Email: cgabs-r@mail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Plate: L14M1507 row: 1 column: 20  
 High quality sequence stop: 717.

FEATURES  
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 1. 718  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
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 /clone\_lib="NIH\_MGC\_122"  
 /lab\_host="DH10B"  
 /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH\_MGC Library."  
 BASE COUNT 144 a 184 c 188 g 201 t 1 others  
 ORIGIN

Query Match 9.8%; Score 48; DB 10; Length 718;  
 Best Local Similarity 100.0%; Pred. No. 1.le-13;  
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATGAGAATTTCGAACACACATTGAGAGATTTCATCCAGTGCTAC 48  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 620 ATGAGAATTTCGAACACACATTGAGAGATTTCATCCAGTGCTAC 667

RESULT 15  
 BF095213  
 LOCUS 309 bp mRNA linear EST 19-OCT-2000  
 DEFINITION IL2-UT0071-050900-144-B03 UT0071 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BF095213  
 VERSION BF095213.1 GI:10900923  
 KEYWORDS EST.  
 SOURCE human.

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 309)  
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 MEDLINE 20202663  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-il2-UT0071-050>)

900-144-B03&t3-2000-09-05&t4-1)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 309.  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="UT0071"  
 /dev\_stage="Adult"  
 /note="Organ: uterus\_tumor; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
 BASE COUNT 110 a 48 c 55 g 96 t  
 ORIGIN

Query Match 9.4%; Score 46; DB 10; Length 309;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-12;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 418 GAGGAAAAAATATTAAGAATTTTTCGAGAGTTTGTACATATG 463  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 110 GAGGAAAAAATATTAAGAATTTTTCGAGAGTTTGTACATATG 155

RESULT 16  
 BI756810  
 LOCUS 817 bp mRNA linear EST 25-SEP-2001  
 DEFINITION 603024487F1 NIH\_MGC\_114 Homo sapiens cDNA clone IMAGE:5194964 5', mRNA sequence.  
 ACCESSION BI756810  
 VERSION BI756810.1 GI:15748388  
 KEYWORDS EST.  
 SOURCE human.

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 817)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Plate: L14M11487 row: n column: 21  
 High quality sequence start: 5  
 High quality sequence stop: 711.  
 Location/Qualifiers  
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 /clone\_lib="NIH\_MGC\_114"  
 /lab\_host="DH10B"  
 /note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH\_MGC Library."

FEATURES  
 source

Db 63 GAGGAAAAAATATTAAAGAAATTTTTCAGAGTTT 97

RESULT 18  
BF088272/c  
LOCUS  
DEFINITION CMI-HT0875-060900-385-a05 HT0875 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF088272  
VERSION BF088272.1 GI:10893982  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 275)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-cm1-HT0875-060  
900-385-a05&t3=2000-09-06&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 4  
High quality sequence stop: 275.  
Location/Qualifiers  
1. .275  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="HT0875"  
/dev\_stage="Adult"  
/note="Organ: head neck; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."  
BASE COUNT 90 a 48 c 45 g 92 t  
ORIGIN  
Query Match 6.5%; Score 32; DB 10; Length 275;  
Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 427 AATATTAAGAATTTTTCAGAGTTTGTACA 458  
|||||  
Db 260 AATATTAAGAATTTTTCAGAGTTTGTACA 229  
|||||

RESULT 19  
BF379349  
LOCUS  
DEFINITION RC2-UT0023-110800-015-g08\_1 UT0023 Homo sapiens cDNA, mRNA  
sequence.  
ACCESSION BF379349  
VERSION BF379349.1 GI:11368474

BASE COUNT 186 a 215 c 209 g 206 t 1 others

Query Match 7.6%; Score 37; DB 10; Length 817;  
Best Local Similarity 100.0%; Pred. No. 4.8e-08;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 GAAGCTGGCATTTCATCTCTTCATTTGGGCTGTTTCA 118  
|||||  
Db 651 GAAGCTGGCATTTCATCTCTTCATTTGGGCTGTTTCA 687  
|||||

RESULT 17  
BE698667  
LOCUS  
DEFINITION RC2-UT0023-290700-011-b01 UT0023 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BE698667  
VERSION BE698667.1 GI:10085736  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 550)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-rc2-UT0023-290  
700-011-b01&t3=2000-07-29&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 7  
High quality sequence stop: 548.  
Location/Qualifiers  
1. .550  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="UT0023"  
/dev\_stage="Adult"  
/note="Organ: uterus tumor; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."  
BASE COUNT 184 a 75 c 104 g 186 t 1 others  
ORIGIN  
Query Match 7.2%; Score 35; DB 10; Length 550;  
Best Local Similarity 100.0%; Pred. No. 5.3e-07;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 418 GAGGAAAAAATATTAAAGAAATTTTTCAGAGTTT 452  
|||||

EST. human. Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 166)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil.  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethum12.pl?tl=RC2&t2=RC2-UT0023-110800-015-908\_1&t3=2000-08-11&t4=1)  
Seq primer: puc 18 forward.  
Location/Qualifiers  
1. 166  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="UT0023"  
/dev\_stage="Adult"  
/note="Organ: uterus\_tumor; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
60 a 26 c 33 g 47 t  
Query Match 6.1%; Score 30; DB 10; Length 166;  
Best Local Similarity 100.0%; Pred No. 0.00021;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 383 TAACAGAAATCTGGATGCAAGAATGTGAGG 412  
|||||  
Db 70 TAACAGAAATCTGGATGCAAGAATGTGAGG 99  
RESULT 20  
AA863763  
LOCUS  
DEFINITION  
IMAGE:1263953 5' similar to gb:U14332 Mus musculus interleukin 15 (MOUSE);, mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 564)  
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and



**KEYWORDS**  
**SOURCE** Norway rat.  
**ORGANISM** Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

**REFERENCE**  
**AUTHORS** 1 (bases 1 to 430)  
**TITLE** Bonaldo,M.F., Lennon,G. and Soares,M.B.  
**JOURNAL** Normalization and subtraction: two approaches to facilitate gene  
**MEDLINE** discovery  
**COMMENT** Genome Res. 6 (9), 791-806 (1996)  
 9704477  
 On Mar 10, 1998 this sequence version replaced gi:2948289.  
 Program for Rat Gene Discovery and Mapping  
 University of Iowa  
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: msoares@blue.weeg.uiowa.edu  
 The sequence tag present in the cDNA between the NotI site and the  
 oligo-dt track served to identify it as a clone from the normalized  
 adult lung library. cDNA Library Preparation: M. Fatima Bonaldo,  
 Ph.D. Clone distribution: clones will be available through Research  
 Genetics This clone is also available through the I.M.A.G.E.  
 Consortium at LLNL (info@image.llnl.gov). IMAGE ID=1767474 The  
 following repetitive elements were found in this cDNA sequence:  
 1-24, >At\_rich#Low\_complexity  
 Seq primer: M13 Forward  
 POLYA=A.

**FEATURES**  
 source  
 1..430  
 /location/Qualifiers  
 /organism="Rattus norvegicus"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /clone="UI-R-A0-aj-a-01-0-UI"  
 /clone\_lib="UI-R-A0"  
 /dev\_stage="adult"  
 /lab\_host="PH10B (Life Technologies)"  
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
 polylinker; Site\_1: Not I; Site\_2: Eco RI; This library  
 consists of a mixture of individually tagged normalized  
 libraries constructed from rat placenta, adult lung, brain  
 , liver, kidney, heart, spleen, ovary, and muscle. The tag  
 is a string of 3-5 nucleotides present between the Not I  
 site and the oligo-dt track which allows identification of  
 the library of origin of a clone within the mixture."  
 124 a 94 c 82 g 130 t

Query Match 5.7%; Score 28; DB 9; Length 430;  
 Best Local Similarity 100.0%; Pred. No. 0.0021;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 455 TACATATTGTCACAAAGTTCATCAACAC 482  
 |||||||||||||||||||||||||||||  
 Db 325 TACATATTGTCACAAAGTTCATCAACAC 298

RESULT 24  
 AA863979  
 LOCUS  
 DEFINITION  
 AA863979 429 bp mRNA linear EST 11-MAR-1998  
 IMAGE:1282208 5' similar to gb:U14332 Mus musculus interleukin 15  
 (MOUSE);, mRNA sequence.  
 ACCESSION  
 VERSION  
 AA863979.1 GI:2956458  
 KEYWORDS  
 EST.  
 SOURCE  
 house mouse.  
 ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

# REFERENCE

## AUTHORS

1 (bases 1 to 429)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

## TITLE

## JOURNAL

## COMMENT

The WashU-HMNI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMNI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMGE Consortium (info@image.llnl.gov) for further information.

MGI:674008

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 415.

# FEATURES

## source

1..429

/location/Qualifiers

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="IMAGE:1282208"

/clone\_lib="Soares\_thymus\_2NbMT"

/sex="male"

/tissue\_type="Thymus"

/dev\_stage="4 weeks"

/lab\_host="DH10B"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dt) primer [5', TGTWACCAATCTGAAGTGGAGCGCGCTTTTGTGTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 115 a 100 c 97 g 117 t

## ORIGIN

## Query Match

Best Local Similarity 100.0%; Pred. No. 0.022;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 GCTGGCATTTCATCTTCATTTTGGG 110

|||||||||||||||||||||||||||

Db 370 GCTGGCATTTCATCTTCATTTTGGG 395

## RESULT 25

BF704348/c

LOCUS

DEFINITION MI-P-03-aba-f-02-1-UM.sl MI-P-03 Sus scrofa cDNA clone

MI-P-03-aba-f-02-1-UM 3', mRNA sequence.

ACCESSION BF704348

VERSION BF704348.1 GI:11989750

KEYWORDS EST.

SOURCE pig.

ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 515)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

CONTACT: Tuggle CK

Molecular Genetics Laboratory, Department of Animal Science  
Iowa State University  
201 Kildee Hall, Ames, IA 50011-3150, USA  
Tel: 5152944252  
Fax: 5152942401  
Email: cktuggle@iastate.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized ovary at estrus day 12 library cDNA Library Preparation: RJ Woods, JEA Green, RS Prather S142 Animal Science Research Center, Department of Animal Science, University of Missouri-Columbia, 65211 Clone Distribution: clones will be available through Research Genetics (www.resgen.com) the following repetitive elements were found in this cDNA sequence: 1-28, >AT-rich#Low\_complexity 81-112, >AT-rich#Low\_complexity  
Seq primer: M13 Forward  
POLYA=Yes.

## FEATURES

source

Location/Qualifiers  
1..515  
/organism="Sus scrofa"  
/strain="crossbreed"  
/db\_xref="taxon:9823"  
/clone="MI-P-03-aba-f-02-1-UM"  
/clone\_lib="MI-P-03"  
/lab\_host="DH10B (Life Technologies)"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: EcoRI; The MI-P-03 library is derived from ovary at estrus day 12. For a detailed description of the library from which this clone was derived, please visit our web site at <http://pigest.genome.iastate.edu/>.  
TAG\_LIB=MI-P-03  
TAG\_TISSUE=ovary at estrus day 12  
TAG\_SEQ=TTGTAC"

BASE COUNT 158 a 91 c 85 g 176 t 5 others  
ORIGIN

Query Match 5.3%; Score 26; DB 10; Length 515;  
Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 388 GAATCTGATCAAGATGTGAGGA 413  
|||||

Db 413 GAATCTGATCAAGATGTGAGGA 388  
|||||

RESULT 26  
AW121368/c AW121368 405 bp mRNA linear EST 22-OCT-1999  
LOCUS  
DEFINITION UI-M-BH2.2-aom-e-04-0-UI.s1 NIH\_BMAP\_M\_S3.2 Mus musculus cDNA clone  
UI-M-BH2.2-aom-e-04-0-UI 3', mRNA sequence.

ACCESSION AW121368

VERSION AW121368.1 GI:6096701

KEYWORDS EST.

SOURCE house mouse.

ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 405)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

CONTACT: Chin, H

National Institute of Mental Health

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD

20892-9643, USA

Tel: 301 443 1706

Fax: 301 443 9890

Email: mEST@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized pineal glands library cDNA Library Preparation: M.B. Soares Lab Clone Distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.  
Seq primer: M13 Forward  
POLYA=Yes.

## FEATURES

source

Location/Qualifiers  
1..405  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UI-M-BH2.2-aom-e-04-0-UI"  
/clone\_lib="NIH\_BMAP\_M\_S3.2"  
/dev\_stage="27-32 days"  
/lab\_host="DH10B (Life Technologies)"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; The NIH\_BMAP\_M\_S3.2 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH\_BMAP\_M\_S3.2, NIH\_BMAP\_M\_S2, NIH\_BMAP\_M\_S1. The subtracted library (NIH\_BMAP\_M\_S3.2) was constructed as follows: PCR amplified cDNA inserts from NIH\_BMAP\_M\_S2 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the NIH\_BMAP\_M\_S2 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the NIH\_BMAP\_M\_S3.2 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)  
TAG\_LIB=NIH\_BMAP\_M\_S3.2  
TAG\_TISSUE=pineal-glands  
TAG\_SEQ=CAAC"

BASE COUNT 119 a 83 c 73 g 130 t  
ORIGIN

Query Match 4.7%; Score 23; DB 9; Length 405;  
Best Local Similarity 100.0%; Pred. No. 0.77;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 460 ATTGTCCAAATGTCATCAACAC 482  
|||||

Db 329 ATTGTCCAAATGTCATCAACAC 307  
|||||

RESULT 27

BE690327/c

LOCUS

DEFINITION

uw66b02.y1 Soares\_mammary\_gland\_NMLMG Mus musculus cDNA clone

IMAGE:3466923 5' similar to gb:U14332 Mus musculus Interleukin 15

(MOUSE); mRNA sequence.

ACCESSION BE690327

VERSION BE690327.1 GI:10077951

KEYWORDS EST.

SOURCE house mouse.

420 bp mRNA linear EST 11-SEP-2000  
Soares\_mammary\_gland\_NMLMG Mus musculus cDNA clone

IMAGE:3466923 5' similar to gb:U14332 Mus musculus Interleukin 15

(MOUSE); mRNA sequence.

BE690327

BE690327.1 GI:10077951

EST.

house mouse.

```

ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 420)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL       Unpublished (1997)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgaps-r@mail.nih.gov
              This clone is available royalty-free through LLNL ; contact the
              IMAGE Consortium (info@image.llnl.gov) for further information.
              MGI:1386283
              Seq primer: -40RP from Gibco
              High quality sequence stop: 367.
FEATURES     source
             1..420
             /organism="Mus musculus"
             /db_xref="taxon:10090"
             /clone="IMAGE:3466923"
             /clone_lib="Soares_mammary_gland_NMLMG"
             /sex="female (lactating)"
             /tissue_type="mammary gland"
             /lab_host="DH10B"
             /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
             polylinker; 1st strand cDNA was prepared from mammary
             gland tissue from a lactating female, and was then primed
             with a Not I - oligo(dT) primer. Double-stranded cDNA was
             ligated to Eco RI adaptors (Pharmacia), digested with Not
             I and cloned into the Not I and Eco RI sites of the
             modified pT7T3 vector. Library is normalized. Library
             was constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT   126 a 87 c 86 g 121 t
ORIGIN
Query Match      4.7%; Score 23; DB 10; Length 420;
Best Local Similarity 100.0%; Pred. No. 0.77;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 460 ATTGTCCTCAATGTTTCATCAACAC 482
|||||
Db 304 ATTGTCCTCAATGTTTCATCAACAC 282

RESULT 28
AI503618/c
LOCUS
DEFINITION      vk38h12.x1 Soares_mammary_gland_NbMWG Mus musculus cDNA clone
IMAGE:948935 3' similar to gb:U14332 Mus musculus Interleukin 15
(MOUSE);, mRNA sequence.
ACCESSION      AI503618.1 GI:4401469
VERSION
KEYWORDS
SOURCE
ORGANISM        house mouse.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 434)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL       Unpublished (1997)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgaps-r@mail.nih.gov
              This clone is available royalty-free through LLNL ; contact the
              IMAGE Consortium (info@image.llnl.gov) for further information.
              MGI:545791
              This clone was previously sequenced on the 5' end only, this new
              data is from the 3' end
              High quality sequence stop: 379.
FEATURES     source
             1..434

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/organism="Mus musculus"
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/lab_host="DH10B"
/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia)
) with a modified polylinker; Site.1: Not I; Site.2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5',
TGTTACCAATCTCAAGTGGAGCGCCGGAATGGTGTGTGTGTGTGTGTGTGTGT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M. Fatima
Bonaldo."
BASE COUNT   131 a 89 c 87 g 125 t 2 others
ORIGIN
Query Match      4.7%; Score 23; DB 9; Length 434;
Best Local Similarity 100.0%; Pred. No. 0.76;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 460 ATTGTCCTCAATGTTTCATCAACAC 482
|||||
Db 315 ATTGTCCTCAATGTTTCATCAACAC 293

RESULT 29
BB825167
LOCUS
DEFINITION      BB825167 RIKEN full-length enriched, mammary gland RCB-0526
JYG-MC(A) cDNA Mus musculus cDNA clone G830036W09 3', mRNA
sequence.
ACCESSION      BB825167.1 GI:17003410
VERSION
KEYWORDS
SOURCE
ORGANISM        house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 438)
AUTHORS      Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii
,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.,
,Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa
,A., Takahashi,F., Takaku-Akaira,S., Tanaka,T., Tomaru,A., Toya,T.,
Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,

```

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/db_xref="taxon:10090"
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/clone_lib="Soares_mammary_gland_NbMMG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="organ: mammary gland; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; lst strand cDNA was primed with a Not I - oligo(dT) primer [5], TgTtACCAATCTGAAGTGGGACGCCGGAATGTTTTTTTTTTTTTTTTTTTTTTT 3'; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."

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BASE COUNT	171 a	108 c	96 g	134 t
ORIGIN				

Query Match	4.7%;	Score 23;	DB 9;	Length 509;
Best Local Similarity	100.0%;	Pred. No. 0.76;		
Matches 23;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Db 404 ATTGTCCAAATGTTTCATCAAC 426

RESULT	31		
AI152482/c			
LOCUS	AI152482	538 bp	mRNA
		linear	EST 30-SEP-1998

ACCESSION

RECEIVED	ALL5248.1	GI:3680951
VERSION	EST.	
KEYWORDS	house mouse.	
SOURCE	Mus musculus	
ORGANISM		

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REFERENCE  
AUTHORS

## AUTHORS

**TITLE**

JOURNAL  
COMMENTFEATURES  
source

/note="vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

Db	565	GCTGGCATTTCATGCTCTTCATT	586
RESULT 33			
LOCUS	Ail161778		
DEFINITION	A006P68U Hybrid aspen plasmid library Populus tremula x Populus tremuloides cDNA 5', mRNA sequence.		
ACCESSION	Ail161778		
VERSION	Ail161778.1	GI:3853063	
KEYWORDS	EST.		
SOURCE	Populus tremula x Populus tremuloides.		
ORGANISM	Populus tremula x Populus tremuloides		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.		
REFERENCE	1 (bases 1 to 560)		
AUTHORS	Sterky,F., Regan,S., Karlsson,J., Hertzberg,M., Rohde,A., Holmberg,A., Aminii,B., Bhalaria,R., Larsson,M., Villarroel,R., Van Montagu,M., Sandberg,G., Olsson,O., Teerli,T.T., Boerjan,W., Gustafsson,P., Uhlen,M., Sundberg,B. and Lundberg,J.		
TITLE	Gene discovery in the wood-forming tissues of poplar: Analysis of 5,692 expressed sequence tags		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	95 (22), 13330-13335 (1998)	
MEDLINE	99007314		
COMMENT	Contact: Sterky F Department of Biotechnology Royal Institute of Technology (KTH) Teknikringen 34, S-100 44 STOCKHOLM, Sweden Tel: +46 8 790 8287 Fax: +46 8 24 54 52 Email: fredrik@biochem.kth.se PCR PRIMERS FORWARD: AAAGGGGATGCTGCTGCAAGCG BACKWARD: GCTTCGGGCTGTATGTTGTG Seq primer: CGTTGTAACGACGCGCAG High quality sequence stop: 560.		
FEATURES	source		
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	/tissue_type="Cambial region"		
	/dev_stage="1.5 m actively growing tree"		
	/lab_host="E.coli"		
	/note="vector: pBluescript SK; Site_1: SalI; Site_2: NotI; Cambial region tissues, including developing xylem, the meristematic cambial zone and the developing and mature phloem, was harvested from 1.5 m actively growing trees. cDNA was prepared and cloned into lambda gt22a. DNA was isolated and subcloned into pBluescript SK using SalI and NotI restriction enzymes."		
BASE COUNT	173 a	76 c	176 g
ORIGIN		133 t	2 others
Query Match			
Best Local Similarity 4.3%; Score 21; DB 9; Length 560;			
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	22	TTGAGAAGTATTTCCATCCAG	42
Db	389	TTGAGAAGTATTTCCATCCAG	409
RESULT 34			
LOCUS	BB664509/c		
DEFINITION	BB664509	652 bp	mRNA
	BB664509	RIKEN full-length enriched, 0 day neonate lung Mus musculus	EST 26-OCT-2001
ACCESSION	BB664509		
VERSION	BB664509.1	GI:16498263	
KEYWORDS	EST.		

/note="vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT	163 a	108 c	103 g
ORIGIN		163 t	1 others
Query Match			
Best Local Similarity 4.7%; Score 23; DB 9; Length 538;			
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	460	ATTGTCACAAATGTCATCAACAC	482
Db	319	ATTGTCACAAATGTCATCAACAC	297
RESULT 32			
LOCUS	BI685688		
DEFINITION	603309529F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5345382 5', mRNA sequence.		
ACCESSION	BI685688		
VERSION	BI685688.1	GI:15648316	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
REFERENCE	1 (bases 1 to 826)		
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs@mail.nih.gov Tissue Procurement: Jeffrey Green M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLAM1877 row: j column: 07 High quality sequence stop: 826.		
FEATURES	source		
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	/db_xref="taxon:10090"		
	/clone IMAGE:5345382"		
	/clone_lib="NCI_CGAP_Mam6"		
	/sex="female, virgin"		
	/tissue_type="infiltrating ductal carcinoma"		
	/dev_stage="5 months"		
	/lab_host="DH10B"		
	/note="organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies Investigator providing samples: Jeffrey Green, M.D., NIH"		
BASE COUNT	212 a	218 c	174 g
ORIGIN		222 t	
Query Match			
Best Local Similarity 4.5%; Score 22; DB 10; Length 826;			
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	85	GCTGCATTCATGCTCTTCATT	106



JOURNAL  
MEDLINE  
COMMENT

expressed sequence tag and genome survey sequence analysis  
Mol. Biochem. Parasitol. 107 (1), 1-32 (2000)  
20183851  
Contact: Nelson, R. G.  
Depts. of Medicine & Pharmaceutical Chemistry  
San Francisco General Hospital-University of California, San  
Francisco  
Box 0811, San Francisco, CA 94143-0811, USA  
Tel: 415 206 8846  
Fax: 415 206 3353  
Email: malaria@itsa.ucsf.edu  
For Annotation Data see <http://medsfgh.ucsf.edu/1d/CpTags/home.html>  
Seq primer: M13(-21) forward  
Class: shotgun.

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Cross. strain:
  Location/Qualifiers
    1. .742
      /organism="Cryptosporidium parvum"
      /strain="IOWA"
      /db_xref="taxon:5807"
      /clone_lib="Cp10WAgpD1"
      /lab_host="E. coli XL2 Blue MRF"
      /notes="Vector: pBluescript II (SK-); Site_1: EcorV; C.
      parvum (IOWA isolate) genomic DNA was hydrodynamically
      sheared to produce fragments variously sized and

```

sheared to produce fragments having a tight size distribution between 2-4 kb by Dr. Yvonne Thorstenson of the Stanford DNA Sequencing and Technology Center (<http://sequence-www.stanford.edu/group/techdev/shear.htm>). The randomly sheared gDNA was chromatographed on Sephacryl S-400 to remove any small fragments and DNA eluting in the void volume was subcloned into an EcoR V-digested, alkaline phosphatase-treated pBlueScript II (SK-) vector and transformed into E. coli strain XL2 Blue MRF'. Recombinant clones from the first plating of the library were selected for sequence analysis using T3 and T7 primers."

205 a	138 c	105 g	293 t	1 others
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BASE COUNT  
ORIGIN

Query Match	4.3%	Score 21;	DB 12;	Length 742;
Best Local Similarity	100.0%;	Pred. No. 7.8;		
Matches 21;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 435	AGAAATTTTTCACAGAGTTTGT	455		
Db 514	AGAAATTTTTCACAGAGTTTGT	534		
RESULT 38				
AQ247270				
LOCUS	AQ247270	820 bp	DNA	linear
DEFINITION	HS-2064_A2_F10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-2064 Col-20 Row=K, DNA sequence.			
ACCESSION	AQ247270			
VERSION	AQ247270.1	GI:3697452		
KEYWORDS	GSS.			
SOURCE	human			

REFERENCE AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 820) Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL MEDLINE	Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel.: (206) 616-3618

Fax: (206) 616-3887  
 Email: jwallace@u.washington.edu  
 Sequence Tagged Connector  
 Plate: 2064 Row: K Column: 20  
 Class: BAC ends  
 High quality sequence stop: 820.  
 Location/Qualifiers  
 1. 820

FEATURES  
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/organism="Homo sapiens"  
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 /sex="male"  
 /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"  
 252 a 152 c 202 g 207 t 7 others

BASE COUNT  
 ORIGIN

Query Match 4.3%; Score 21; DB 12; Length 820;  
 Best Local Similarity 100.0%; Pred. No. 7.7;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 380 ATATAACAGAACTGGATGCA 400  
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 Db 503 ATATAACAGAACTGGATGCA 523

RESULT 39  
 LOCUS

BB467257 204 bp mRNA linear EST 22-JUL-2000  
 BB467257 RIKEN full-length enriched, 12 days embryo eyeball Mus  
 musculus cDNA clone D230013C16 3' similar to S59342 nuclear pore  
 complex glycoprotein p62, mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE

BB467257.1 GI:9384446

EST.  
 house mouse.  
 Mus musculus

ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 204)

REFERENCE  
 AUTHORS

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci  
 P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,  
 Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,  
 Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,  
 Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,  
 Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,  
 Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata  
 Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.,  
 Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya  
 T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I.,  
 Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino  
 M., Muramatsu, M. and Hayashizaki, Y.  
 RIKEN Mouse ESTs (Konno, H., et al.)  
 Unpublished (2000)

TITLE  
 JOURNAL  
 COMMENT

Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216

Email: genome-res@sc.riken.go.jp  
 URL: http://genome.res.riken.go.jp/  
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagakawa, S., Sasaki  
 N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Thermostabilization and thermoactivation of thermolabile enzymes by  
 trehalose and its application for the synthesis of full length  
 cDNA. Proc Natl Acad Sci U.S.A. 95 (2), 520-524 (1998)  
 Itoh, M., Kikuchi, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,  
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki  
 Y. and Hayashizaki, Y.

Automated filtration-based high-throughput plasmid preparation  
 system. Genome Res. 9 (5), 463-470 (1999)  
 Carninci, P. and Hayashizaki, Y.  
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 19-44 (1999)  
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 further details.

FEATURES  
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Location/Qualifiers  
 1. 204  
 /organism="Mus musculus"  
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 /clone="D230013C16"  
 /clone\_lib="RIKEN full-length enriched, 12 days embryo  
 eyeball"  
 /tissue\_type="eyeball"  
 /dev\_stage="12 days embryo"  
 /lab\_host="DH10B"  
 /note="Site\_1: Sali; Site\_2: BamHI; cDNA library was  
 prepared and sequenced in Mouse Genome Encyclopedia  
 Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in  
 RIKEN. Division of Experimental Animal Research in Riken  
 contributed to prepare mouse tissues. 1st strand cDNA was  
 primed with a primer [5'  
 GAGAGAGAGCGCGCAACTCGAGTTTCTTTTCTTTTNN 3'], cDNA was  
 prepared by using trehalose thermo-activated reverse  
 transcriptase and subsequently enriched for full-length by  
 cap-trapper. Second strand cDNA was prepared with the  
 primer adapter of sequence [5'  
 GAGAGAGAGTCGAGTTAAATTAATTCCTCCCGCCCCCCC 3']. cDNA  
 was cleaved with BamHI and XhoI. Vector: a modified  
 pBluescript KS(+) after bulk excision from Lambda FLC I."

BASE COUNT  
 ORIGIN

48 a 46 c 37 g 73 t

Query Match 4.1%; Score 20; DB 9; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 TGAAGCTGGCATTTCATGCTCT 100  
 |||||  
 Db 95 TGAAGCTGGCATTTCATGCTCT 114

RESULT 40  
 LOCUS

BB213861 224 bp mRNA linear EST 30-JUN-2000  
 BB213861 RIKEN full-length enriched, adult male aorta and vein Mus  
 musculus cDNA clone A530014K14 3' similar to S59342 nuclear pore  
 complex glycoprotein p62, mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE

BB213861.1 GI:8878814

EST.  
 house mouse.  
 Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 224)  
 Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci  
 P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,  
 Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,  
 Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,  
 Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,  
 Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,  
 Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata  
 Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.,  
 Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya  
 T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I.,  
 Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino  
 M., Muramatsu, M. and Hayashizaki, Y.  
 RIKEN Mouse ESTs (Konno, H., et al.)  
 Unpublished (2000)

## COMMENT

Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center(GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan  
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 URL: http://genome.gsc.riken.go.jp/  
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 N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
 Thermotabilization and thermoactivation of thermolabile enzymes by  
 trehalose and its application for the synthesis of full length  
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
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 Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki  
 Y. and Hayashizaki,Y.  
 Automated filtration-based high-throughput plasmid preparation  
 system. Genome Res. 9 (5), 463-470 (1999)  
 Carninci,P. and Hayashizaki,Y.  
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
 19-44 (1999)  
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 further details.

FEATURES  
source

Location/Qualifiers  
 1. .224  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone="A530014K14"  
 /clone\_lib="RIKEN full-length enriched, adult male aorta  
 and vein"  
 /sex="male"  
 /tissue\_type="aorta and vein"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /note="Site.1: Salt; Site.2: BamHI; cDNA library was  
 prepared and sequenced in Mouse Genome Encyclopedia  
 Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in  
 RIKEN. Division of Experimental Animal Research in Riken  
 contributed to prepare mouse tissues. 1st strand cDNA was  
 primed with a primer [5'  
 GAGAGAGAAGGATCCAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was  
 prepared by using trehalose thermo-activated reverse  
 transcriptase and subsequently enriched for full-length by  
 cap-trapper. cDNA went through one round of normalization  
 to Rot = 20.0 and subtraction to Rot = 459.0. Second  
 strand cDNA was prepared with the primer adapter of  
 sequence [5' GAGAGAGATCTCGAGTTAATTAATATCCCCCCCCC  
 3']. cDNA was cleaved with XhoI and BamHI. Vector: a  
 modified pBluescript KS(+) after bulk excision from Lambda  
 FLC I."

BASE COUNT 51 a 51 c 38 g 84 t  
 ORIGIN

Query Match 4.1%; Score 20; DB 9; Length 224;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 TGAAGTCGCATTCATGCT 100  
 Db 119 TGAAGTCGCATTCATGCT 138

RESULT 41  
 A1447397/c  
 LOCUS  
 DEFINITION m36f10.x1 Soares\_thymus\_2NbMT Mus musculus cDNA clone IMAGE:583435  
 A1447397  
 ACCESSION A1447397  
 VERSION A1447397.1 GI:4303701  
 KEYWORDS EST.

SOURCE  
ORGANISM

house mouse.  
 Mus musculus

REFERENCE  
AUTHORS  
TITLE

1 (bases 1 to 253)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)

JOURNAL  
COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 This clone was previously sequenced on the 5' end only, this new  
 data is from the 3' end  
 High quality sequence stop: 247.

FEATURES  
source

Location/Qualifiers  
 1. .253  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:583435"  
 /clone\_lib="Soares\_thymus\_2NbMT"  
 /sex="male"  
 /tissue\_type="Thymus"  
 /dev\_stage="4 weeks"  
 /lab\_host="DH10B"  
 /note="Vector: p7T3D-Pac (Pharmacia) with a modified  
 polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA  
 was primed with a Not I - oligo(dT) primer [5'  
 TGTTACCAATCTGAAGTGGAGCGCGCGTTTTTTTTTTTTTTTTTTTTT  
 3']; double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified p7T3 vector. RNA  
 provided by Dr. Bertrand Jordan. Library went through two  
 rounds of normalization, and was constructed by Bento  
 Soares and M.Fatima Bonaldo."

BASE COUNT  
ORIGIN

55 a 36 c 22 g 140 t

Query Match 4.1%; Score 20; DB 9; Length 253;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 AAAAATTAAGAATTTT 443

Db 176 AAAAATTAAGAATTTT 157

RESULT 42  
LOCUS

BB141025 286 bp mRNA linear EST 28-JUN-2000  
 BB141025 RIKEN full-length enriched, adult female vagina Mus  
 musculus cDNA clone 993003P08 3' similar to S59342 nuclear pore  
 complex glycoprotein p62, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS

BB141025  
 BB141025.1 GI:8795962  
 EST.

SOURCE  
ORGANISM

house mouse.  
 Mus musculus

REFERENCE  
AUTHORS

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 1 (bases 1 to 286)  
 Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci  
 P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,  
 Hirozawa,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,  
 Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,  
 Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.,  
 Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,  
 Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata  
 Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.,  
 Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya

,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.  
RIKEN Mouse ESTs (Konno,H., et al.)  
Unpublished (2000)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.go.jp,  
URL:http://genome.gsc.riken.go.jp/  
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Thermotabilization and thermoactivation of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.  
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)  
Carninci,P. and Hayashizaki,Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

TITLE  
JOURNAL  
COMMENT

FEATURES  
source

Location/Qualifiers  
1. .286  
/organism="Mus musculus"  
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/clone\_lib="RIKEN full-length enriched, adult female vagina"  
/sex="female"  
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/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Site\_1: Sall; Site\_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'  
GAGAGAGAGAGATCCAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCGAGTTAATTAATCCCGCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

BASE COUNT 67 a 62 c 53 g 103 t 1 others  
ORIGIN

Query Match 4.1% Score 20; DB 9; Length 286;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 TGAAGCTGGCATTGCTCT 100  
|||||  
DB 184 TGAAGCTGGCATTGCTCT 203

RESULT 43  
BB003966  
LOCUS

BB003966 288 bp mRNA linear EST 22-JUN-2000

DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BB003966 RIKEN full-length enriched, 10 day neonate skin Mus  
musculus cDNA clone 4732457L13 3' similar to S59342 nuclear pore complex glycoprotein p62, mRNA sequence.  
BB003966.1 GI:8093414  
EST.  
house mouse  
Mus musculus

REFERENCE  
AUTHORS

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 288)  
Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.  
RIKEN Mouse ESTs (Konno,H., et al.)  
Unpublished (2000)  
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The Institute of Physical and Chemical Research (RIKEN)  
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URL:http://genome.gsc.riken.go.jp/  
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Thermotabilization and thermoactivation of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
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High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
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TITLE  
JOURNAL  
COMMENT

Location/Qualifiers  
1. .286  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone\_lib="4732457L13"  
/clone\_lib="RIKEN full-length enriched, 10 day neonate skin"  
/sex="mixed"  
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/note="Site\_1: Sall; Site\_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'  
GAGAGAGAGATCCAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCGAGTTAATTAATCCCGCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

FEATURES  
Source

Location/Qualifiers  
1. .286  
/organism="Mus musculus"  
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/db\_xref="taxon:10090"  
/clone\_lib="4732457L13"  
/clone\_lib="RIKEN full-length enriched, 10 day neonate skin"  
/sex="mixed"  
/tissue\_type="skin"  
/dev\_stage="10 days neonate"  
/lab\_host="DH10B"  
/note="Site\_1: Sall; Site\_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'  
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Fax: 81-45-503-9216  
 Email: genome-resgsc.riken.go.jp,  
 URL: http://genome.gsc.riken.go.jp/  
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 Y. and Hayashizaki, Y.  
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 system. Genome Res. 9 (5), 463-470 (1999)  
 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
 19-44 (1999)  
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 further details.

#### FEATURES

Location/Qualifiers  
 1. .294  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
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 /tissue\_type="parthenogenote"  
 /dev\_stage="9.5 days embryo"  
 /lab\_host="DH10B"  
 /note="Site\_1: Sall; Site\_2: BamHI; cDNA library was  
 prepared and sequenced in Mouse Genome Encyclopedia  
 Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in  
 RIKEN. Division of Experimental Animal Research in Riken  
 contributed to prepare mouse tissues. 1st strand cDNA was  
 primed with a primer [5'  
 GAGAGAGAGATCTCGAGTTAAATTAATTCACCCGCCCC 3']. cDNA was  
 prepared by using trehalose thermo-activated reverse  
 transcriptase and subsequently enriched for full-length by  
 cap-trapper. cDNA went through one round of subtraction to  
 Rot = 229.0 Second strand cDNA was prepared with the  
 primer adapter of sequence [5'  
 GAGAGAGATCTCGAGTTAAATTAATTCACCCGCCCC 3']. cDNA  
 was cleaved with XhoI and BamHI. Vector: a modified  
 pBluescript KS(+) after bulk excision from Lambda FLC I."  
 60 a 91 c 46 g 97 t

#### BASE COUNT

ORIGIN

Query Match 4.1%; Score 20; DB 9; Length 294;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 TGAAGCTGCATTCATGTCT 100

DB 191 TGAAGCTGCATTCATGTCT 210

#### RESULT 46

LOCUS

BB135090  
 BB135090 RIKEN full-length enriched, adult male bone Mus musculus  
 cDNA clone 9830122A02 3' similar to S59342 nuclear pore complex  
 glycoprotein p62, mRNA sequence.

DEFINITION

BB135090

ACCESSION

BB135090

VERSION

BB135090.1

KEYWORDS

EST

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

1 (bases 1 to 295)

AUTHORS

Konno H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci  
 P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,

Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,  
 Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,  
 Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,  
 Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,  
 Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata,  
 Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.,  
 Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya,  
 T., Tsunoda, Y., Watanabe, S., Watanabe, S., Yamamura, T., Yamanaka, I.,  
 Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino,  
 M., Muramatsu, M. and Hayashizaki, Y.  
 RIKEN Mouse ESTs (Konno, H., et al.)

#### TITLE

JOURNAL

COMMENT

Unpublished (2000)

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-resgsc.riken.go.jp,

URL: http://genome.gsc.riken.go.jp/  
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki  
 N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Thermotabilization and thermoactivation of thermolabile enzymes by  
 trehalose and its application for the synthesis of full length  
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
 Itoh, M., Kitsumai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,  
 Tomaru, Y., Carninci, P., Shibusawa, Y., Ozawa, Y., Muramatsu, M., Okazaki  
 Y. and Hayashizaki, Y.  
 Automated filtration-based high-throughput plasmid preparation  
 system. Genome Res. 9 (5), 463-470 (1999)  
 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
 19-44 (1999)  
 Please visit our web site (http://genome.rtc.riken.go.jp) for  
 further details.

#### FEATURES

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/organism="Mus musculus"

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/clone="9830122A02"

/clone\_lib="RIKEN full-length enriched, adult male bone"

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/note="Site\_1: Sall; Site\_2: BamHI; cDNA library was  
 prepared and sequenced in Mouse Genome Encyclopedia  
 Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in  
 RIKEN. Division of Experimental Animal Research in Riken  
 contributed to prepare mouse tissues. 1st strand cDNA was  
 primed with a primer [5'  
 GAGAGAGAGATCTCGAGTTAAATTAATTCACCCGCCCC 3']. cDNA was  
 prepared by using trehalose thermo-activated reverse  
 transcriptase and subsequently enriched for full-length by  
 cap-trapper. cDNA went through one round of normalization  
 to Rot = 10.0 and subtraction to Rot = 185.0. Second  
 strand cDNA was prepared with the primer adapter of  
 sequence [5' GAGAGAGATCTCGAGTTAAATTAATTCACCCGCCCC  
 3']. cDNA was cleaved with XhoI and BamHI. Vector: a  
 modified pBluescript KS(+) after bulk excision from Lambda  
 FLC I."

BASE COUNT 70 a 68 c 57 g 100 t  
 ORIGIN

Query Match 4.1%; Score 20; DB 9; Length 295;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 TGAAGCTGCATTCATGTCT 100

|||||

Db 190 TGAAGCTGGCATTTCATGTCT 209

# RESULT 47

## BB157192

LOCUS BB157192 RIKEN full-length enriched, 16 days neonate thymus Mus  
DEFINITION musculus cDNA clone Al30035D04 3' similar to S59342 nuclear pore  
complex glycoprotein p62, mRNA sequence.

## ACCESSION

BB157192.1 GI:8813122

## VERSION

EST.

## KEYWORDS

house mouse.

## SOURCE

Mus musculus

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 295)

## REFERENCE

### AUTHORS

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci  
, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,  
Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,  
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,  
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,  
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,  
Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata  
, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.,  
Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya  
, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamana, I.,  
Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino  
, M., Muramatsu, M. and Hayashizaki, Y.  
RIKEN Mouse ESTs (Konno, H., et al.)

## TITLE

## JOURNAL

## COMMENT

Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/  
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sakai  
, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Thermotabilization and thermoactivation of thermolabile enzymes by  
trehalose and its application for the synthesis of full length  
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
Itoh, M., Kitsuai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,  
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki  
, Y. and Hayashizaki, Y.  
Automated filtration-based high-throughput plasmid preparation  
system. Genome Res. 9 (5), 463-470 (1999)  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for  
further details.

## FEATURES

### source

Location/Qualifiers  
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/organism="Mus musculus"  
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/tissue\_type="thymus"  
/dev\_stage="16 days neonate"  
/lab\_host="PH108"  
/note="Site\_1: SalI; Site\_2: BamHI; cDNA library was  
prepared and sequenced in Mouse Genome Encyclopedia  
Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN. Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer [5'  
GAGAGAGAGAGATCCCAAGAGCTCTTTTTTTTTTTTTTTTTTTVN 3'], cDNA was

prepared by using trehalose thermo-activated reverse  
transcriptase and subsequently enriched for full-length by  
cap-trapper. cDNA went through one round of normalization  
to Rot = 10.0 and subtraction to Rot = 185.0. Second  
strand cDNA was prepared with the primer adapter of  
sequence [5' GAGAGAGATCTCGAGTAAATTAATTAATCCCCCCCCCCC  
3']. cDNA was cleaved with XhoI and BamHI. Vector: a  
modified pBluescript KS(+) after bulk excision from Lambda  
FLC I."

BASE COUNT 64 a 71 c 55 g 105 t  
ORIGIN

Query Match 4.1%; Score 20; DB 9; Length 295;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 TGAAGCTGGCATTTCATGTCT 100

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Db 190 TGAAGCTGGCATTTCATGTCT 209

## RESULT 48

BB714486

ID BB714486 standard; RNA; EST; 307 BP.

XX AC BB714486;

XX SV BB714486.1

XX

DT 09-OCT-2001 (Rel. 69, Created)

DT 09-OCT-2001 (Rel. 69, Last updated, Version 1)

DE Mus musculus 9.5 days embryo parthenogenote cDNA, RIKEN full-length

DE enriched library, clone: B130060L02, 3' end partial sequence.

XX

KW EST (expressed sequence tag).

XX

OS Mus musculus (house mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

XX

RP [1]

RA Akimura T., Arakawa T., Carninci P., Furuno M., Hanagaki T., Hayatsu N.,

RA Hiramoto K., Hiraoka T., Hirozane T., Imotani K., Ishii Y., Ito M.,

RA Kawai J., Kojima Y., Konno H., Kouda M., Matsuyama T., Nakamura M.,

RA Nishi K., Nomura K., Numasaki R., Okazaki Y., Okido T., Saito R., Sakai C.,

RA Sakai K., Sakazume N., Sasaki D., Sato K., Shibata K., Shinagawa A.,

RA Shiraki T., Sogabe Y., Suzuki H., Tagawa A., Takahashi F.,

RA Takaku-Akahira S., Tanaka T., Tomaru A., Toya T., Watahiki A.,

RA Yasunishi A., Muramatsu M., Hayashizaki Y.;

RT Submitted (28-SEP-2001) to the EMBL/GenBank/DBJ databases.

RL Yoshihide Hayashizaki, The Institute of Physical and Chemical Research

RL (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic

RL Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho,

RL Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

RL (E-mail: genome-res@gsc.riken.go.jp, URL: <http://genome.gsc.riken.go.jp/>;

RL Tel: 81-45-503-9222, Fax: 81-45-503-9216)

XX

RN [2]

RA Akimura T., Arakawa T., Carninci P., Furuno M., Hanagaki T., Hayatsu N.,

RA Hiramoto K., Hiraoka T., Hirozane T., Imotani K., Ishii Y., Ito M.,

RA Kawai J., Kojima Y., Konno H., Kouda M., Matsuyama T., Nakamura M.,

RA Nishi K., Nomura K., Numasaki R., Okazaki Y., Okido T., Saito R., Sakai C.,

RA Sakai K., Sakazume N., Sasaki D., Sato K., Shibata K., Shinagawa A.,

RA Shiraki T., Sogabe Y., Suzuki H., Tagawa A., Takahashi F.,

RA Takaku-Akahira S., Tanaka T., Tomaru A., Toya T., Watahiki A.,

RA Yasunishi A., Muramatsu M., Hayashizaki Y.;

RT "RIKEN Encyclopedia of Mouse Full-length cDNAs";

RT Unpublished.

XX

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NN Konno H., Fukunishi Y., Shibata K., Itoh M., Carninci P., Sugahara Y.,
RA Hayashizaki Y.;
RT "Computer-based methods for the mouse full-length cDNA encyclopedia:
RT real-time sequence clustering for construction of a nonredundant cDNA
RT library";
RL Genome Res. 11:281-289(2001).
XX

[4]
NN Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare
RT full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630(2000).
XX

[5]
NN Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishii K., Kitsuunai T., Tashiro H., Itoh M., Sumi N.,
RA Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R.,
RA Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaki S.,
RA Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y.,
RA Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y.,
RA Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing
RT pipeline with 384 multicapillary sequencer";
RL Genome Res. 10:1757-1771(2000).
XX

CC Please visit our web site (http://genome.gsc.riken.go.jp/) for
CC further details.
CC cDNA library was prepared and sequenced in Mouse Genome
CC Encyclopedia Project of Genome Exploration Research Group in Riken
CC Genomic Sciences Center and Genome Science Laboratory in Riken.
CC Division of Experimental Animal Research in Riken contributed to
CC prepare mouse tissues.
XX
FH Key Location/Qualifiers
FH
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FT /sequenced_mol="cDNA to mRNA"
FT /organism="Mus musculus"
FT /clone="B130060L02"
FT /clone_lib="RIKEN full-length enriched mouse cDNA library"
FT /dev_stage="9.5 days embryo"
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QY 81 TGAAGCTGGCATTTCATGCT 100
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Db 199 TGAAGCTGGCATTTCATGCT 218

RESULT 49
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LOCUS BB165365 RIKEN full-length enriched, 16 days neonate thymus Mus
DEFINITION musculus cDNA clone Al30082J05 3' similar to S59342 nuclear pore
complex glycoprotein p62, mRNA sequence.
ACCESSION BB165365
VERSION BB165365.1 GI:8821306
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 347)

```

## AUTHORS

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, Y., Sobabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

## TITLE

RIKEN Mouse ESTs (Konno, H., et al.)

## JOURNAL

Unpublished (2000)

## COMMENT

Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gs.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/  
N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Thermotabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
Ito, M., Kitsuunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.  
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
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## FEATURES

Location/Qualifiers  
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/dev\_stage="16 days neonate"  
/lab\_host="DH10B"  
/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'  
GAGAGAGAGAGGATCCAGAGCTCTTTTTTTTTTTTNN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATCTCGAGTTAATTAATCCCTCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLX I."

BASE COUNT  
ORIGIN

74 a 87 c 73 g 113 t  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 TGAAGCTGGCATTTCATGTCT 100  
|||||  
Db 244 TGAAGCTGGCATTTCATGTCT 263

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VERSION B35094.1 GI:2534463  
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SOURCE human.  
ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 430)  
Mahaïras,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S.,  
Traicoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E.  
Construction of a Characterized Clone Resource for Genomic  
Sequencing: Generation and Preliminary Analysis of 20,000 Sequence  
Tagged Connectors  
Unpublished (1997)  
Contact: Mahaïras GG, Zackrone KD, Hood L  
University of Washington  
Seattle, WA 98195, USA  
Tel: (206) 616-8744  
Fax: (206) 685-7301  
Email: kzackron@u.washington.edu  
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Plate: CT 806 row: A column: 1  
Class: BAC ends  
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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 6, 2002, 21:31:16 ; Search time 67.77 Seconds  
(without alignments)  
1772.389 Million cell updates/sec

Title: US-09-724-841-4

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Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

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Minimum DB seq length: 0

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6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	489	100.0	489	1	US-08-726-817-4
4	489	100.0	489	1	US-08-504-042-1
5	489	100.0	489	1	US-08-392-317B-1
6	489	100.0	489	2	US-08-725-969-4
7	489	100.0	489	2	US-08-794-524-4
8	489	100.0	489	3	US-09-134-132-1
9	489	100.0	489	4	US-09-134-456-1
10	489	100.0	489	4	US-09-134-456-1
11	489	100.0	489	4	US-09-196-427-1
12	489	100.0	489	4	US-09-189-193-4
13	489	100.0	489	5	PCT-US94-03793-1
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15	345	70.6	345	1	US-08-726-817-13
16	345	70.6	345	2	US-08-725-969-13
17	345	70.6	345	2	US-08-794-524-13
18	345	70.6	345	4	US-09-189-193-13
19	107	21.9	489	1	US-08-031-399-4
20	107	21.9	489	1	US-08-393-305-1
21	107	21.9	489	1	US-08-535-733-1
22	107	21.9	489	1	US-08-726-817-1
23	107	21.9	489	1	US-08-504-042-4
24	107	21.9	489	1	US-08-392-317B-2
25	107	21.9	489	2	US-08-725-969-1
26	107	21.9	489	2	US-08-794-524-1
27	107	21.9	489	3	US-08-842-947-5

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29	107	21.9	489	3	US-09-134-132-2	Sequence 2, Appli
30	107	21.9	489	4	US-03-134-134A-2	Sequence 2, Appli
31	107	21.9	489	4	US-09-134-456-2	Sequence 2, Appli
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36	107	21.9	1202	3	US-08-962-503-11	Sequence 1, Appli
37	95	19.4	1248	2	US-09-200-141-1	Sequence 12, Appli
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39	80	16.4	345	1	US-08-726-817-12	Sequence 12, Appli
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41	80	16.4	345	2	US-08-794-524-12	Sequence 12, Appli
42	80	16.4	345	4	US-09-189-193-12	Sequence 435, App
43	27	5.5	32	2	US-08-859-998-435	Sequence 435, App
44	27	5.5	32	4	US-09-225-928-435	Sequence 4, Appli
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51	21	4.3	36	4	US-09-196-427-10	Sequence 10, Appli
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54	21	4.3	69	3	US-09-134-132-9	Sequence 9, Appli
55	21	4.3	69	4	US-09-134-134A-9	Sequence 9, Appli
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66	18	3.7	18	2	US-09-200-141-43	Sequence 2, Appli
67	18	3.7	26	3	US-08-842-947-2	Sequence 7, Appli
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69	18	3.7	39	3	US-09-134-132-7	Sequence 7, Appli
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73	18	3.7	45	3	US-09-134-132-8	Sequence 8, Appli
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83	18	3.7	6129	1	US-08-136-809A-1	Sequence 1, Appli
84	18	3.7	6129	2	US-08-951-912-1	Sequence 5, Appli
85	18	3.7	6129	2	US-08-691-605-1	Sequence 1, Appli
86	18	3.7	6129	3	US-09-248-026-1	Sequence 1, Appli
87	18	3.7	6129	3	US-08-681-838A-1	Sequence 1, Appli
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89	18	3.7	6129	4	US-09-174-077-5	Sequence 16, Appli
90	18	3.7	6130	5	PCT-US93-11667-1	Sequence 16, Appli
91	18	3.7	6130	2	US-08-466-886-16	Sequence 1, Appli
92	18	3.7	6130	2	US-08-604-488-1	Sequence 1, Appli
93	18	3.7	6130	2	US-08-469-461-1	Sequence 1, Appli
94	18	3.7	6130	3	US-07-890-609-1	Sequence 1, Appli
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C 102	18	3.7	6146	6	5240846-4	Patent No. 5240846	16	3.3	1792	3	US-08-747-2218-18	Sequence 18, Appl
C 103	18	3.7	8225	4	US-08-793-618-1	Sequence 1, Appl	16	3.3	1792	3	US-08-747-2218-20	Sequence 20, Appl
C 104	18	3.7	9572	3	US-08-836-022A-3	Sequence 3, Appl	16	3.3	1792	4	US-09-005-051-18	Sequence 18, Appl
C 105	18	3.7	9972	4	US-09-427-048A-3	Sequence 3, Appl	16	3.3	1792	4	US-09-005-051-20	Sequence 20, Appl
C 106	18	3.7	22846	2	US-08-469-461-3	Sequence 3, Appl	16	3.3	1867	1	US-07-955-905A-1	Sequence 1, Appl
C 107	18	3.7	22846	3	US-07-890-609-3	Sequence 3, Appl	16	3.3	2136	1	US-08-321-587-1	Sequence 1, Appl
C 108	17	3.5	18	2	US-09-200-141-39	Sequence 39, Appl	16	3.3	2763	1	US-08-176-413-1	Sequence 1, Appl
C 109	17	3.5	1011	1	US-08-332-312-3	Sequence 3, Appl	16	3.3	2763	1	US-08-612-542B-1	Sequence 1, Appl
C 110	17	3.5	1133	1	US-07-750-080A-2	Sequence 2, Appl	16	3.3	2763	2	US-08-772-113-1	Sequence 1, Appl
C 111	17	3.5	1133	1	US-07-750-080A-3	Sequence 3, Appl	16	3.3	2763	2	US-09-199-137-1	Sequence 1, Appl
C 112	17	3.5	1133	3	US-08-651-472-2	Sequence 2, Appl	16	3.3	2763	4	PCT-US94-14919-1	Sequence 1, Appl
C 113	17	3.5	1133	4	US-08-651-472-3	Sequence 3, Appl	16	3.3	2763	5	PCT-US94-14920-1	Sequence 1, Appl
C 114	17	3.5	1133	4	US-08-358-928-2	Sequence 2, Appl	16	3.3	3250	3	US-08-617-860B-1	Sequence 1, Appl
C 115	17	3.5	1133	4	US-08-358-928-3	Sequence 3, Appl	16	3.3	3271	3	US-08-545-196B-22	Sequence 22, Appl
C 116	17	3.5	1209	1	US-07-750-080A-22	Sequence 22, Appl	16	3.3	3279	5	PCT-US93-03077-2	Sequence 2, Appl
C 117	17	3.5	1209	3	US-08-651-472-22	Sequence 22, Appl	16	3.3	4203	2	US-08-288-630-3	Sequence 3, Appl
C 118	17	3.5	1209	4	US-08-358-928-22	Sequence 22, Appl	16	3.3	15	3	US-08-649-654-2	Sequence 2, Appl
C 119	17	3.5	1448	1	US-08-298-426-1	Sequence 1, Appl	15	3.1	32	2	US-08-859-998-436	Sequence 436, App
C 120	17	3.5	1449	4	US-08-936-165A-100	Sequence 100, App	15	3.1	32	4	US-09-225-928-436	Sequence 436, App
C 121	17	3.5	1776	1	US-08-298-426-3	Sequence 3, Appl	15	3.1	114	1	US-08-184-941-11	Sequence 11, Appl
C 122	17	3.5	3878	3	US-08-651-472-65	Sequence 65, Appl	15	3.1	313	4	US-09-040-984-64	Sequence 64, Appl
C 123	17	3.5	3878	4	US-08-358-928-65	Sequence 65, Appl	15	3.1	313	4	US-09-123-912-64	Sequence 64, Appl
C 124	17	3.5	4145	3	US-08-651-472-62	Sequence 62, Appl	15	3.1	431	2	US-08-691-814B-84	Sequence 84, Appl
C 125	17	3.5	4145	4	US-08-358-928-62	Sequence 62, Appl	15	3.1	447	3	US-09-358-580-5	Sequence 5, Appl
C 126	17	3.5	4277	3	US-08-651-472-63	Sequence 63, Appl	15	3.1	489	2	US-08-334-254-7	Sequence 7, Appl
C 127	17	3.5	4277	4	US-08-358-928-63	Sequence 63, Appl	15	3.1	489	2	US-08-848-131-7	Sequence 7, Appl
C 128	17	3.5	4659	1	US-08-232-463-10	Sequence 10, Appl	15	3.1	602	4	PCT-US95-14792-7	Sequence 7, Appl
C 129	17	3.5	4701	3	US-08-651-472-64	Sequence 64, Appl	15	3.1	617	4	US-09-328-111-220	Sequence 220, App
C 130	17	3.5	4701	4	US-08-358-928-64	Sequence 64, Appl	15	3.1	747	4	US-09-385-982-170	Sequence 170, App
C 131	17	3.5	4818	1	US-08-232-463-11	Sequence 11, Appl	15	3.1	821	1	US-09-385-982-540	Sequence 540, App
C 132	17	3.5	4821	1	US-08-232-463-12	Sequence 12, Appl	15	3.1	821	1	US-09-396-452-3	Sequence 3, Appl
C 133	17	3.5	4824	1	US-08-232-463-13	Sequence 13, Appl	15	3.1	821	4	US-09-169-119-3	Sequence 3, Appl
C 134	17	3.5	5532	3	US-08-651-472-72	Sequence 72, Appl	15	3.1	854	4	US-09-064-683A-24	Sequence 24, Appl
C 135	17	3.5	5532	4	US-08-358-928-72	Sequence 72, Appl	15	3.1	912	1	US-08-764-100-15	Sequence 15, Appl
C 136	17	3.5	6060	5	PCT-US96-09430-7	Sequence 7, Appl	15	3.1	912	1	US-08-764-100-22	Sequence 22, Appl
C 137	17	3.5	6474	3	US-08-651-472-66	Sequence 66, Appl	15	3.1	1093	1	US-08-525-505A-3	Sequence 3, Appl
C 138	17	3.5	6474	4	US-08-358-928-66	Sequence 66, Appl	15	3.1	1129	4	US-09-227-357-40	Sequence 40, Appl
C 139	17	3.5	6601	1	US-08-232-463-15	Sequence 15, Appl	15	3.1	1197	4	US-09-383-586-5	Sequence 5, Appl
C 140	17	3.5	6811	3	US-08-651-472-67	Sequence 67, Appl	15	3.1	1272	2	US-08-869-037-1	Sequence 1, Appl
C 141	17	3.5	6811	4	US-08-358-928-67	Sequence 67, Appl	15	3.1	1296	2	US-08-401-068-3	Sequence 3, Appl
C 142	17	3.5	6926	3	US-08-651-472-69	Sequence 69, Appl	15	3.1	1296	2	US-08-846-338-3	Sequence 3, Appl
C 143	17	3.5	6926	4	US-08-358-928-69	Sequence 69, Appl	15	3.1	1323	4	US-08-307-499-36	Sequence 36, Appl
C 144	17	3.5	7218	1	US-08-232-463-14	Sequence 14, Appl	15	3.1	1323	4	US-09-299-268-36	Sequence 36, Appl
C 145	17	3.5	9890	1	US-08-232-463-18	Sequence 18, Appl	15	3.1	1551	4	US-09-197-063-1	Sequence 1, Appl
C 146	17	3.5	9916	1	US-08-232-463-17	Sequence 17, Appl	15	3.1	1650	2	US-08-500-635A-11	Sequence 11, Appl
C 147	17	3.5	9917	1	US-08-232-463-16	Sequence 16, Appl	15	3.1	1650	4	US-09-167-151-11	Sequence 11, Appl
C 148	17	3.5	10408	1	US-08-232-463-6	Sequence 6, Appl	15	3.1	1749	1	US-07-649-591B-2	Sequence 2, Appl
C 149	17	3.5	10408	1	US-08-232-463-7	Sequence 7, Appl	15	3.1	1749	1	US-08-277-540-2	Sequence 2, Appl
C 150	17	3.5	13910	4	US-09-263-933-1	Sequence 1, Appl	15	3.1	1749	1	US-08-430-787A-2	Sequence 2, Appl
C 151	17	3.5	13910	4	US-09-263-933-8	Sequence 8, Appl	15	3.1	1789	2	US-08-895-521-2	Sequence 2, Appl
C 152	17	3.5	13910	4	US-09-263-933-15	Sequence 15, Appl	15	3.1	1789	3	US-09-235-218-2	Sequence 2, Appl
C 153	17	3.5	13999	3	US-08-444-644-24	Sequence 24, Appl	15	3.1	1794	3	US-09-012-515A-13	Sequence 13, Appl
C 154	17	3.5	13999	4	US-08-232-463A-24	Sequence 24, Appl	15	3.1	1794	3	US-08-360-144A-13	Sequence 13, Appl
C 155	16	3.3	18	2	US-09-200-141-27	Sequence 27, Appl	15	3.1	1794	5	PCT-US95-06722-13	Sequence 13, Appl
C 156	16	3.3	383	4	US-09-020-956-166	Sequence 166, App	15	3.1	1803	1	US-08-021-608D-7	Sequence 7, Appl
C 157	16	3.3	383	4	US-09-030-607-166	Sequence 166, App	15	3.1	1803	1	US-08-726-160-7	Sequence 7, Appl
C 158	16	3.3	383	4	US-09-439-313-166	Sequence 166, App	15	3.1	1803	5	PCT-US94-01782-7	Sequence 7, Appl
C 159	16	3.3	444	3	US-08-545-196B-2	Sequence 2, Appl	15	3.1	1817	1	US-08-179-738-1	Sequence 1, Appl
C 160	16	3.3	444	3	US-08-545-196B-4	Sequence 4, Appl	15	3.1	1817	2	US-08-628-145-1	Sequence 1, Appl
C 161	16	3.3	709	1	US-08-469-667-12	Sequence 12, Appl	15	3.1	1833	1	US-08-179-738-6	Sequence 6, Appl
C 162	16	3.3	709	4	US-09-224-110-12	Sequence 12, Appl	15	3.1	1833	2	US-08-628-145-6	Sequence 6, Appl
C 163	16	3.3	709	5	PCT-US95-07289-12	Sequence 12, Appl	15	3.1	1862	1	US-08-179-738-4	Sequence 4, Appl
C 164	16	3.3	1315	1	US-08-741-406-1	Sequence 1, Appl	15	3.1	1862	2	US-08-628-145-4	Sequence 4, Appl
C 165	16	3.3	1315	3	US-09-024-472-1	Sequence 1, Appl	15	3.1	1993	4	US-09-148-680-1	Sequence 1, Appl
C 166	16	3.3	1408	3	US-08-545-196B-11	Sequence 11, Appl	15	3.1	2056	4	US-09-334-601-12	Sequence 12, Appl
C 167	16	3.3	1408	3	US-08-545-196B-13	Sequence 13, Appl	15	3.1	2100	1	US-08-332-576-1	Sequence 1, Appl
C 168	16	3.3	1590	3	US-08-747-221B-23	Sequence 23, Appl	15	3.1	2100	5	PCT-US95-13672-1	Sequence 1, Appl
C 169	16	3.3	1590	4	US-09-005-051-23	Sequence 23, Appl	15	3.1	2262	3	US-09-276-400-3	Sequence 3, Appl
C 170	16	3.3	1650	3	US-08-747-221B-21	Sequence 21, Appl	15	3.1	2262	4	US-09-448-076-3	Sequence 3, Appl
C 171	16	3.3	1650	3	US-08-747-221B-22	Sequence 22, Appl	15	3.1	2381	1	US-08-021-608D-9	Sequence 9, Appl
C 172	16	3.3	1650	4	US-09-005-051-21	Sequence 21, Appl	15	3.1	2381	1	US-08-726-160-9	Sequence 9, Appl
C 173	16	3.3	1650	4	US-09-005-051-22	Sequence 22, Appl	15	3.1	2381	5	PCT-US94-01782-9	Sequence 9, Appl

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249	15	3.1	2384	5	PCT-US94-01782-1	Sequence 1, Appli	c 322	14	2.9	367	3	US-09-040-699A-2	Sequence 2, Appli
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257	15	3.1	2920	3	US-09-276-400-1	Sequence 3, Appli	c 330	14	2.9	499	1	US-08-650-528-8	Sequence 8, Appli
258	15	3.1	2920	4	US-09-448-076-1	Sequence 1, Appli	c 331	14	2.9	499	3	US-09-060-584-8	Sequence 8, Appli
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264	15	3.1	3264	4	US-09-262-773-5	Sequence 5, Appli	c 337	14	2.9	573	1	US-08-847-429A-21	Sequence 21, Appli
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266	15	3.1	3319	2	US-08-960-022-19	Sequence 19, Appli	c 339	14	2.9	573	3	US-09-065-474-21	Sequence 21, Appli
267	15	3.1	3378	1	US-08-261-206A-76	Sequence 76, Appli	c 340	14	2.9	584	1	US-08-054-985-2	Sequence 2, Appli
268	15	3.1	3872	5	PCT-US93-12169-1	Sequence 1, Appli	c 341	14	2.9	595	4	US-09-276-531-63	Sequence 63, Appli
269	15	3.1	3879	4	US-08-916-352-1	Sequence 1, Appli	c 342	14	2.9	605	4	US-09-385-982-501	Sequence 501, App
270	15	3.1	4743	3	US-09-339-964-1	Sequence 1, Appli	c 343	14	2.9	612	3	US-08-906-769-146	Sequence 146, App
271	15	3.1	4970	1	US-08-764-100-14	Sequence 14, Appli	c 344	14	2.9	612	3	US-08-906-769-146	Sequence 146, App
272	15	3.1	4970	1	US-08-764-100-20	Sequence 20, Appli	c 345	14	2.9	612	3	US-08-639-075A-146	Sequence 146, App
273	15	3.1	5093	2	US-08-468-036-23	Sequence 23, Appli	c 346	14	2.9	612	4	US-09-012-431-146	Sequence 146, App
274	15	3.1	5093	2	US-08-376-843-23	Sequence 4, Appli	c 347	14	2.9	612	4	US-09-012-693-146	Sequence 146, App
275	15	3.1	5110	2	US-08-404-531B-5	Sequence 5, Appli	c 348	14	2.9	612	4	US-08-906-613-146	Sequence 146, App
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279	15	3.1	5110	3	US-08-488-546A-5	Sequence 3, Appli	c 352	14	2.9	651	1	US-08-998-416-173	Sequence 173, App
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281	15	3.1	5232	3	US-09-617-053A-3	Sequence 3, Appli	c 354	14	2.9	680	4	US-08-998-416-739	Sequence 739, App
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283	15	3.1	5632	3	US-09-560-594-3	Sequence 1, Appli	c 356	14	2.9	686	2	US-08-522-421-7	Sequence 1140, Ap
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314	14	2.9	183	3	US-08-513-974B-306	Sequence 306, App	c 387	14	2.9	1048	3	US-09-065-474-138	Sequence 138, App
315	14	2.9	211	3	US-08-513-974B-307	Sequence 307, App	c 388	14	2.9	1056	3	US-09-065-474-140	Sequence 140, App
316	14	2.9	211	3	US-08-248-474-95	Sequence 95, Appli	c 389	14	2.9	1056	3	US-08-476-102A-8	Sequence 8, Appli
317	14	2.9	256	4	US-08-756-849-95	Sequence 95, Appli	c 390	14	2.9	1078	4	US-09-492-543-28	Sequence 28, Appli
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319	14	2.9	331	3	US-08-171-385-1	Sequence 1, Appli	c 392	14	2.9	1078	4	US-09-492-543-29	Sequence 29, Appli
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C 393	14	2.9	1111	3	US-09-267-031-15	Sequence 15, Appl	466	14	2.9	1811	3	US-09-050-603A-9	Sequence 9, Appl
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C 395	14	2.9	1174	2	US-08-477-504A-39	Sequence 39, Appl	468	14	2.9	1811	4	US-09-497-698-9	Sequence 9, Appl
C 396	14	2.9	1174	2	US-08-486-756A-39	Sequence 39, Appl	469	14	2.9	1826	4	US-09-286-691-11	Sequence 11, Appl
C 397	14	2.9	1174	2	US-08-485-862B-39	Sequence 39, Appl	470	14	2.9	1826	4	US-09-687-147-11	Sequence 11, Appl
C 398	14	2.9	1174	3	US-08-787-739-39	Sequence 39, Appl	C 471	14	2.9	1830	2	US-08-933-750C-79	Sequence 79, Appl
C 399	14	2.9	1174	3	US-08-487-077A-39	Sequence 39, Appl	C 472	14	2.9	1830	3	US-09-234-613-79	Sequence 6, Appl
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C 401	14	2.9	1174	4	US-08-485-049D-39	Sequence 39, Appl	474	14	2.9	1855	3	US-09-150-141-6	Sequence 6, Appl
C 402	14	2.9	1174	4	US-09-178-115-39	Sequence 39, Appl	475	14	2.9	1855	4	US-09-374-493-6	Sequence 6, Appl
C 403	14	2.9	1174	4	US-09-177-776-39	Sequence 39, Appl	476	14	2.9	1855	4	US-09-374-824-6	Sequence 6, Appl
C 404	14	2.9	1189	1	US-08-307-581-2	Sequence 2, Appl	477	14	2.9	1855	4	US-08-313-842-1	Sequence 6, Appl
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C 407	14	2.9	1227	1	US-09-031-485-17	Sequence 17, Appl	480	14	2.9	1935	2	US-08-328-322-9	Sequence 9, Appl
C 408	14	2.9	1227	1	US-09-031-485-18	Sequence 18, Appl	481	14	2.9	1964	1	US-08-961-083-203	Sequence 203, App
C 409	14	2.9	1227	1	US-08-847-429A-17	Sequence 17, Appl	482	14	2.9	1972	3	US-08-811-949-38	Sequence 38, Appl
C 410	14	2.9	1227	1	US-08-847-429A-18	Sequence 18, Appl	C 483	14	2.9	1974	2	US-09-052-089A-7	Sequence 7, Appl
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C 412	14	2.9	1227	3	US-09-065-474-18	Sequence 18, Appl	C 485	14	2.9	2019	2	5187089-1	Sequence 46, Appl
C 413	14	2.9	1228	1	US-09-065-474-18	Sequence 18, Appl	C 486	14	2.9	2019	2	5187089-1	Sequence 46, Appl
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C 422	14	2.9	1257	5	PCT-US94-00238-1	Sequence 5, Appl	C 495	14	2.9	2032	6	5187089-1	Sequence 46, Appl
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C 442	14	2.9	1660	3	US-08-957-742-2	Sequence 2, Appl	C 515	14	2.9	2032	6	5187089-1	Sequence 46, Appl
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C 452	14	2.9	1784	3	US-08-808-323-19	Sequence 19, Appl	C 525	14	2.9	2032	6	5187089-1	Sequence 46, Appl
C 453	14	2.9	1784	3	US-09-050-603A-19	Sequence 19, Appl	C 526	14	2.9	2032	6	5187089-1	Sequence 46, Appl
C 454	14	2.9	1784	4	US-09-102-420B-19	Sequence 19, Appl	C 527	14	2.9	2032	6	5187089-1	Sequence 46, Appl
C 455	14	2.9	1784	4	US-09-497-698-19	Sequence 19, Appl	C 528	14	2.9	2032	6	5187089-1	Sequence 46, Appl
C 456	14	2.9	1791	1	US-08-245-294-7	Sequence 7, Appl	C 529	14	2.9	2032	6	5187089-1	Sequence 46, Appl
C 457	14	2.9	1791	1	US-08-474-499-7	Sequence 7, Appl	C 530	14	2.9	2032	6	5187089-1	Sequence 46, Appl
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C 465	14	2.9	1811	3	US-08-808-323-9	Sequence 9, Appl	C 538	14	2.9	2032	6	5187089-1	Sequence 46, Appl

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c 543	14	2.9	2883	2	US-08-742-923A-7	Sequence 7, Appli	616	14	2.9	4483	2	US-08-456-240-5	Sequence 5, Appli
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c 547	14	2.9	2960	3	US-08-913-842-3	Sequence 3, Appli	620	14	2.9	4529	1	US-08-565-386-1	Sequence 1, Appli
c 548	14	2.9	3000	1	US-07-841-997A-3	Sequence 3, Appli	621	14	2.9	4619	2	US-08-874-186-38	Sequence 38, Appli
c 549	14	2.9	3000	1	US-08-290-301-3	Sequence 3, Appli	622	14	2.9	4766	5	PCT-US93-07261-10	Sequence 10, Appli
c 550	14	2.9	3065	1	US-08-156-866-1	Sequence 1, Appli	623	14	2.9	4817	2	US-07-951-715A-18	Sequence 18, Appli
c 551	14	2.9	3092	1	US-08-426-627-3	Sequence 3, Appli	624	14	2.9	4817	2	US-08-459-448A-18	Sequence 18, Appli
c 552	14	2.9	3095	6	5231168-1	Patent No. 5231168	625	14	2.9	4817	3	US-08-459-595A-18	Sequence 18, Appli
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c 554	14	2.9	3104	1	US-08-371-320-1	Sequence 1, Appli	627	14	2.9	4817	4	US-08-459-444-18	Sequence 18, Appli
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c 561	14	2.9	3328	1	US-08-159-340A-1	Sequence 1, Appli	634	14	2.9	5235	1	US-09-031-485-36	Sequence 36, Appli
c 562	14	2.9	3337	2	US-08-072-610-1	Sequence 1, Appli	635	14	2.9	5235	1	US-08-847-429A-35	Sequence 35, Appli
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c 564	14	2.9	3337	4	US-09-092-458-1	Sequence 1, Appli	637	14	2.9	5235	3	US-09-065-474-35	Sequence 35, Appli
c 565	14	2.9	3381	3	US-08-937-195-1	Sequence 1, Appli	638	14	2.9	5235	3	US-09-065-474-36	Sequence 36, Appli
c 566	14	2.9	3381	3	US-08-937-195-2	Sequence 2, Appli	639	14	2.9	5407	4	US-09-269-040-7	Sequence 7, Appli
c 567	14	2.9	3381	4	US-08-915-152-1	Sequence 1, Appli	640	14	2.9	5503	1	US-09-031-485-32	Sequence 32, Appli
c 568	14	2.9	3381	4	US-08-915-152-2	Sequence 2, Appli	641	14	2.9	5503	1	US-09-031-485-34	Sequence 34, Appli
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c 725	14	2.9	4403765	4	US-09-103-840A-2	Sequence 2, Appli	c 796	13	2.7	117	1	US-08-239-498A-41	Sequence 41, Appl
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c 732	13	2.7	19	2	US-08-331-389A-33	Sequence 33, Appl	c 803	13	2.7	157	1	US-08-457-304A-11	Sequence 11, Appl
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c 833	13	2.7	271	2	US-08-458-109-18	Sequence 18, Appl	c 906	13	2.7	538	1	US-08-525-507-13	Sequence 13, Appl
c 834	13	2.7	271	3	US-08-231-196-18	Sequence 18, Appl	c 907	13	2.7	542	4	US-09-305-639-5	Sequence 5, Appl
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ALIGNMENTS

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; Sequence 1, Application US/08031399  
; Patent No. 5552303  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: Epithelium-derived T-cell Factor  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/031,399  
; FILING DATE: 19930308  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Launer, Charlene  
; REGISTRATION NUMBER: 33,035  
; REFERENCE/DOCKET NUMBER: 2811  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-587-0430  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
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; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/393,305  
; FILING DATE: 22-FEB-1995

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; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET INFORMATION: 480052.409C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..489
; US-08-393-305-4

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Best Local Similarity 100.0%; Pred. No. 3.7e-235;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 4, Application US/08726817
; Patent No. 5707616
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Anderson, Dirk
; APPLICANT: Eisenman, June
; APPLICANT: Fung, Victor
; APPLICANT: Rauch, Charles
; TITLE OF INVENTION: EPIPHILIUM-DERIVED T-CELL FACTOR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
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; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726.817
; FILING DATE: 04-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/393,305
; FILING DATE: 22-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 480052.409C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..489
; US-08-726-817-4
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Best Local Similarity 100.0%; Pred. No. 3.7e-235;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 301 GAGTCGGAGATACAGATATTTATGATACAGTAAAGTCTTATATACAGAAAGTGATTCAC 360
DB 301 GAGTCGGAGATACAGATATTTATGATACAGTAAAGTCTTATATACAGAAAGTGATTCAC 360
QY 361 ATCTTGTCTTCTAATGGGAATATAACAGAAATCTGGATGCAAGAAATGTGAGGAAC 420
DB 361 ATCTTGTCTTCTAATGGGAATATAACAGAAATCTGGATGCAAGAAATGTGAGGAAC 420
QY 421 GAAAAAATATTAAAGAAATTTTTCAGAGTTTGTACATATTTCCAAATGTTTCATCAAC 480
DB 421 GAAAAAATATTAAAGAAATTTTTCAGAGTTTGTACATATTTCCAAATGTTTCATCAAC 480
QY 481 ACTTCTTGA 489
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Db 481 ACTTCTTGA 489
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RESULT 4
US-08-504-042-1
; Sequence 1, Application US/08504042
; Patent No. 5747024
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Anderson, Dirk
; APPLICANT: Eisenman, June
; APPLICANT: Fung, Victor
; APPLICANT: Rauch, Charles
; TITLE OF INVENTION: Epithelium-derived T-cell Factor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/504,042
; FILING DATE: 19-JUL-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/031,399
; FILING DATE: 08-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Launer, Charlene
; REGISTRATION NUMBER: 33,035
; REFERENCE/DOCKET NUMBER: 2811
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..489
US-08-504-042-1

Query Match 100.0%; Score 489; DB 1; Length 489;
Best Local Similarity 100.0%; Pred. No. 3.7e-235;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAACACCATTTGAGAGTATTTCCATCCAGTGCCTACTGTGTTACTT 60
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Db 1 ATGAGATTTCGAACACCATTTGAGAGTATTTCCATCCAGTGCCTACTGTGTTACTT 60
|||||
QY 61 CTAAGAGTCATTTTCTAACTGAAGCTGCATTCATGTCTTTCATTTGGGCTGTTTCAGT 120
|||||
Db 61 CTAAGAGTCATTTTCTAACTGAAGCTGCATTCATGTCTTTCATTTGGGCTGTTTCAGT 120
|||||
QY 121 GCAGGGCTCCCTAAACAGACCCCAACTGGGTGAATGTAATTAAGTATTTGAAAAAAT 180
|||||
Db 121 GCAGGGCTCCCTAAACAGACCCCAACTGGGTGAATGTAATTAAGTATTTGAAAAAAT 180
|||||
QY 181 GAAGATCTTATTCAATCTATGCTATTTATGCTACTTTATATACAGAAAGTATGTTCCAC 240
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Db 181 GAAGATCTTATTCAATCTATGCTATTTATGCTACTTTATATACAGAAAGTATGTTCCAC 240
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QY 241 CCCAGTTGCAAGGTAACAGCAATGAAGTCTTCTCTTGGAGTTGCAAGTTATTTTCACAT 300
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Db 241 CCCAGTTGCAAGGTAACAGCAATGAAGTCTTCTCTTGGAGTTGCAAGTTATTTTCACAT 300
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QY 301 GAGTCGGGAGATACAGATATTTCATGATACAGTAGAGAAAAATCTTATCATCTAGCAACAAC 360
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Db 301 GAGTCGGGAGATACAGATATTTCATGATACAGTAGAGAAAAATCTTATCATCTAGCAACAAC 360
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QY 361 ATCTTGTCTTCTAAATGGGAATATAACAGAAATCTGGATGCAAGAAATGTCAGGAAGTACAG 420
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Db 361 ATCTTGTCTTCTAAATGGGAATATAACAGAAATCTGGATGCAAGAAATGTCAGGAAGTACAG 420
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QY 421 GAAAAAATATTAAAGAAATTTTTCAGAGATTTTGTACATATTTGTCCAAATGTTTCATCAAC 480
|||||
Db 421 GAAAAAATATTAAAGAAATTTTTCAGAGATTTTGTACATATTTGTCCAAATGTTTCATCAAC 480
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QY 481 ACTTCTTGA 489
|||||
Db 481 ACTTCTTGA 489
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RESULT 5
US-08-392-317B-1
; Sequence 1, Application US/08392317B
; Patent No. 5795966
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Paxton, Raymond
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Antagonists of IL-15
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Word for Windows 95, 7.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/392,317B
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..342
US-08-392-317B-1

Query Match 100.0%; Score 489; DB 1; Length 489;
Best Local Similarity 100.0%; Pred. No. 3.7e-235;
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Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAACACCAATTTGAGAAGTATTTCCATCCAGTGTCTACCTGTTTACTT 60  
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Db 1 ATGAGAAATTCGAACACCAATTTGAGAAGTATTTCCATCCAGTGTCTACCTGTTTACTT 60  
|||||  
QY 61 CTAAGAGTCATTTCTTAAGTGGCATTGCTTCTTCAATTTGGGCTGTTTCAGT 120  
|||||  
Db 61 CTAAGAGTCATTTCTTAAGTGGCATTGCTTCTTCAATTTGGGCTGTTTCAGT 120  
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QY 121 GCAGGGCTCCCTAAACAGAACCCAACTGGGTGAATGTAATAGTCAATTTGAAAAAATT 180  
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Db 121 GCAGGGCTCCCTAAACAGAACCCAACTGGGTGAATGTAATAGTCAATTTGAAAAAATT 180  
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QY 181 GAAGATCTTATTCAATCTATGATATTTGATGCTACTTTATATACAGAAAGTGTTCAC 240  
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Db 181 GAAGATCTTATTCAATCTATGATATTTGATGCTACTTTATATACAGAAAGTGTTCAC 240  
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QY 241 CCCAGTTGCAAGGTAACAGCAATGAAGTGTCTTCTTGGAGTTGCAAGTTATTTTCACAT 300  
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Db 241 CCCAGTTGCAAGGTAACAGCAATGAAGTGTCTTCTTGGAGTTGCAAGTTATTTTCACAT 300  
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QY 301 GAGTCGGAGATACAGATATTCATGATACAGTAGAAAAATCTTATCATCCTAGCAACAAC 360  
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Db 301 GAGTCGGAGATACAGATATTCATGATACAGTAGAAAAATCTTATCATCCTAGCAACAAC 360  
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QY 361 ATCTTGTCTTCTTAATGGGAATATAACAGAACTCTGGATGCAAGAAATGTGAGGAAC TAGAG 420  
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Db 361 ATCTTGTCTTCTTAATGGGAATATAACAGAACTCTGGATGCAAGAAATGTGAGGAAC TAGAG 420  
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QY 421 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTTGTCCAAATGTTTCATCAAC 480  
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Db 421 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTTGTCCAAATGTTTCATCAAC 480  
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QY 481 ACTTCTTGA 489  
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Db 481 ACTTCTTGA 489  
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RESULT 6  
US-08-725-969-4  
; Sequence 4, Application US/08725969  
; Patent No. 5892001  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/725,969  
; FILING DATE: 04-OCT-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/393,305  
; FILING DATE: 22-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963

; REFERENCE/DOCKET NUMBER: 480052.409C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-622-4900  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..489  
US-08-725-969-4

Query Match 100.0%; Score 489; DB 2; Length 489;  
Best Local Similarity 100.0%; Pred. No. 3.7e-235;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAACACCAATTTGAGAAGTATTTCCATCCAGTGTCTACCTGTTTACTT 60  
|||||  
Db 1 ATGAGAAATTCGAACACCAATTTGAGAAGTATTTCCATCCAGTGTCTACCTGTTTACTT 60  
|||||  
QY 61 CTAAGAGTCATTTCTTAAGTGGCATTGCTTCTTCAATTTGGGCTGTTTCAGT 120  
|||||  
Db 61 CTAAGAGTCATTTCTTAAGTGGCATTGCTTCTTCAATTTGGGCTGTTTCAGT 120  
|||||  
QY 121 GCAGGGCTCCCTAAACAGAACCCAACTGGGTGAATGTAATAGTCAATTTGAAAAAATT 180  
|||||  
Db 121 GCAGGGCTCCCTAAACAGAACCCAACTGGGTGAATGTAATAGTCAATTTGAAAAAATT 180  
|||||  
QY 181 GAAGATCTTATTCAATCTATGATATTTGATGCTACTTTATATACAGAAAGTGTTCAC 240  
|||||  
Db 181 GAAGATCTTATTCAATCTATGATATTTGATGCTACTTTATATACAGAAAGTGTTCAC 240  
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QY 241 CCCAGTTGCAAGGTAACAGCAATGAAGTGTCTTCTTGGAGTTGCAAGTTATTTTCACAT 300  
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Db 241 CCCAGTTGCAAGGTAACAGCAATGAAGTGTCTTCTTGGAGTTGCAAGTTATTTTCACAT 300  
|||||  
QY 301 GAGTCGGAGATACAGATATTCATGATACAGTAGAAAAATCTTATCATCCTAGCAACAAC 360  
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Db 301 GAGTCGGAGATACAGATATTCATGATACAGTAGAAAAATCTTATCATCCTAGCAACAAC 360  
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QY 361 ATCTTGTCTTCTTAATGGGAATATAACAGAACTCTGGATGCAAGAAATGTGAGGAAC TAGAG 420  
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Db 361 ATCTTGTCTTCTTAATGGGAATATAACAGAACTCTGGATGCAAGAAATGTGAGGAAC TAGAG 420  
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QY 421 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTTGTCCAAATGTTTCATCAAC 480  
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Db 421 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTTGTCCAAATGTTTCATCAAC 480  
|||||  
QY 481 ACTTCTTGA 489  
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Db 481 ACTTCTTGA 489  
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RESULT 7  
US-08-794-524-4  
; Sequence 4, Application US/08794524  
; Patent No. 5985262  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington

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/ COUNTRY: USA
/ ZIP: 98104
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/794,524
/ FILING DATE: 03-FEB-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/393,305
/ FILING DATE: 22-FEB-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McMasters, David D.
/ REGISTRATION NUMBER: 33,963
/ REFERENCE/DOCKET NUMBER: 480052.409C2
/ TELEPHONE: 206-622-4900
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 489 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..489
/ US-08-794-524-4

Query Match 100.0%; Score 489; DB 2; Length 489;
Best Local Similarity 100.0%; Pred. No. 3.7e-235;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACCAACATTTGAGAAGTATTTCATCCAGTGCCTGCTGTGTACTT 60
Db 1 ATGAGAAATTCGAAACCAACATTTGAGAAGTATTTCATCCAGTGCCTGCTGTGTACTT 60
QY 61 CTAAGAGTCATTTCTAACTGAAGTGGCATTTCATGCTTCTCATTTGGGCTGTTTCAGT 120
Db 61 CTAAGAGTCATTTCTAACTGAAGTGGCATTTCATGCTTCTCATTTGGGCTGTTTCAGT 120
QY 121 GCAGGGCTCCCTAAACACAGAACCCAACTGGGTGAATGTAATAGTGATTTGAAAAAATT 180
Db 121 GCAGGGCTCCCTAAACACAGAACCCAACTGGGTGAATGTAATAGTGATTTGAAAAAATT 180
QY 181 GAAGATCTTTATTCATCTATGCATATTGATGCTACTTTATATACAGAAAGTGATGTTCA 240
Db 181 GAAGATCTTTATTCATCTATGCATATTGATGCTACTTTATATACAGAAAGTGATGTTCA 240
QY 241 CCCAGTGCAGGTAAACAGCAATGGAATGCTTCTCTTGGAGTTGCAAGTTATTTTCACAT 300
Db 241 CCCAGTGCAGGTAAACAGCAATGGAATGCTTCTCTTGGAGTTGCAAGTTATTTTCACAT 300
QY 301 GAGTCGGAGATACAGATATTTCATGATACAGTAGAAAAATCTTATCATCTAGCAAAACAC 360
Db 301 GAGTCGGAGATACAGATATTTCATGATACAGTAGAAAAATCTTATCATCTAGCAAAACAC 360
QY 361 ATCTGCTCTTCTAATGGGAATATAACAGAACTGATGCTGATGCAAGAAATGAGGAACTAG 420
Db 361 ATCTGCTCTTCTAATGGGAATATAACAGAACTGATGCTGATGCAAGAAATGAGGAACTAG 420
QY 421 GAAAAAATATTAAAGAAATTTTGGCAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480
Db 421 GAAAAAATATTAAAGAAATTTTGGCAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480
QY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489
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RESULT 8
US-09-134-132-1
/ Sequence 1, Application US/09134132
/ Patent No. 6013480
/ GENERAL INFORMATION:
/ APPLICANT: Grabstein, Kenneth
/ APPLICANT: Paxton, Raymond
/ APPLICANT: Pettit, Dean
/ TITLE OF INVENTION: Antagonists of IL-15
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Immunex Corporation
/ STREET: 51 University Street
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: USA
/ ZIP: 98101
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC Compatible
/ OPERATING SYSTEM: Word for Windows 95, 7.0
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/134,132
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/392,317
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Malaska, Stephen L.
/ REGISTRATION NUMBER: 32,655
/ REFERENCE/DOCKET NUMBER: 2831
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-587-0430
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 489 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..342
/ US-09-134-132-1

Query Match 100.0%; Score 489; DB 3; Length 489;
Best Local Similarity 100.0%; Pred. No. 3.7e-235;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACCAACATTTGAGAAGTATTTCATCCAGTGCCTGCTGTGTACTT 60
Db 1 ATGAGAAATTCGAAACCAACATTTGAGAAGTATTTCATCCAGTGCCTGCTGTGTACTT 60
QY 61 CTAAGAGTCATTTCTAACTGAAGTGGCATTTCATGCTTCTCATTTGGGCTGTTTCAGT 120
Db 61 CTAAGAGTCATTTCTAACTGAAGTGGCATTTCATGCTTCTCATTTGGGCTGTTTCAGT 120
QY 121 GCAGGGCTCCCTAAACACAGAACCCAACTGGGTGAATGTAATAGTGATTTGAAAAAATT 180
Db 121 GCAGGGCTCCCTAAACACAGAACCCAACTGGGTGAATGTAATAGTGATTTGAAAAAATT 180
QY 181 GAAGATCTTTATTCATCTATGCATATTGATGCTACTTTATATACAGAAAGTGATGTTCA 240
Db 181 GAAGATCTTTATTCATCTATGCATATTGATGCTACTTTATATACAGAAAGTGATGTTCA 240
QY 241 CCCAGTGCAGGTAAACAGCAATGGAATGCTTCTCTTGGAGTTGCAAGTTATTTTCACAT 300
Db 241 CCCAGTGCAGGTAAACAGCAATGGAATGCTTCTCTTGGAGTTGCAAGTTATTTTCACAT 300
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QY 301 GAGTCGGAGATACAGATATTCATGATACAGTAGAGAAATCTTATCATCTAGCAACAAC 360  
DB 301 GAGTCGGAGATACAGATATTCATGATACAGTAGAGAAATCTTATCATCTAGCAACAAC 360  
QY 361 ATCTTCTCTCTTAATGGGAATATAACAGAAATCTGGATGCAAGAAATGTGAGGAACCTAGAG 420  
DB 361 ATCTTCTCTCTTAATGGGAATATAACAGAAATCTGGATGCAAGAAATGTGAGGAACCTAGAG 420  
QY 421 GAAAAAATATTAAAGAAATTTTGGAGAGTTTGTGATACATATTTGTCCTCAATGTTTCATCAAC 480  
DB 421 GAAAAAATATTAAAGAAATTTTGGAGAGTTTGTGATACATATTTGTCCTCAATGTTTCATCAAC 480  
QY 481 ACTTCTTGA 489  
DB 481 ACTTCTTGA 489

RESULT 9  
US-09-134-134A-1  
; Sequence 1, Application US/09134134A  
; Patent No. 6165466  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Paxton, Raymond  
; APPLICANT: Pettit, Dean  
; TITLE OF INVENTION: Antagonists of IL-15  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: Word for Windows 95, 7.0  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: 08/392,317  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Malaska, Stephen L.  
; REGISTRATION NUMBER: 32,655  
; REFERENCE/DOCKET NUMBER: 2831  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-587-0430  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..342  
; US-09-134-134A-1

Query Match 100.0%; Score 489; DB 4; Length 489;  
Best Local Similarity 100.0%; Pred. No. 3.7e-235; Indels 0; Gaps 0;  
Matches 489; Conservative 0; Mismatches 0;  
QY 1 ATGAGAATTTGGAACACACATTTGAGAAGTATTTCCATCCAGTGCTACCTGTGTTACTT 60

DB 1 ATGAGAATTTGGAACACACATTTGAGAAGTATTTCCATCCAGTGCTACCTGTGTTACTT 60  
QY 61 CTAAAGAGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCAATTTTGGGCTGTTTCAGT 120  
DB 61 CTAAAGAGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCAATTTTGGGCTGTTTCAGT 120  
QY 121 GCAGGCTCCCTAAAACAGAGCCAACTGGTGAATGTAATAAGTGATTTGAAAAAAAT 180  
DB 121 GCAGGCTCCCTAAAACAGAGCCAACTGGTGAATGTAATAAGTGATTTGAAAAAAAT 180  
QY 181 GAAGATCTTATTTCAATCTATGTCATATTTGATGCTACTTTATATACAGAAAGTGATTTCAAC 240  
DB 181 GAAGATCTTATTTCAATCTATGTCATATTTGATGCTACTTTATATACAGAAAGTGATTTCAAC 240  
QY 241 CCCAGTTGCAAGTAACAGCAATGAAGTGCTTTCTCTTGGAGTTGCAAGTTATTTTACAT 300  
DB 241 CCCAGTTGCAAGTAACAGCAATGAAGTGCTTTCTCTTGGAGTTGCAAGTTATTTTACAT 300  
QY 301 GAGTCGGAGATACAGATATTCATGATACAGTAGAGAAATCTTATCATCTAGCAACAAC 360  
DB 301 GAGTCGGAGATACAGATATTCATGATACAGTAGAGAAATCTTATCATCTAGCAACAAC 360  
QY 361 ATCTTCTCTCTTAATGGGAATATAACAGAAATCTGGATGCAAGAAATGTGAGGAACCTAGAG 420  
DB 361 ATCTTCTCTCTTAATGGGAATATAACAGAAATCTGGATGCAAGAAATGTGAGGAACCTAGAG 420  
QY 421 GAAAAAATATTAAAGAAATTTTGGAGAGTTTGTGATACATATTTGTCCTCAATGTTTCATCAAC 480  
DB 421 GAAAAAATATTAAAGAAATTTTGGAGAGTTTGTGATACATATTTGTCCTCAATGTTTCATCAAC 480  
QY 481 ACTTCTTGA 489  
DB 481 ACTTCTTGA 489

RESULT 10  
US-09-134-456-1  
; Sequence 1, Application US/09134456  
; Patent No. 6168783  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Paxton, Raymond  
; APPLICANT: Pettit, Dean  
; TITLE OF INVENTION: Antagonists of IL-15  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: Word for Windows 95, 7.0  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: 08/392,317  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Malaska, Stephen L.  
; REGISTRATION NUMBER: 32,655  
; REFERENCE/DOCKET NUMBER: 2831  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-587-0430  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..342  
; US-09-134-134A-1

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;
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..342
US-09-134-456-1

Query Match          100.0%; Score 489; DB 4; Length 489;
Best Local Similarity 100.0%; Pred. No. 3.7e-235;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAATTCGAAACACACATTTGAGAAGTATTTCCATCCAGTGTACCTGTGTTACTT 60
Db 1 ATGAGAATTCGAAACACACATTTGAGAAGTATTTCCATCCAGTGTACCTGTGTTACTT 60
QY 61 CTAAGAGTCTATTTCTAACTGAAGCTGGCATTCATCTCTCATTTTGGGCTGTTTCAGT 120
Db 61 CTAAGAGTCTATTTCTAACTGAAGCTGGCATTCATCTCTCATTTTGGGCTGTTTCAGT 120
QY 121 GCAGGGCTCCCTAAACAGAGCCAACTGGGTGAATGTAATAAGTGAATTTGAAAAAATT 180
Db 121 GCAGGGCTCCCTAAACAGAGCCAACTGGGTGAATGTAATAAGTGAATTTGAAAAAATT 180
QY 181 GAAGATCTTATTCATCTATTCATATTCATATTCATATTCATATTCATATTCATATTC 240
Db 181 GAAGATCTTATTCATCTATTCATATTCATATTCATATTCATATTCATATTCATATTC 240
QY 241 CCCAGTTGCAAGGTAACAGCAATGAAGTGTCTTCTTGGAGTTGCAAGTTATTTTCACAT 300
Db 241 CCCAGTTGCAAGGTAACAGCAATGAAGTGTCTTCTTGGAGTTGCAAGTTATTTTCACAT 300
QY 301 GAGTCCGGAGATACAGATATTCATGATACAGTACAGTACAGTACAGTACAGTACAGTAC 360
Db 301 GAGTCCGGAGATACAGATATTCATGATACAGTACAGTACAGTACAGTACAGTACAGTAC 360
QY 361 ATCTTGCTCTTAATGGGAATATACAGAACTCTGGAATGGAATGGAATGGAATGGAATG 420
Db 361 ATCTTGCTCTTAATGGGAATATACAGAACTCTGGAATGGAATGGAATGGAATGGAATG 420
QY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGTCACATATTTGCCAAATGTTCAACAAC 480
Db 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGTCACATATTTGCCAAATGTTCAACAAC 480
QY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489

RESULT 11
US-09-196-427-1
; Sequence 1, Application US/09196427
; Patent No. 6177079
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Paxton, Raymond
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Antagonists of IL-15
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Word for Windows 95, 7.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/196,427
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/392,317
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..342
US-09-196-427-1
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Query Match          100.0%; Score 489; DB 4; Length 489;
Best Local Similarity 100.0%; Pred. No. 3.7e-235;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAATTCGAAACACACATTTGAGAAGTATTTCCATCCAGTGTACCTGTGTTACTT 60
Db 1 ATGAGAATTCGAAACACACATTTGAGAAGTATTTCCATCCAGTGTACCTGTGTTACTT 60
QY 61 CTAAGAGTCTATTTCTAACTGAAGCTGGCATTCATCTCTCATTTTGGGCTGTTTCAGT 120
Db 61 CTAAGAGTCTATTTCTAACTGAAGCTGGCATTCATCTCTCATTTTGGGCTGTTTCAGT 120
QY 121 GCAGGGCTCCCTAAACAGAGCCAACTGGGTGAATGTAATAAGTGAATTTGAAAAAATT 180
Db 121 GCAGGGCTCCCTAAACAGAGCCAACTGGGTGAATGTAATAAGTGAATTTGAAAAAATT 180
QY 181 GAAGATCTTATTCATCTATTCATATTCATATTCATATTCATATTCATATTCATATTC 240
Db 181 GAAGATCTTATTCATCTATTCATATTCATATTCATATTCATATTCATATTCATATTC 240
QY 241 CCCAGTTGCAAGGTAACAGCAATGAAGTGTCTTCTTGGAGTTGCAAGTTATTTTCACAT 300
Db 241 CCCAGTTGCAAGGTAACAGCAATGAAGTGTCTTCTTGGAGTTGCAAGTTATTTTCACAT 300
QY 301 GAGTCCGGAGATACAGATATTCATGATACAGTACAGTACAGTACAGTACAGTACAGTAC 360
Db 301 GAGTCCGGAGATACAGATATTCATGATACAGTACAGTACAGTACAGTACAGTACAGTAC 360
QY 361 ATCTTGCTCTTAATGGGAATATACAGAACTCTGGAATGGAATGGAATGGAATGGAATG 420
Db 361 ATCTTGCTCTTAATGGGAATATACAGAACTCTGGAATGGAATGGAATGGAATGGAATG 420
QY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGTCACATATTTGCCAAATGTTCAACAAC 480
Db 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGTCACATATTTGCCAAATGTTCAACAAC 480
QY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489

RESULT 12
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US-09-189-193-4  
; Sequence 4, Application US/09189193  
; Patent No. 6184359  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: EPIHELUM-DERIVED T-CELL FACTOR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/189,193  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/393,305  
; FILING DATE: 22-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 480052.409C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-622-4900  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..489  
US-09-189-193-4

Query Match 100.0%; Score 489; DB 4; Length 489;  
Best Local Similarity 100.0%; Pred. No. 3.7e-235;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAATTCGAAACACATTTGAGAAGTATTTCCATCCAGTCTACCTGTTTACTT 60  
Db 1 ATGAGAATTCGAAACACATTTGAGAAGTATTTCCATCCAGTCTACCTGTTTACTT 60  
Qy 61 CTAAGAGTCAATTTCTAACTGAAGTGGCATTCATGCTTCTATTTGGGCTGTTTCACT 120  
Db 61 CTAAGAGTCAATTTCTAACTGAAGTGGCATTCATGCTTCTATTTGGGCTGTTTCACT 120  
Qy 121 GCAGGGCTCCCTAAACAGAGCCCACTGGGTGAATTAAGTGAATTTGAAAAAATT 180  
Db 121 GCAGGGCTCCCTAAACAGAGCCCACTGGGTGAATTAAGTGAATTTGAAAAAATT 180  
Qy 181 GAAGATCTTATTCATCTATGATGCTACTTATATATACAGAAAGTGATGTTCACT 240  
Db 181 GAAGATCTTATTCATCTATGATGCTACTTATATATACAGAAAGTGATGTTCACT 240  
Qy 241 CCCAGTTGCAAGGTAAACAGCAATGAAGTGGCTTCTCTTGGAGTGGCAAGTTATTTCACT 300  
Db 241 CCCAGTTGCAAGGTAAACAGCAATGAAGTGGCTTCTCTTGGAGTGGCAAGTTATTTCACT 300  
Qy 301 GAGTCCGGAGATACAGATATTTCATGATACAGTAGAAAAATCTTATCATCTAGCAAAAC 360

Db 301 GAGTCCGGAGATACAGATATTTCATGATACAGTAGAAAAATCTTATCATCTAGCAAAAC 360  
Qy 361 ATCTTGCTCTTAATGGGAATATAACAGATCTGGATGCAAGAAATGTGAGGAAGTAGAG 420  
Db 361 ATCTTGCTCTTAATGGGAATATAACAGATCTGGATGCAAGAAATGTGAGGAAGTAGAG 420  
Qy 421 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480  
Db 421 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480  
Qy 481 ACTTCTTGA 489  
Db 481 ACTTCTTGA 489  
RESULT 13  
PCT-US94-03793-1  
; Sequence 1, Application PC/TUS9403793  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: Interleukin-15  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/03793  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Launer, Charlene  
; REGISTRATION NUMBER: 33,035  
; REFERENCE/DOCKET NUMBER: 2811  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-587-0430  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..489  
PCT-US94-03793-1

Query Match 100.0%; Score 489; DB 5; Length 489;  
Best Local Similarity 100.0%; Pred. No. 3.7e-235;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAATTCGAAACACATTTGAGAAGTATTTCCATCCAGTCTACCTGTTTACTT 60  
Db 1 ATGAGAATTCGAAACACATTTGAGAAGTATTTCCATCCAGTCTACCTGTTTACTT 60  
Qy 61 CTAAGAGTCAATTTCTAACTGAAGTGGCATTCATGCTTCTATTTGGGCTGTTTCACT 120

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; NAME/KEY: CDS
; LOCATION: 1..345
; US-08-393-305-13

Query Match 70.6%; Score 345; DB 1: Length 345;
Best Local Similarity 100.0%; Pred. No. 3e-163;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTTGAAGATCTTATTCATCTATGTCAT 204
Db 1 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTTGAAGATCTTATTCATCTATGTCAT 60
QY 205 ATTGATGCTACTTTATATACAGAAAGTGTTCACCCCAAGTTGCAAGGTAACAGCAATG 264
Db 61 ATTGATGCTACTTTATATACAGAAAGTGTTCACCCCAAGTTGCAAGGTAACAGCAATG 120
QY 265 AAGTGCTTTCTCTGGAGTTGCAAGTTATTTACATGAGTCCGAGATACAGATATTTCAT 324
Db 121 AAGTGCTTTCTCTGGAGTTGCAAGTTATTTACATGAGTCCGAGATACAGATATTTCAT 180
QY 325 GATACAGTAGAAATCTTATCATCTCTAGCAACAACATCTTGTCTCTAATGGAATATA 384
Db 181 GATACAGTAGAAATCTTATCATCTCTAGCAACAACATCTTGTCTCTAATGGAATATA 240
QY 385 ACAGAACTGGATGCAAAAGAAATGTGAGGAAGTGTGAGGAACTAGAGAAAAAATATTAAAGAAATTTTG 444
Db 241 ACAGAACTGGATGCAAAAGAAATGTGAGGAACTAGAGAAAAAATATTAAAGAAATTTTG 300
QY 445 CAGAGTTTTGTACATATTGTCCAAATGTTTCATCAACACTTCTTGA 489
Db 301 CAGAGTTTTGTACATATTGTCCAAATGTTTCATCAACACTTCTTGA 345

RESULT 15
US-08-726-817-13
; Sequence 13, Application US/08726817
; Patent No. 5707616
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Anderson, Dirk
; APPLICANT: Eisenman, June
; APPLICANT: Fung, Victor
; APPLICANT: Rauch, Charles
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,305
; FILING DATE: 22-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 480052.409C2
; TELEPHONE: 206-622-4900
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 345 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: 1..345
; US-08-393-305-13

Query Match 70.6%; Score 345; DB 1: Length 345;
Best Local Similarity 100.0%; Pred. No. 3e-163;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTTGAAGATCTTATTCATCTATGTCAT 204
Db 1 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTTGAAGATCTTATTCATCTATGTCAT 60
QY 205 ATTGATGCTACTTTATATACAGAAAGTGTTCACCCCAAGTTGCAAGGTAACAGCAATG 264
Db 61 ATTGATGCTACTTTATATACAGAAAGTGTTCACCCCAAGTTGCAAGGTAACAGCAATG 120
QY 265 AAGTGCTTTCTCTGGAGTTGCAAGTTATTTACATGAGTCCGAGATACAGATATTTCAT 324
Db 121 AAGTGCTTTCTCTGGAGTTGCAAGTTATTTACATGAGTCCGAGATACAGATATTTCAT 180
QY 325 GATACAGTAGAAATCTTATCATCTCTAGCAACAACATCTTGTCTCTAATGGAATATA 384
Db 181 GATACAGTAGAAATCTTATCATCTCTAGCAACAACATCTTGTCTCTAATGGAATATA 240
QY 385 ACAGAACTGGATGCAAAAGAAATGTGAGGAAGTGTGAGGAACTAGAGAAAAAATATTAAAGAAATTTTG 444
Db 241 ACAGAACTGGATGCAAAAGAAATGTGAGGAACTAGAGAAAAAATATTAAAGAAATTTTG 300
QY 445 CAGAGTTTTGTACATATTGTCCAAATGTTTCATCAACACTTCTTGA 489
Db 301 CAGAGTTTTGTACATATTGTCCAAATGTTTCATCAACACTTCTTGA 345

RESULT 15
US-08-726-817-13
; Sequence 13, Application US/08726817
; Patent No. 5707616
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Anderson, Dirk
; APPLICANT: Eisenman, June
; APPLICANT: Fung, Victor
; APPLICANT: Rauch, Charles
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,305
; FILING DATE: 22-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 480052.409C2
; TELEPHONE: 206-622-4900
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 345 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
;
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;/ LENGTH: 345 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ FEATURE:  
;/ NAME/KEY: CDS  
;/ LOCATION: 1..345  
US-08-726-817-13

Query Match 70.6%; Score 345; DB 1; Length 345;  
Best Local Similarity 100.0%; Pred. No. 3e-163;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTCAGAGATCTTATTCAATCTATGCAT 204  
DB 1 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTCAGAGATCTTATTCAATCTATGCAT 60  
QY 205 ATTGATGCTACTTTATATACAGAAAGTGATGTTCAACCCAGTTGCAAGGTAACAGCAATG 264  
DB 61 ATTGATGCTACTTTATATACAGAAAGTGATGTTCAACCCAGTTGCAAGGTAACAGCAATG 120  
QY 265 AACTGCTTTCTCTGGAGTTGCAAGTTATTTTCACATGAGTCCGGAGATACAGATATTTCAT 324  
DB 121 AACTGCTTTCTCTGGAGTTGCAAGTTATTTTCACATGAGTCCGGAGATACAGATATTTCAT 180  
QY 325 GATACAGTAGAAAAATCTTATCATCTAGCAAAACAACATCTTGTCTTCTAATGGGAATATA 384  
DB 181 GATACAGTAGAAAAATCTTATCATCTAGCAAAACAACATCTTGTCTTCTAATGGGAATATA 240  
QY 385 ACAGAATCTGGATGCAAAAGATGTGAGGAAGTCTAGAGGAAAAAATAATTAAGAAATTTTG 444  
DB 241 ACAGAATCTGGATGCAAAAGATGTGAGGAAGTCTAGAGGAAAAAATAATTAAGAAATTTTG 300  
QY 445 CAGAGTTTGTACATATTGTCCAAATGTTTCATCAACACTTCTTGA 489  
DB 301 CAGAGTTTGTACATATTGTCCAAATGTTTCATCAACACTTCTTGA 345

RESULT 16  
US-08-725-969-13  
; Sequence 13, Application US/08725969  
; Patent No. 5892001  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/725,969  
; FILING DATE: 04-OCT-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/393,305  
; FILING DATE: 22-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mcmasters, David D.  
; REGISTRATION NUMBER: 33,963

;/ REFERENCE/DOCKET NUMBER: 480052.409C2  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: 206-622-4900  
;/ INFORMATION FOR SEQ ID NO: 13:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 345 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ FEATURE:  
;/ NAME/KEY: CDS  
;/ LOCATION: 1..345  
US-08-725-969-13

Query Match 70.6%; Score 345; DB 2; Length 345;  
Best Local Similarity 100.0%; Pred. No. 3e-163;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTCAGAGATCTTATTCAATCTATGCAT 204  
DB 1 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTCAGAGATCTTATTCAATCTATGCAT 60  
QY 205 ATTGATGCTACTTTATATACAGAAAGTGATGTTCAACCCAGTTGCAAGGTAACAGCAATG 264  
DB 61 ATTGATGCTACTTTATATACAGAAAGTGATGTTCAACCCAGTTGCAAGGTAACAGCAATG 120  
QY 265 AACTGCTTTCTCTGGAGTTGCAAGTTATTTTCACATGAGTCCGGAGATACAGATATTTCAT 324  
DB 121 AACTGCTTTCTCTGGAGTTGCAAGTTATTTTCACATGAGTCCGGAGATACAGATATTTCAT 180  
QY 325 GATACAGTAGAAAAATCTTATCATCTAGCAAAACAACATCTTGTCTTCTAATGGGAATATA 384  
DB 181 GATACAGTAGAAAAATCTTATCATCTAGCAAAACAACATCTTGTCTTCTAATGGGAATATA 240  
QY 385 ACAGAATCTGGATGCAAAAGATGTGAGGAAGTCTAGAGGAAAAAATAATTAAGAAATTTTG 444  
DB 241 ACAGAATCTGGATGCAAAAGATGTGAGGAAGTCTAGAGGAAAAAATAATTAAGAAATTTTG 300  
QY 445 CAGAGTTTGTACATATTGTCCAAATGTTTCATCAACACTTCTTGA 489  
DB 301 CAGAGTTTGTACATATTGTCCAAATGTTTCATCAACACTTCTTGA 345

RESULT 17  
US-08-794-524-13  
; Sequence 13, Application US/08794524  
; Patent No. 5985262  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/794,524  
; FILING DATE: 03-FEB-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:

```
;
; APPLICATION NUMBER: US 08/393,305
; FILING DATE: 22-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 480052.409C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 345 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..345
; US-08-794-524-13

Query Match 70.6%; Score 345; DB 2; Length 345;
Best Local Similarity 100.0%; Pred. No. 3e-163;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATGAAGATCTTATTCAATCTATGCAT 204
Db 1 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATGAAGATCTTATTCAATCTATGCAT 60
QY 205 ATTGATGCTACTTTATATACAGAAAGTGATTTACACCCAGTTGCAAGGTAACAGCAATG 264
Db 61 ATTGATGCTACTTTATATACAGAAAGTGATTTACACCCAGTTGCAAGGTAACAGCAATG 120
QY 265 AAGTGCCTTTCTCTGGAGTTGCAAGTTATTTCACATGAGTCCGCGAGATACAGATATTTCAT 324
Db 121 AAGTGCCTTTCTCTGGAGTTGCAAGTTATTTCACATGAGTCCGCGAGATACAGATATTTCAT 180
QY 325 GATACAGTAGAATAATCTTATCATCTAGCAAAACACATCTTGCTTCTAATGGGAATATA 384
Db 181 GATACAGTAGAATAATCTTATCATCTAGCAAAACACATCTTGCTTCTAATGGGAATATA 240
QY 385 ACAGAAATCTGGATGCAAAAGAAATGTGAGGAACTAGAGGAAAAAATATTAAAGAAATTTTG 444
Db 241 ACAGAAATCTGGATGCAAAAGAAATGTGAGGAACTAGAGGAAAAAATATTAAAGAAATTTTG 300

RESULT 18
US-09-189-193-13
; Sequence 13, Application US/09189193
; Patent No. 6184359
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Anderson, Dirk
; APPLICANT: Eisenman, June
; APPLICANT: Fung, Victor
; APPLICANT: Rauch, Charles
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/189,193
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/393,305
; APPLICATION NUMBER: US 08/393,305
; FILING DATE: 22-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 480052.409C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 345 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..345
; US-09-189-193-13

Query Match 70.6%; Score 345; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 3e-163;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATGAAGATCTTATTCAATCTATGCAT 204
Db 1 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATGAAGATCTTATTCAATCTATGCAT 60
QY 205 ATTGATGCTACTTTATATACAGAAAGTGATTTACACCCAGTTGCAAGGTAACAGCAATG 264
Db 61 ATTGATGCTACTTTATATACAGAAAGTGATTTACACCCAGTTGCAAGGTAACAGCAATG 120
QY 265 AAGTGCCTTTCTCTGGAGTTGCAAGTTATTTCACATGAGTCCGCGAGATACAGATATTTCAT 324
Db 121 AAGTGCCTTTCTCTGGAGTTGCAAGTTATTTCACATGAGTCCGCGAGATACAGATATTTCAT 180
QY 325 GATACAGTAGAATAATCTTATCATCTAGCAAAACACATCTTGCTTCTAATGGGAATATA 384
Db 181 GATACAGTAGAATAATCTTATCATCTAGCAAAACACATCTTGCTTCTAATGGGAATATA 240
QY 385 ACAGAAATCTGGATGCAAAAGAAATGTGAGGAACTAGAGGAAAAAATATTAAAGAAATTTTG 444
Db 241 ACAGAAATCTGGATGCAAAAGAAATGTGAGGAACTAGAGGAAAAAATATTAAAGAAATTTTG 300

RESULT 19
US-08-031-399-4
; Sequence 4, Application US/08031399
; Patent No. 5552303
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Anderson, Dirk
; APPLICANT: Eisenman, June
; APPLICANT: Fung, Victor
; APPLICANT: Rauch, Charles
; TITLE OF INVENTION: Epithelium-derived T-cell Factor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
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COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/031,399  
FILING DATE: 19930308  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Launer, Charlene  
REGISTRATION NUMBER: 33,035  
REFERENCE/DOCKET NUMBER: 2811  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0430  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..489  
US-08-031-399-4

Query Match 21.9%; Score 107; DB 1; Length 489;  
Best Local Similarity 99.4%; Pred. No. 2.2e-44;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTTCATTTTGGGCTGTTTCAGTCGAGG 126  
Db 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTTCATTTTGGGCTGTTTCAGTCGAGG 126  
QY 127 CTCCTAAACAGAACCCAACTGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186  
Db 127 CTCCTAAACAGAACCCAACTGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186  
QY 187 CTTATTCATCTATGCATATTCATGCTACTTTATATAC 224  
Db 187 CTTATTCATCTATGCATATTCATGCTACTTTATATAC 224

RESULT 20  
US-08-393-305-1  
Sequence 1, Application US/08393305  
Patent No. 5574138  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Elsenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/393,305  
FILING DATE: 22-FEB-1995  
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 480052.409C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..489  
US-08-393-305-1  
Query Match 21.9%; Score 107; DB 1; Length 489;  
Best Local Similarity 99.4%; Pred. No. 2.2e-44;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTTCATTTTGGGCTGTTTCAGTCGAGG 126  
Db 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTTCATTTTGGGCTGTTTCAGTCGAGG 126  
QY 127 CTCCTAAACAGAACCCAACTGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186  
Db 127 CTCCTAAACAGAACCCAACTGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186  
QY 187 CTTATTCATCTATGCATATTCATGCTACTTTATATAC 224  
Db 187 CTTATTCATCTATGCATATTCATGCTACTTTATATAC 224  
RESULT 21  
US-08-535-733-1  
Sequence 1, Application US/08535733  
Patent No. 5660824  
GENERAL INFORMATION:  
APPLICANT: Quinn, LeBris  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Troutt, Anthony B.  
TITLE OF INVENTION: Muscle-Trophic Factor  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: System 7, Word 5.1a  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/535,733  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2833  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0430  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..489  
US-08-535-733-1

Query Match 21.9%; Score 107; DB 1; Length 489;  
Best Local Similarity 99.4%; Pred. No. 2.2e-44;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCATTTTGGGCTGTTTTCAGTCAGGG 126  
|||||  
Db 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCATTTTGGGCTGTTTTCAGTCAGGG 126  
|||||  
QY 127 CTCCTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTGAAGAT 186  
|||||  
Db 127 CTCCTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTGAAGAT 186  
|||||  
QY 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224  
|||||  
Db 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224  
|||||

## RESULT 22

US-08-726-817-1  
; Sequence 1, Application US/08726817  
; Patent No. 5707616  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/726.817  
; FILING DATE: 04-OCT-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/393,305  
; FILING DATE: 22-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 480052.409C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-622-4900  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..489  
US-08-726-817-1

Query Match 21.9%; Score 107; DB 1; Length 489;  
Best Local Similarity 99.4%; Pred. No. 2.2e-44;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCATTTTGGGCTGTTTTCAGTCAGGG 126  
|||||  
Db 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCATTTTGGGCTGTTTTCAGTCAGGG 126  
|||||  
QY 127 CTCCTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTGAAGAT 186  
|||||  
Db 127 CTCCTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTGAAGAT 186  
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QY 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224  
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Db 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224  
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## RESULT 23

US-08-504-042-4  
; Sequence 4, Application US/08504042  
; Patent No. 5747024  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: Epithelium-derived T-cell Factor  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/504.042  
; FILING DATE: 19-JUL-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/031,399  
; FILING DATE: 08-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Launer, Charlene  
; REGISTRATION NUMBER: 33,035  
; REFERENCE/DOCKET NUMBER: 2811  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-587-0430  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..489  
US-08-504-042-4

Query Match 21.9%; Score 107; DB 1; Length 489;  
Best Local Similarity 99.4%; Pred. No. 2.2e-44;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCATTTTGGGCTGTTTTCAGTCAGGG 126  
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Db 67 AGTCATTTTCTAACTGAAGCTGGCATTGCTTTCATTTTGGGCTGTTTTCAGTGCAGGG 126

QY 127 CTCCTTAAACAGAGCCAACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGAT 186

Db 127 CTTCTTAAACAGAGCCAACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGAT 186

QY 187 CTTATTCAATCTATGCATATTTGATGCTACTTTATATAC 224

Db 187 CTTATTCAATCTATGCATATTTGATGCTACTTTATATAC 224

RESULT 24

US-08-392-317B-2

; Sequence 2, Application US/08392317B

; Patent No. 5795966

GENERAL INFORMATION:

; APPLICANT: Grabstein, Kenneth

; APPLICANT: Paxton, Raymond

; APPLICANT: Pettit, Dean

; TITLE OF INVENTION: Antagonists of IL-15

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation

; STREET: 51 University Street

; City: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98101

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC Compatible

; OPERATING SYSTEM: Word for Windows 95, 7.0

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/392,317B

; FILING DATE:

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Malaska, Stephen L.

; REGISTRATION NUMBER: 32,655

; REFERENCE/DOCKET NUMBER: 2831

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-587-0430

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 489 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..489

US-08-392-317B-2

Query Match 21.9%; Score 107; DB 1; Length 489;

Best Local Similarity 99.4%; Pred. No. 2.2e-44;

Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTGCTTTCATTTTGGGCTGTTTTCAGTGCAGGG 126

Db 67 AGTCATTTTCTAACTGAAGCTGGCATTGCTTTCATTTTGGGCTGTTTTCAGTGCAGGG 126

QY 127 CTCCTTAAACAGAGCCAACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGAT 186

Db 127 CTTCTTAAACAGAGCCAACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGAT 186

QY 187 CTTATTCAATCTATGCATATTTGATGCTACTTTATATAC 224

Db 187 CTTATTCAATCTATGCATATTTGATGCTACTTTATATAC 224

RESULT 25

US-08-725-969-1

; Sequence 1, Application US/08725969

; Patent No. 5892001

GENERAL INFORMATION:

; APPLICANT: Grabstein, Kenneth

; APPLICANT: Anderson, Dirk

; APPLICANT: Eisenman, June

; APPLICANT: Fung, Victor

; APPLICANT: Raugh, Charles

; TITLE OF INVENTION: EPITHELIMUM-DERIVED T-CELL FACTOR

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Seed and Berry

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; City: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98104

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/725,969

; FILING DATE: 04-OCT-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/393,305

; FILING DATE: 22-FEB-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Mcmasters, David D.

; REGISTRATION NUMBER: 33,963

; REFERENCE/DOCKET NUMBER: 480052.409C2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-622-4900

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 489 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..489

US-08-725-969-1

Query Match 21.9%; Score 107; DB 2; Length 489;

Best Local Similarity 99.4%; Pred. No. 2.2e-44;

Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTGCTTTCATTTTGGGCTGTTTTCAGTGCAGGG 126

Db 67 AGTCATTTTCTAACTGAAGCTGGCATTGCTTTCATTTTGGGCTGTTTTCAGTGCAGGG 126

QY 127 CTCCTTAAACAGAGCCAACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGAT 186

Db 127 CTTCTTAAACAGAGCCAACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGAT 186

QY 187 CTTATTCAATCTATGCATATTTGATGCTACTTTATATAC 224

Db 187 CTTATTCAATCTATGCATATTTGATGCTACTTTATATAC 224

RESULT 26

US-08-794-524-1

; Sequence 1, Application US/08794524

; Patent No. 5985262

GENERAL INFORMATION:

; APPLICANT: Grabstein, Kenneth

; APPLICANT: Anderson, Dirk

APPLICANT: Eisenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/794,524  
FILING DATE: 03-FEB-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/393,305  
FILING DATE: 22-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 480052.409C2  
TELEPHONE: 206-622-4900  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..489  
US-08-794-524-1

Query Match 21.9%; Score 107; DB 2; Length 489;  
Best Local Similarity 99.4%; Pred. No. 2.2e-44;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTTCATTTTGGGCTGTTTCAGTCAGGG 126  
DB 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTTCATTTTGGGCTGTTTCAGTCAGGG 126  
QY 127 CTCCTAAACAGAACCCCACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTTGAAGAT 186  
DB 127 CTCCTAAACAGAACCCCACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTTGAAGAT 186  
QY 187 CTTATTCATCTATGCATATTGATGCTACTTTATATAC 224  
DB 187 CTTATTCATCTATGCATATTGATGCTACTTTATATAC 224

RESULT 27  
US-08-842-947-5  
; Sequence 5, Application US/08842947  
; Patent No. 6001973  
; GENERAL INFORMATION:  
; APPLICANT: Strom, Terry B.  
; APPLICANT: Maslinski, Wlodzimierz  
; TITLE OF INVENTION: ANTAGONISTS OF INTERLEUKIN-15  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA

COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/842,947  
FILING DATE: 25-APR-1997  
CLASSIFICATION: 432  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/016,634  
FILING DATE: 26-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 01948/039001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...486  
OTHER INFORMATION:  
US-08-842-947-5

Query Match 21.9%; Score 107; DB 3; Length 489;  
Best Local Similarity 99.4%; Pred. No. 2.2e-44;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTTCATTTTGGGCTGTTTCAGTCAGGG 126  
DB 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTTCATTTTGGGCTGTTTCAGTCAGGG 126  
QY 127 CTCCTAAACAGAACCCCACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTTGAAGAT 186  
DB 127 CTCCTAAACAGAACCCCACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTTGAAGAT 186  
QY 187 CTTATTCATCTATGCATATTGATGCTACTTTATATAC 224  
DB 187 CTTATTCATCTATGCATATTGATGCTACTTTATATAC 224

RESULT 28  
US-08-842-947-7  
; Sequence 7, Application US/08842947  
; Patent No. 6001973  
; GENERAL INFORMATION:  
; APPLICANT: Strom, Terry B.  
; APPLICANT: Maslinski, Wlodzimierz  
; TITLE OF INVENTION: ANTAGONISTS OF INTERLEUKIN-15  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/842,947  
FILING DATE: 25-APR-1997  
CLASSIFICATION: 432  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/016,634  
FILING DATE: 26-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 01948/039001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1..486  
OTHER INFORMATION:  
US-08-842-947-7

Query Match 21.9%; Score 107; DB 3; Length 489;

Best Local Similarity 99.4%; Pred. No. 2.2e-44;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCAATTTTGGGCTGTTTCAGTGCAGGG 126  
|||||  
Db 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCAATTTTGGGCTGTTTCAGTGCAGGG 126  
QY 127 CTCCTAAACAGACAGCCAACTGGTGAATGTAATAGTGAATTTGAAAAAATTTGAAGAT 186  
|||||  
Db 127 CTCCTAAACAGACAGCCAACTGGTGAATGTAATAGTGAATTTGAAAAAATTTGAAGAT 186  
QY 187 CTTATTCATCTATGCATATTGATGCTACTTTATATAC 224  
|||||  
Db 187 CTTATTCATCTATGCATATTGATGCTACTTTATATAC 224

## RESULT 29

US-09-134-132-2  
Sequence 2, Application US/09134132  
Patent No. 6013480  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Paxton, Raymond  
APPLICANT: Pettit, Dean  
TITLE OF INVENTION: Antagonists of IL-15  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: Word for Windows 95, 7.0  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/134,132  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/392,317  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2831  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0430  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..489  
US-09-134-132-2

Query Match 21.9%; Score 107; DB 3; Length 489;

Best Local Similarity 99.4%; Pred. No. 2.2e-44;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCAATTTTGGGCTGTTTCAGTGCAGGG 126  
|||||  
Db 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCAATTTTGGGCTGTTTCAGTGCAGGG 126  
QY 127 CTCCTAAACAGACAGCCAACTGGTGAATGTAATAGTGAATTTGAAAAAATTTGAAGAT 186  
|||||  
Db 127 CTCCTAAACAGACAGCCAACTGGTGAATGTAATAGTGAATTTGAAAAAATTTGAAGAT 186  
QY 187 CTTATTCATCTATGCATATTGATGCTACTTTATATAC 224  
|||||  
Db 187 CTTATTCATCTATGCATATTGATGCTACTTTATATAC 224

## RESULT 30

US-09-134-134A-2  
Sequence 2, Application US/09134134A  
Patent No. 6165466  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Paxton, Raymond  
APPLICANT: Pettit, Dean  
TITLE OF INVENTION: Antagonists of IL-15  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: Word for Windows 95, 7.0  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/134,134A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/392,317  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2831  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0430  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 base pairs

; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..489  
US-09-134-134A-2

Query Match 21.9%; Score 107; DB 4; Length 489;  
Best Local Similarity 99.4%; Pred. No. 2.2e-44;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 67 AGTCATTTTCTAACTGAAGCTGGCAATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126  
|||  
Db 67 AGTCATTTTCTAACTGAAGCTGGCAATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126  
|||  
  
QY 127 CTCCTAAACAGACGCAACTGGTGAATGTAATAGTGATTTGAAAAAATTGAAGAT 186  
|||  
Db 127 CTCCTAAACAGACGCAACTGGTGAATGTAATAGTGATTTGAAAAAATTGAAGAT 186  
|||  
  
QY 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224  
|||  
Db 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224  
|||

RESULT 31  
US-09-134-456-2  
; Sequence 2, Application US/09134456  
; Patent No. 6188783  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Paxton, Raymond  
; APPLICANT: Pettit, Dean  
; TITLE OF INVENTION: Antagonists of IL-15  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: Word for Windows 95, 7.0  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/134,456  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/392,317  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Malaska, Stephen L.  
; REGISTRATION NUMBER: 32,655  
; REFERENCE/DOCKET NUMBER: 2831  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-587-0430  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..489  
US-09-134-456-2

Query Match 21.9%; Score 107; DB 4; Length 489;  
Best Local Similarity 99.4%; Pred. No. 2.2e-44;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 67 AGTCATTTTCTAACTGAAGCTGGCAATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126  
|||  
Db 67 AGTCATTTTCTAACTGAAGCTGGCAATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126  
|||  
  
QY 127 CTCCTAAACAGACGCAACTGGTGAATGTAATAGTGATTTGAAAAAATTGAAGAT 186  
|||  
Db 127 CTCCTAAACAGACGCAACTGGTGAATGTAATAGTGATTTGAAAAAATTGAAGAT 186  
|||  
  
QY 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224  
|||  
Db 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224  
|||

RESULT 32  
US-09-196-427-2  
; Sequence 2, Application US/09196427  
; Patent No. 6177079  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Paxton, Raymond  
; APPLICANT: Pettit, Dean  
; TITLE OF INVENTION: Antagonists of IL-15  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: Word for Windows 95, 7.0  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/196,427  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/392,317  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Malaska, Stephen L.  
; REGISTRATION NUMBER: 32,655  
; REFERENCE/DOCKET NUMBER: 2831  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-587-0430  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..489  
US-09-196-427-2

Query Match 21.9%; Score 107; DB 4; Length 489;  
Best Local Similarity 99.4%; Pred. No. 2.2e-44;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 67 AGTCATTTTCTAACTGAAGCTGGCAATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126  
|||  
Db 67 AGTCATTTTCTAACTGAAGCTGGCAATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126  
|||

Db 67 AGTCATTTTCTAACTGAAGCTGCATTGCTCTTCATTTTGGCGTCTTTTCAGTCGAGG 126  
QY 127 CTCCTAAACACAGACCACTGGTGAATGTAATAGTGATTTGAAAAAATTGAAGAT 186  
Db 127 CTCCTAAACACAGACCACTGGTGAATGTAATAGTGATTTGAAAAAATTGAAGAT 186  
QY 187 CTTATTCAATCTATGCATATTGATGCTACTTTTATATAC 224  
Db 187 CTTATTCAATCTATGCATATTGATGCTACTTTTATATAC 224

RESULT 33  
US-09-189-193-1  
; Sequence 1, Application US/09189193  
; Patent No. 6184359  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: EPITHELIIUM-DERIVED T-CELL FACTOR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/189,193  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/393,305  
; FILING DATE: 22-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mcmasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 480052.409C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-622-4900  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..489  
US-09-189-193-1

Query Match 21.9%; Score 107; DB 4; Length 489;  
Best Local Similarity 99.4%; Pred. No. 2.2e-44;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGCATTGCTCTTCATTTTGGCGTCTTTTCAGTCGAGG 126  
Db 67 AGTCATTTTCTAACTGAAGCTGCATTGCTCTTCATTTTGGCGTCTTTTCAGTCGAGG 126  
QY 127 CTCCTAAACACAGACCACTGGTGAATGTAATAGTGATTTGAAAAAATTGAAGAT 186  
Db 127 CTCCTAAACACAGACCACTGGTGAATGTAATAGTGATTTGAAAAAATTGAAGAT 186  
QY 187 CTTATTCAATCTATGCATATTGATGCTACTTTTATATAC 224

Db 187 CTTATTCAATCTATGCATATTGATGCTACTTTTATATAC 224

RESULT 34  
PCT-US94-03793-4  
; Sequence 4, Application PC/TUS9403793  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: Interleukin-15  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/03793  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Launer, Charlene  
; REGISTRATION NUMBER: 33,035  
; REFERENCE/DOCKET NUMBER: 2811  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-587-0430  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..489  
PCT-US94-03793-4

Query Match 21.9%; Score 107; DB 5; Length 489;  
Best Local Similarity 99.4%; Pred. No. 2.2e-44;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGCATTGCTCTTCATTTTGGCGTCTTTTCAGTCGAGG 126  
Db 67 AGTCATTTTCTAACTGAAGCTGCATTGCTCTTCATTTTGGCGTCTTTTCAGTCGAGG 126  
QY 127 CTCCTAAACACAGACCACTGGTGAATGTAATAGTGATTTGAAAAAATTGAAGAT 186  
Db 127 CTCCTAAACACAGACCACTGGTGAATGTAATAGTGATTTGAAAAAATTGAAGAT 186  
QY 187 CTTATTCAATCTATGCATATTGATGCTACTTTTATATAC 224  
Db 187 CTTATTCAATCTATGCATATTGATGCTACTTTTATATAC 224

RESULT 35  
PCT-US96-06423-1  
; Sequence 1, Application PC/TUS9606423  
; GENERAL INFORMATION:  
; APPLICANT: Immunex Corporation  
; TITLE OF INVENTION: Muscle Trophic Factor

; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: System 7, Word 6.0  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/06423  
; FILING DATE: 07 May 1996  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Malaska, Stephen L.  
; REGISTRATION NUMBER: 32,655  
; REFERENCE/DOCKET NUMBER: 2833-WO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-587-0430  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..489  
PCT-US96-06423-1

Query Match 21.9%; Score 107; DB 5; Length 489;  
Best Local Similarity 99.4%; Pred. No. 2.2e-44;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 67 AGTCATTTTCTTAAGCTGCGCATTCATGCTTTCATTTTGGGCTGTTTCAGTGCAGG 126  
Db 67 AGTCATTTTCTTAAGCTGCGCATTCATGCTTTCATTTTGGGCTGTTTCAGTGCAGG 126  
Qy 127 CTCCTTAAACAGACGACCAACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGAT 186  
Db 127 CTCCTTAAACAGACGACCAACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGAT 186  
Qy 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224  
Db 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224

RESULT 36  
US-08-962-503-11  
; Sequence 11, Application US/08962503  
; Patent No. 6087172  
; GENERAL INFORMATION:  
; APPLICANT: Veerapaneni, Dange  
; APPLICANT: Hamanaka, Shoji  
; APPLICANT: NO. 6087172awa, Iwao  
; TITLE OF INVENTION: RIBOZYMES TARGETED TO IL-15 MRNA  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/962,503  
; FILING DATE: 31-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haile, Ph.D., Lisa A  
; REGISTRATION NUMBER: 38,347  
; REFERENCE/DOCKET NUMBER: 09326/002001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 619/678-5099  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1202 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-962-503-11

Query Match 21.9%; Score 107; DB 3; Length 1202;  
Best Local Similarity 99.4%; Pred. No. 2.2e-44;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 67 AGTCATTTTCTTAAGCTGCGCATTCATGCTTTCATTTTGGGCTGTTTCAGTGCAGG 126  
Db 383 AGTCATTTTCTTAAGCTGCGCATTCATGCTTTCATTTTGGGCTGTTTCAGTGCAGG 442  
Qy 127 CTCCTTAAACAGACGACCAACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGAT 186  
Db 443 CTCCTTAAACAGACGACCAACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGAT 502  
Qy 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224  
Db 503 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 540

RESULT 37  
US-09-200-141-1  
; Sequence 1, Application US/09200141  
; Patent No. 5985663  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Lex M. Cowser  
; TITLE OF INVENTION: ANTISENSE MODULATION OF Interleukin-15 EXPRESSION  
; FILE REFERENCE: RTS-0022  
; CURRENT APPLICATION NUMBER: US/09/200,141  
; CURRENT FILING DATE: 1998-11-25  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 1  
; LENGTH: 1248  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (519)..(926)  
US-09-200-141-1

Query Match 19.4%; Score 95; DB 2; Length 1248;  
Best Local Similarity 100.0%; Pred. No. 2.1e-38;  
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 130 CCTAAAAACAGACGACCAACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGATCTT 189  
Db 567 cctaaacagaaagcccaactggggaatgtaataagtgattgaaaaaaattgaagatctt 626  
Qy 190 ATTCAATCTATGCATATTGATGCTACTTTATATAC 224  
Db 627 attcaatctatgcataattgatgctactttatataac 661

RESULT 38  
US-08-393-305-12  
; Sequence 12, Application US/08393305  
; Patent No. 5574138  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/393,305  
; FILING DATE: 22-FEB-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 480052.409C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-622-4900  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 345 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..345  
; US-08-393-305-12

Query Match 16.4%; Score 80; DB 1; Length 345;  
Best Local Similarity 100.0%; Pred. No. 6.7e-31;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 145 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGATCTTATTCAATCTATGCAT 204  
Db 1 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGATCTTATTCAATCTATGCAT 60  
QY 205 ATTGATGCTACTTTATATAC 224  
Db 61 ATTGATGCTACTTTATATAC 80

RESULT 39  
US-08-726-817-12  
; Sequence 12, Application US/08726817  
; Patent No. 5707616  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/726,817  
; FILING DATE: 04-OCT-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/393,305  
; FILING DATE: 22-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 480052.409C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-622-4900  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 345 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..345  
; US-08-726-817-12

Query Match 16.4%; Score 80; DB 1; Length 345;  
Best Local Similarity 100.0%; Pred. No. 6.7e-31;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 145 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGATCTTATTCAATCTATGCAT 204  
Db 1 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGATCTTATTCAATCTATGCAT 60  
QY 205 ATTGATGCTACTTTATATAC 224  
Db 61 ATTGATGCTACTTTATATAC 80

RESULT 40  
US-08-725-969-12  
; Sequence 12, Application US/08725969  
; Patent No. 5892001  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25

```
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/725,969
; FILING DATE: 04-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/393,305
; FILING DATE: 22-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 480052.409C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 345 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..345
; US-08-725-969-12

Query Match          16.4%; Score 80; DB 2; Length 345;
Best Local Similarity 100.0%; Pred. No. 6.7e-31;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTTGAAGATCTTTATTCATCTATGCAT 204
Db 1 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTTGAAGATCTTTATTCATCTATGCAT 60

QY 205 ATTGATGCTACTTTATATAC 224
Db 61 ATTGATGCTACTTTATATAC 80

RESULT 41
US-08-794-524-12
; Sequence 12, Application US/08/794524
; Patent No. 5985262
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Anderson, Dirk
; APPLICANT: Eisenman, June
; APPLICANT: Fung, Victor
; APPLICANT: Rauch, Charles
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/794,524
; FILING DATE: 03-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/393,305
; FILING DATE: 22-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 480052.409C2
```

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 345 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..345
; US-08-794-524-12

Query Match          16.4%; Score 80; DB 2; Length 345;
Best Local Similarity 100.0%; Pred. No. 6.7e-31;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTTGAAGATCTTTATTCATCTATGCAT 204
Db 1 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTTGAAGATCTTTATTCATCTATGCAT 60

QY 205 ATTGATGCTACTTTATATAC 224
Db 61 ATTGATGCTACTTTATATAC 80

RESULT 42
US-09-189-193-12
; Sequence 12, Application US/09189193
; Patent No. 6184359
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Anderson, Dirk
; APPLICANT: Eisenman, June
; APPLICANT: Fung, Victor
; APPLICANT: Rauch, Charles
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/189,193
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/393,305
; FILING DATE: 22-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 480052.409C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 345 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..345
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US-09-189-193-12

Query Match 16.4%; Score 80; DB 4; Length 345;  
Best Local Similarity 100.0%; Pred. No. 6.7e-31;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 AACTGGGTGAATGTAATGAAGTTTGAAGAAATTCAGATCTTATTCATCTATGCAT 204  
|||||  
Db 1 AACTGGGTGAATGTAATGAAGTTTGAAGAAATTCAGATCTTATTCATCTATGCAT 60

QY 205 ATTGATGCTACTTTATATAC 224  
|||||  
Db 61 ATTGATGCTACTTTATATAC 80

RESULT 43

US-08-859-998-435  
; Sequence 435, Application US/08859998  
; Patent No. 5994076

; GENERAL INFORMATION:

; APPLICANT: Chenchik, Alex  
; APPLICANT: Jokhadze, George  
; APPLICANT: Bibilashvili, Robert

; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL

; TITLE OF INVENTION: EXPRESSION

; NUMBER OF SEQUENCES: 1375

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish &amp; Richardson, P.C.

; STREET: 2200 Sand Hill Road, Suite 100

; CITY: Menlo Park

; STATE: CA

; COUNTRY: US

; ZIP: 94025

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/859,998

; FILING DATE: 21-MAY-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Field, Bret E.

; REGISTRATION NUMBER: 37,620

; REFERENCE/DOCKET NUMBER: 09096/002001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-322-5070

; TELEFAX: 415-854-0875

; INFORMATION FOR SEQ ID NO: 435:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 32 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

; FEATURE:

; OTHER INFORMATION: oligonucleotide primer

US-08-859-998-435

Query Match 5.5%; Score 27; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 0.0002;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TTGAGAAGTATTTCCATCCAGTCTAC 48  
|||||  
Db 1 TTGAGAAGTATTTCCATCCAGTCTAC 27

RESULT 44

US-09-225-928-435

; Sequence 435, Application US/09225928  
; Patent No. 6352829

; GENERAL INFORMATION:

; APPLICANT: Chenchik, Alex  
; APPLICANT: Jokhadze, George  
; APPLICANT: Bibilashvili, Robert

; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL

; EXPRESSION

; NUMBER OF SEQUENCES: 1375

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish &amp; Richardson, P.C.

; STREET: 2200 Sand Hill Road, Suite 100

; CITY: Menlo Park

; STATE: CA

; COUNTRY: US

; ZIP: 94025

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/225,928

; FILING DATE: 05-Jan-1999

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/859,998

; FILING DATE: 21-MAY-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Field, Bret E.

; REGISTRATION NUMBER: 37,620

; REFERENCE/DOCKET NUMBER: 09096/002001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-322-5070

; TELEFAX: 415-854-0875

; INFORMATION FOR SEQ ID NO: 435:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 32 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

; FEATURE:

; OTHER INFORMATION: oligonucleotide primer

; SEQUENCE DESCRIPTION: SEQ ID NO: 435:

US-09-225-928-435

Query Match 5.5%; Score 27; DB 4; Length 32;  
Best Local Similarity 100.0%; Pred. No. 0.0002;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TTGAGAAGTATTTCCATCCAGTCTAC 48  
|||||  
Db 1 TTGAGAAGTATTTCCATCCAGTCTAC 27

RESULT 45

US-08-962-503-4

; Sequence 4, Application US/08962503.  
; Patent No. 6087172

; GENERAL INFORMATION:

; APPLICANT: Veerapaneni, Dange

; APPLICANT: Hamaoka, Shoji

; APPLICANT: No. 6087172awa, Iwao

; TITLE OF INVENTION: RIBOZYMES TARGETED TO IL-15 MRNA

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish &amp; Richardson P.C.

; STREET: 4225 Executive Square, Suite 1400

```
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/962,503
; FILING DATE: 31-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Halle, Ph.D., Lisa A
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 09326/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; US-08-962-503-4
```

```
Query Match 4.3%; Score 21; DB 3; Length 21;
Best Local Similarity 52.4%; Pred. No. 0.2;
Matches 11; Conservative 10; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 88 GGCATTTCATGCTTCATTG 108
Db 1 GGCAUUAUGUCCUUAUUUG 21
```

```
RESULT 46
US-08-962-503-6
; Sequence 6, Application US/08962503
; Patent No. 6087172
; GENERAL INFORMATION:
; APPLICANT: Veerapaneni, Dange
; APPLICANT: Hamanaka, Shoji
; APPLICANT: No. 6087172awa, Iwao
; TITLE OF INVENTION: RIBOZYMES TARGETED TO IL-15 MRNA
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/962,503
; FILING DATE: 31-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Halle, Ph.D., Lisa A
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 09326/002001
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
```

```
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; US-08-962-503-6
;
; Query Match 4.3%; Score 21; DB 3; Length 21;
; Best Local Similarity 81.0%; Pred. No. 0.2;
; Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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```
QY 294 TTCACATGAGTCGCGAGATAC 314
Db 1 UUCACAUGAGUCCGAGATAC 21
```

```
RESULT 47
US-08-962-503-10
; Sequence 10, Application US/08962503
; Patent No. 6087172
; GENERAL INFORMATION:
; APPLICANT: Veerapaneni, Dange
; APPLICANT: Hamanaka, Shoji
; APPLICANT: No. 6087172awa, Iwao
; TITLE OF INVENTION: RIBOZYMES TARGETED TO IL-15 MRNA
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/962,503
; FILING DATE: 31-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Halle, Ph.D., Lisa A
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 09326/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; US-08-962-503-10
```

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Query Match 4.3%; Score 21; DB 3; Length 21;
Best Local Similarity 61.9%; Pred. No. 0.2;
Matches 13; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
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QY 454 GTACATATTGCCAAATGTTTC 474
Db 1 GUACAUAUUGUCCAAAUUC 21
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```
RESULT 48
US-08-392-317B-10/c
; Sequence 10, Application US/08392317B
; Patent No. 5795966
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
```

```
; APPLICANT: Paxton, Raymond
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Antagonists of IL-15
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Word for Windows 95, 7.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/392,317B
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; US-08-392-317B-10

Query Match 4.3%; Score 21; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 469 ATGTTTCATCAACACTTCTTGA 489
Db 36 ATGTTTCATCAACACTTCTTGA 16

RESULT 49
US-09-134-132-10/c
; Sequence 10, Application US/09134132
; Patent No. 6013480
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Paxton, Raymond
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Antagonists of IL-15
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Word for Windows 95, 7.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,132
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US/08/392,317
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; US-09-134-132-10

Query Match 4.3%; Score 21; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 469 ATGTTTCATCAACACTTCTTGA 489
Db 36 ATGTTTCATCAACACTTCTTGA 16

RESULT 50
US-09-134-134A-10/c
; Sequence 10, Application US/09134134A
; Patent No. 6165466
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Paxton, Raymond
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Antagonists of IL-15
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Word for Windows 95, 7.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,134A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/392,317
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; US-09-134-134A-10
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QY 469 ATGTTTCATCAACACTTCTTGA 489  
|||||  
Db 36 ATGTTTCATCAACACTTCTTGA 16

Search completed: August 6, 2002, 21:31:41  
Job time: 4638 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 6, 2002, 21:37:06 ; Search time 293.09 Seconds  
(without alignments)  
2864.551 Million cell updates/sec

Title: US-09-724-841-4  
Perfect score: 489  
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Scoring table: OLIGO\_NUC  
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22: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.\*  
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	489	100.0	489	16	Simian interleukin
2	489	100.0	489	16	Simian IL-15 clone
3	489	100.0	489	17	Human epithelium d
4	489	100.0	489	17	Simian epithelium-
5	489	100.0	489	17	Simian interleukin
6	489	100.0	489	19	Human epithelium d
7	489	100.0	489	20	Human epithelium-d
8	489	100.0	489	21	Simian interleukin
9	489	100.0	489	21	Human epithelium-d

10	489	100.0	489	22	AAF57018	Human ETF (hETF) p
11	345	70.6	345	16	AAT00525	Simian interleukin
12	345	70.6	345	22	AAF57025	Human ETF (hETF) m
13	107	21.9	489	16	AAT00526	Human interleukin-
14	107	21.9	489	16	AAQ84584	Human IL-15 clone
15	107	21.9	489	17	AAT49455	Simian epithelium
16	107	21.9	489	17	AAT42243	Human epithelium-d
17	107	21.9	489	17	AAT36635	Human interleukin-
18	107	21.9	489	18	AAT97227	Wild-type interleuk
19	107	21.9	489	18	AAT97228	Mutant interleukin
20	107	21.9	489	18	AAT58404	Interleukin-15 cod
21	107	21.9	489	19	AAV23554	Human interleukin-
22	107	21.9	489	19	AAV02873	Simian epithelium
23	107	21.9	489	20	AAZ29479	Simian epithelium-
24	107	21.9	489	21	AAZ90032	Human interleukin-
25	107	21.9	489	21	AAZ38244	Simian epithelium-
26	107	21.9	489	22	AAF57017	Human interleukin
27	107	21.9	489	22	AAF57017	Simian ETF (sETF)
28	107	21.9	1202	20	AAZ56368	Human IL-15 DNA.
29	107	21.9	1202	21	AAZ21342	Human low adenosin
30	107	21.9	1202	21	AAZ58044	Human interleukin-
31	107	21.9	1202	21	AAZ35220	Human adenosine re
32	107	21.9	1202	21	AAZ88708	Human IL-15 cDNA
33	107	21.9	17904	21	AAF21345	Human low adenosin
34	95	19.4	1248	21	AAF21341	Human low adenosin
35	95	19.4	1248	21	AAZ35219	Human adenosine re
36	95	19.4	1248	21	AAZ37358	Human interleukin-
37	95	19.4	17844	21	AAZ35223	Human adenosine re
38	84	17.2	486	21	AAF21344	Human low adenosin
39	84	17.2	486	21	AAZ35222	Human adenosine re
40	80	16.4	345	16	AAT00527	Human interleukin-
41	80	16.4	345	22	AAF57024	Simian ETF (sETF)
42	72	14.7	14968	21	AAF21343	Human low adenosin
43	72	14.7	14968	21	AAZ35221	Human adenosine re
44	72	14.7	14968	22	AAZ14464	Human IL-15 gene a
45	72	14.7	14968	22	AAZ15838	Human interleukin
46	29	5.9	384	22	AAZ25950	Human breast cancer
47	29	5.9	474	22	AAZ19115	Human breast cancer
48	29	5.9	506	22	AAZ08205	Human breast cancer
49	27	5.5	30	21	AAZ88711	Human IL-15 target
50	23	4.7	25	21	AAZ88714	Human IL-15 target
51	21	4.3	21	20	AAZ56361	Human IL-15 DNA/RN
52	21	4.3	21	20	AAZ56363	Human IL-15 DNA/RN
53	21	4.3	21	20	AAZ56367	Human IL-15 DNA/RN
54	21	4.3	24	21	AAZ88716	Human IL-15 target
55	21	4.3	27	21	AAZ88713	Human IL-15 target
56	21	4.3	60	18	AAZ97226	Mutant interleukin
57	21	4.3	565	22	AAZ35436	Human colon cancer
58	21	4.3	17369	23	ABL02754	Drosophila melanog
59	20	4.1	20	20	AAZ56365	Human IL-15 DNA/RN
60	20	4.1	20	21	AAZ58050	Human interleukin-
61	20	4.1	20	21	AAZ58052	Human interleukin-
62	20	4.1	700	22	AAZ93090	Human inflammatory
63	20	4.1	8387	22	AAZ05409	Human reproductive
64	20	4.1	31949	22	AAZ05410	Human reproductive
65	20	4.1	32186	22	AAZ05411	Human reproductive
66	19	3.9	25	18	AAZ97224	Mature interleukin
67	19	3.9	936	21	AAZ70183	Plasmodium falcipa
68	19	3.9	8964	24	ABL33534	Human immune syste
69	19	3.9	8964	24	AAZ61276	Human gene regulat
70	19	3.9	19131	22	AAZ46717	Tumour suppressor
71	19	3.9	24601	20	AAZ13160	Enterococcus faeca
72	19	3.9	58407	19	AAZ21210	Methanococcus jann
73	18	3.7	18	21	AAZ37343	Interleukin-15 ant
74	18	3.7	18	21	AAZ37345	Interleukin-15 ant
75	18	3.7	18	21	AAZ37346	Interleukin-15 ant
76	18	3.7	18	21	AAZ37352	Interleukin-15 ant
77	18	3.7	18	21	AAZ37355	Interleukin-15 ant
78	18	3.7	18	21	AAZ37374	Interleukin-15 ant
79	18	3.7	18	21	AAZ37377	Interleukin-15 ant
80	18	3.7	20	21	AAZ58054	Human interleukin-
81	18	3.7	24	21	AAZ88715	Human IL-15 target
82	18	3.7	26	21	AAZ97225	Mature interleukin

83	18	3.7	39	17	AAT36636	Interleukin-15 PCR	c 156	17	3.5	537	22	AA18314	Human breast cancer
c 84	18	3.7	45	17	AAT36637	Interleukin-15 PCR	c 157	17	3.5	538	22	ABA60948	Human foetal liver
c 85	18	3.7	144	20	AAH86344	Human single nucle	c 158	17	3.5	558	22	AAK09238	Human brain expres
c 86	18	3.7	467	22	ABA58913	Human foetal liver	c 159	17	3.5	558	22	AAK35128	Human bone marrow
c 87	18	3.7	467	22	AAK07075	Human brain expres	c 160	17	3.5	558	22	AAI40845	Probe #9531 used t
c 88	18	3.7	467	22	AAK32815	Human bone marrow	c 161	17	3.5	575	22	AAI40845	Human foetal liver
c 89	18	3.7	467	22	AAI38630	Probe #7316 used t	c 162	17	3.5	575	22	AAK09586	Human brain expres
c 90	18	3.7	582	22	ABA62535	Human foetal liver	c 163	17	3.5	575	22	AAK35480	Human bone marrow
c 91	18	3.7	582	22	ABA29862	Probe #8328 for ge	c 164	17	3.5	575	22	AAI41194	Probe #9880 used t
c 92	18	3.7	582	22	AAK10890	Human brain expres	c 165	17	3.5	617	21	AAK77163	Human OREF ORF2718
c 93	18	3.7	582	22	AAK36752	Human brain expres	c 166	17	3.5	722	21	AAK65805	Human immune/haema
c 94	18	3.7	582	22	AAI17599	Human bone marrow	c 167	17	3.5	731	22	AAK65804	Human immune/haema
c 95	18	3.7	582	22	AAI42517	Probe #11203 used	c 168	17	3.5	731	22	AAK65806	Human immune/haema
c 96	18	3.7	649	23	AAH81461	DNA encoding novel	c 169	17	3.5	788	22	AAH05570	Human cDNA clone (
c 97	18	3.7	1887	24	AAI67644	F. necrophorum tru	c 170	17	3.5	894	18	AAV74880	Staphylococcus aur
c 98	18	3.7	2016	23	AAH56129	Salmonella typhi D	c 171	17	3.5	946	20	AAV20347	Borrelia burgdorfe
c 99	18	3.7	4443	22	AAH84742	DNA encoding cysti	c 172	17	3.5	1011	22	AAAT33202	F22b7.7 potassium
c 100	18	3.7	4560	20	AAI11643	CFTF protein encod	c 173	17	3.5	1133	14	AAQ40246	Caenorhabditis ele
c 101	18	3.7	4894	12	AAQ13605	Cystic fibrosis tr	c 174	17	3.5	1133	14	AAQ40247	Sequence of a DNA
c 102	18	3.7	5635	15	AAQ68002	Ad2/CFTF-1 nucleot	c 175	17	3.5	1133	14	AAH89813	Sequence of a DNA
c 103	18	3.7	6126	12	AAQ13053	CFTF delta 1507.	c 176	17	3.5	1133	21	AAH89814	Partial pN2-gptb D
c 104	18	3.7	6126	12	AAQ13053	DeltaF508 cystic f	c 177	17	3.5	1133	21	AAH89814	Partial pN2-gptb D
c 105	18	3.7	6127	12	AAQ11371	Mutant cystic fibr	c 178	17	3.5	1133	22	AAI12731	Vaccinia virus P7.
c 106	18	3.7	6128	12	AAQ13072	CFTF 3659 del C.	c 179	17	3.5	1133	22	AAI12732	Vaccinia virus P7.
c 107	18	3.7	6128	12	AAQ13068	CFTF 556 del A. H	c 180	17	3.5	1209	22	AAH89833	NotI cassette #2.
c 108	18	3.7	6129	12	AAQ13071	CFTF 1717 -1G -> A	c 181	17	3.5	1209	22	AAI12751	Plasmid pdhr-gpt D
c 109	18	3.7	6129	12	AAQ13054	CFTF G85E. Homo S	c 182	17	3.5	1449	18	AAH89833	DNA encoding a Sta
c 110	18	3.7	6129	12	AAQ13055	CFTF I148T. Homo	c 183	17	3.5	1449	19	AAV53400	DNA encoding a Sta
c 111	18	3.7	6129	12	AAQ13056	CFTF G178R. Homo	c 184	17	3.5	1466	22	ABA08564	Human Grb7 effecto
c 112	18	3.7	6129	12	AAQ13057	CFTF A455E. Homo	c 185	17	3.5	1575	21	AAK35960	Arabidopsis thalia
c 113	18	3.7	6129	12	AAQ13058	CFTF Q493X. Homo	c 186	17	3.5	1776	16	AAQ86521	Heliothis virescen
c 114	18	3.7	6129	12	AAQ13059	CFTF G542X. Homo	c 187	17	3.5	1784	23	AAH89257	DNA encoding novel
c 115	18	3.7	6129	12	AAQ13060	CFTF S549R. Homo	c 188	17	3.5	1785	20	AAK61658	B. burgdorferi ant
c 116	18	3.7	6129	12	AAQ13061	CFTF G51D. Homo	c 189	17	3.5	1807	20	AAZ28316	Fatty acyl-CoA elo
c 117	18	3.7	6129	12	AAQ13062	CFTF R560T. Homo	c 190	17	3.5	1847	21	AAK98932	Human pancreatic c
c 118	18	3.7	6129	12	AAQ13063	CFTF R563N. Homo	c 191	17	3.5	1878	20	AAK61657	B. burgdorferi ant
c 119	18	3.7	6129	12	AAQ13064	CFTF P574H. Homo	c 192	17	3.5	1891	23	AAH81171	DNA encoding novel
c 120	18	3.7	6129	12	AAQ13065	CFTF L1077P. Homo	c 193	17	3.5	1943	22	AAI60162	Human polynucleoti
c 121	18	3.7	6129	12	AAQ13066	CFTF Y1092X. Homo	c 194	17	3.5	1943	22	AAK51625	Human polynucleoti
c 122	18	3.7	6129	12	AAQ13067	CFTF 129G -> C. H	c 195	17	3.5	1986	22	AAK52986	DNA encoding human
c 123	18	3.7	6129	16	AAQ94067	DNA encoding the C	c 196	17	3.5	2053	22	AAK52986	DNA encoding human
c 124	18	3.7	6129	16	AAQ87795	Cystic fibrosis tr	c 197	17	3.5	2088	22	AAK52986	Human polynucleoti
c 125	18	3.7	6129	16	AAQ84724	Human cystic fibro	c 198	17	3.5	2093	21	AAK98123	Human polynucleoti
c 126	18	3.7	6129	20	AAK35552	DNA encoding a cys	c 199	17	3.5	2120	22	AAK51624	Human colon cancer
c 127	18	3.7	6129	20	AAK35554	G551D cystic fibro	c 200	17	3.5	2485	23	ABL13126	Human polynucleoti
c 128	18	3.7	6129	20	AAK35554	Human CFTF nucleot	c 201	17	3.5	2506	23	ABL13126	Human polynucleoti
c 129	18	3.7	6129	22	AAH57522	Human pancreas cel	c 202	17	3.5	2553	22	AAK52608	Drosophila melanog
c 130	18	3.7	6129	22	AAH57522	Cystic fibrosis ge	c 203	17	3.5	2553	22	AAK52608	Drosophila melanog
c 131	18	3.7	6130	13	AAQ11046	Human cystic fibro	c 204	17	3.5	2553	22	AAK52609	Human polynucleoti
c 132	18	3.7	6130	13	AAQ24280	Cystic fibrosis ge	c 205	17	3.5	2553	22	AAK52610	Human polynucleoti
c 133	18	3.7	6130	20	AAK04300	Human cystic fibro	c 206	17	3.5	2787	22	ABA07987	Human ovarian and
c 134	18	3.7	6131	20	AAK16105	DNA encoding a cys	c 207	17	3.5	2787	22	AAK05661	Human reproductive
c 135	18	3.7	6131	20	AAK16105	DNA encoding a cys	c 208	17	3.5	2787	22	AAH5965	Human immune/haema
c 136	18	3.7	6131	20	AAK16105	F. necrophorum leu	c 209	17	3.5	2821	22	AAH5965	Human cDNA sequenc
c 137	18	3.7	9972	17	AAI27557	Shuttle vector pad	c 210	17	3.5	2971	22	AAH5965	Human cDNA sequenc
c 138	18	3.7	11130	24	AAI67647	F. necrophorum leu	c 211	17	3.5	2971	22	AAH5965	Human cDNA sequenc
c 139	18	3.7	12143	20	AAV33952	DNA sequence of ex	c 212	17	3.5	2971	22	AAH5965	Human cDNA sequenc
c 140	18	3.7	19795	23	ABL02606	Drosophila melanog	c 213	17	3.5	3353	22	AAH5965	Human cDNA sequenc
c 141	18	3.7	32449	22	AAK04931	Human reproductive	c 214	17	3.5	3353	22	AAH5965	Human cDNA sequenc
c 142	18	3.7	36335	15	AAQ68003	Ad2/-ORF6/PGK-CFTF	c 215	17	3.5	3508	22	AAH5965	Human cDNA sequenc
c 143	18	3.7	73334	24	ABL34125	Human immune syste	c 216	17	3.5	3508	22	AAH5965	Human cDNA sequenc
c 144	17	3.5	18	21	AAZ37354	Interleukin-15 ant	c 217	17	3.5	3797	22	AAH5965	Human cDNA sequenc
c 145	17	3.5	263	22	AAI80333	Human polynucleoti	c 218	17	3.5	3797	22	AAH5965	Human cDNA sequenc
c 146	17	3.5	302	14	AAK59747	Human brain expres	c 219	17	3.5	3816	22	AAH5965	Human cDNA sequenc
c 147	17	3.5	309	22	AAK59144	Human immune/haema	c 220	17	3.5	3816	22	AAH5965	Human cDNA sequenc
c 148	17	3.5	343	22	AAK74601	Human immune/haema	c 221	17	3.5	3816	22	AAH5965	Human cDNA sequenc
c 149	17	3.5	343	22	AAK74602	Human immune/haema	c 222	17	3.5	3816	22	AAH5965	Human cDNA sequenc
c 150	17	3.5	357	22	AAI80357	Human polynucleoti	c 223	17	3.5	3816	22	AAH5965	Human cDNA sequenc
c 151	17	3.5	403	21	AAK02705	Human secreted pro	c 224	17	3.5	3816	22	AAH5965	Human cDNA sequenc
c 152	17	3.5	434	21	AAK99179	Human pancreatic c	c 225	17	3.5	3816	22	AAH5965	Human cDNA sequenc
c 153	17	3.5	466	22	ABA56227	Human foetal liver	c 226	17	3.5	3816	22	AAH5965	Human cDNA sequenc
c 154	17	3.5	466	22	AAK04414	Human brain expres	c 227	17	3.5	3816	22	AAH5965	Human cDNA sequenc
c 155	17	3.5	466	22	AAI35873	Probe #4559 used t	c 228	17	3.5	4338	22	AAH5965	Human diagnostic a

229	17	3.5	4406	22	AAF63930	Human tankyrase2 c	302	16	3.3	262	22	AAK20323	Human brain expres
230	17	3.5	4512	22	AAO02578	Human tankyrase ho	303	16	3.3	262	22	AAK46406	Human bone marrow
231	17	3.5	4641	14	AAQ40294	Sequence of plasm	304	16	3.3	262	22	AAI52293	Probe #20979 used
232	17	3.5	4701	21	AAA89875	Plasmid PTZ-L2. S	c 305	16	3.3	264	18	AAV78845	Staphylococcus aur
233	17	3.5	4701	22	AAI12793	Plasmid pTZ-L2 DNA	c 306	16	3.3	289	22	AAI20254	Human breast cance
234	17	3.5	4967	22	AAI560957	Human cancer agent	c 307	16	3.3	298	21	AAA42207	Human secreted exp
235	17	3.5	4992	22	AAF63953	Human tankyrase2 T	c 308	16	3.3	298	22	ABAI1158	Human nervous syst
236	17	3.5	5002	22	AAF63952	Human tankyrase2 T	c 309	16	3.3	305	22	AAI38817	Novel human diagno
237	17	3.5	5005	22	AAF89706	Human adult T-cell	c 310	16	3.3	312	22	AAK58906	Human immune/haema
238	17	3.5	5019	22	AAF82427	Moraxella catarrha	c 311	16	3.3	313	21	AAI11692	Aspergillus niger
239	17	3.5	5472	14	AAQ41005	Sequence of plasm	c 312	16	3.3	316	14	AAQ60349	Human brain expres
240	17	3.5	5532	21	AAA89883	Plasmid pN2gpta-FI	c 313	16	3.3	326	21	AAO06156	Human secreted pro
241	17	3.5	5532	22	AAI12901	Plasmid pN2-gpta-F	c 314	16	3.3	331	22	AAI17149	Human ion channel-
242	17	3.5	6019	22	AAI85294	Human SPANK CDNA	c 315	16	3.3	342	22	AAK74021	Human immune/haema
243	17	3.5	6060	18	AAI48454	Human beta-globin	c 316	16	3.3	345	21	AAO06158	Human secreted pro
244	17	3.5	6416	23	ABL23040	Drosophila melanog	c 317	16	3.3	363	21	AAK30048	Human secreted pro
245	17	3.5	6446	22	AAI46328	Tumour suppressor	c 318	16	3.3	368	21	AAK42430	Arabidopsis thalia
246	17	3.5	6470	22	AAI58376	Human polynucleoti	c 319	16	3.3	372	22	AAI83885	Human polynucleoti
247	17	3.5	6474	14	AAQ40300	Sequence of plasm	c 320	16	3.3	380	23	AAI89312	DNA encoding novel
248	17	3.5	6474	21	AAA89877	Plasmid pSelp-gp16	c 321	16	3.3	383	19	AAV61320	cDNA sequence of p
249	17	3.5	6474	22	AAI12795	Plasmid pSelp-gp16	c 322	16	3.3	383	19	AAV58639	Prostate tumour sp
250	17	3.5	6636	24	ABL32791	Human immune syste	c 323	16	3.3	383	21	AAO06402	Human immunogenic
251	17	3.5	6811	14	AAQ41004	Sequence of plasm	c 324	16	3.3	383	22	AAI63610	Human prostate CDN
252	17	3.5	6811	21	AAA89878	Plasmid pN2-gptapr	c 325	16	3.3	383	22	AAI0161	Human prostate tum
253	17	3.5	6811	22	AAI12796	Plasmid pN2-gptapr	c 326	16	3.3	383	22	AAH93518	Human prostate-spe
254	17	3.5	6926	14	AAQ40281	Sequence of clone	c 327	16	3.3	383	22	AAH84832	Human prostate-spe
255	17	3.5	6926	21	AAA89880	pp2-gp 16OMN. Syn	c 328	16	3.3	383	22	AAH02583	Prostate tumour an
256	17	3.5	6926	22	ABL12798	Plasmid p2-gp160m	c 329	16	3.3	385	22	AAI66533	Novel human polynu
257	17	3.5	6959	23	ABL05196	Drosophila melanog	c 330	16	3.3	386	22	AAI13287	Human cDNA clone (
258	17	3.5	7533	8	AAI70491	Entire sequence of	c 331	16	3.3	389	22	AAI82244	Human polynucleoti
259	17	3.5	7533	9	AAI81970	Plasmid pEMpl-tPA.	c 332	16	3.3	391	21	AAO00946	Human secreted pro
260	17	3.5	7918	23	ABL03498	Drosophila melanog	c 333	16	3.3	400	18	AAV78689	Staphylococcus aur
261	17	3.5	9399	20	AAI20261	Borrelia burgdorfe	c 334	16	3.3	402	18	AAV78644	Staphylococcus aur
262	17	3.5	9842	20	AAI20259	Borrelia burgdorfe	c 335	16	3.3	402	20	AAI84700	Human metastatic m
263	17	3.5	10649	23	ABL12972	Drosophila melanog	c 336	16	3.3	408	21	AAO06157	Human secreted pro
264	17	3.5	11152	19	AAI32373	Complete sequence	c 337	16	3.3	410	22	AAK96588	Human secreted g
265	17	3.5	11152	21	AAI59047	Nucleotide sequenc	c 338	16	3.3	410	22	AAK98081	Human neuregulin g
266	17	3.5	11152	24	ABA94256	Nucleotide sequenc	c 339	16	3.3	418	22	AAI11355	Human neuregulin g
267	17	3.5	11336	14	AAQ43497	Approximate nucleo	c 340	16	3.3	426	21	AAO2912	Human secreted pro
268	17	3.5	12622	23	ABL06818	Drosophila melanog	c 341	16	3.3	426	22	AAK07659	Human brain expres
269	17	3.5	12667	23	ABL06006	Drosophila melanog	c 342	16	3.3	426	22	AAK33469	Human bone marrow
270	17	3.5	13085	23	ABL03680	Drosophila melanog	c 343	16	3.3	426	22	AAI39243	Probe #7929 used t
271	17	3.5	13910	21	AAI51002	Recombinant fusion	c 344	16	3.3	427	21	AAO06159	Human secreted pro
272	17	3.5	13910	21	AAI51003	Recombinant viral	c 345	16	3.3	432	22	AAI39493	cDNA encoding nove
273	17	3.5	13910	21	AAI51004	Recombinant viral	c 346	16	3.3	432	22	AAK88392	Human digestive sy
274	17	3.5	13939	14	AAQ43845	Plasmid pAH4611.	c 347	16	3.3	432	22	AAK88392	N. meningitidis pa
275	17	3.5	14455	19	AAI32374	Complete sequence	c 348	16	3.3	444	17	AAI28257	Survival motor neu
276	17	3.5	14455	21	AAI59050	Nucleotide sequenc	c 349	16	3.3	444	17	AAI17248	Survival motor neu
277	17	3.5	14455	21	AAI59050	Nucleotide sequenc	c 350	16	3.3	447	17	AAI18569	Cauphylobacter jej
278	17	3.5	15044	22	AAI36290	Human cardiovascular	c 351	16	3.3	447	22	ABA43708	Human breast cell
279	17	3.5	15046	22	AAI36291	Human cardiovascular	c 352	16	3.3	449	22	ABA54165	Human foetal liver
280	17	3.5	16736	23	ABL26478	Drosophila melanog	c 353	16	3.3	449	22	ABA23910	Probe #2376 for ge
281	17	3.5	21591	20	AAI13047	Enterococcus faeca	c 354	16	3.3	449	22	AAK02435	Human brain expres
282	17	3.5	32250	22	AAI06975	Human reproductive	c 355	16	3.3	449	22	AAK27876	Human bone marrow
283	17	3.5	32763	22	AAK68779	Human immune/haema	c 356	16	3.3	449	22	AAI12457	Probe #2390 for ge
284	17	3.5	32763	21	AAI68779	Human immune/haema	c 357	16	3.3	449	22	AAI33811	Probe #2497 used t
285	17	3.5	89047	22	AAI28547	Genomic fragment #	c 358	16	3.3	449	22	AAI02368	Probe #2359 used t
286	17	3.5	96583	21	AAI22297	BAC containing rep	c 359	16	3.3	459	15	AAO68707	Murine protein tyr
287	17	3.5	110000	22	AAI84800	Nucleotide sequenc	c 360	16	3.3	476	21	AAI64720	C. trachomatis LGV
288	17	3.5	349980	22	AAH41225	Pyrococcus abyssi	c 361	16	3.3	476	22	ABA44854	Human breast cell
289	17	3.5	349980	22	AAH41226	Pyrococcus abyssi	c 362	16	3.3	476	22	ABA55315	Human foetal liver
290	17	3.5	611590	21	AAI22303	Arabidopsis thalia	c 363	16	3.3	476	22	ABA25050	Probe #3516 for ge
291	17	3.5	910715	20	AAI20248	Borrelia burgdorfe	c 364	16	3.3	476	22	AAK03560	Human brain expres
292	16	3.3	18	21	AAI337372	Interleukin-15 ant	c 365	16	3.3	476	22	AAI29019	Human bone marrow
293	16	3.3	19	21	AAI58671	Nucleotide sequenc	c 366	16	3.3	476	22	AAI13605	Probe #3538 for ge
294	16	3.3	19	21	AAI58680	Nucleotide sequenc	c 367	16	3.3	476	22	AAI34968	Probe #3654 used t
295	16	3.3	20	20	AAI04958	PCR primer used to	c 368	16	3.3	476	22	AAH56223	Chlamydia trachoma
296	16	3.3	156	20	AAI09663	Nucleic acid seque	c 369	16	3.3	478	22	AAH35386	Human colon cancer
297	16	3.3	180	21	AAI09540	Human gene expres	c 370	16	3.3	483	16	AAI04236	CDNA up to the fou
298	16	3.3	183	20	AAI14277	Human gene expres	c 371	16	3.3	486	22	ABA43386	Human breast cell
299	16	3.3	229	20	AAI87510	EST clone BV15. H	c 372	16	3.3	486	22	ABA53830	Human foetal liver
300	16	3.3	234	23	ABL23987	Drosophila melanog	c 373	16	3.3	486	22	ABA23575	Probe #2041 for ge
301	16	3.3	256	22	AAI58621	Human immune/haema	c 374	16	3.3	486	22	AAI20090	Human brain expres



521	16	3.3	2763	16	AAT15167	Methylthioadenosin	c 594	16	3.3	6643	22	AAK84930	Human immune/haema
522	16	3.3	2763	16	AAQ92813	Human MTase, Homo	595	16	3.3	6802	22	AAS46282	Tumour suppressor
523	16	3.3	2763	18	AAT85305	Human methylthioad	596	16	3.3	6802	22	AAS61068	Human gene regulat
524	16	3.3	2763	20	AAZ00866	Human MTase DNA,	c 597	16	3.3	6882	20	AAZ10631	Splice variant ZAP
525	16	3.3	2763	22	AAF86091	Pseudomonas putida	c 598	16	3.3	6950	23	ABL18490	Drosophila melanog
526	16	3.3	2784	16	AAQ99202	Protein phosphatas	599	16	3.3	7087	24	ABL33583	Human immune syste
527	16	3.3	2787	20	AAI15661	Drosophila melanog	600	16	3.3	7137	23	ABL23480	Drosophila melanog
528	16	3.3	2804	23	ABL26440	Drosophila melanog	601	16	3.3	7384	24	ABL32747	Human immune syste
529	16	3.3	2821	22	AAI63835	Human polynucleoti	602	16	3.3	7430	18	AAV74571	Staphylococcus aur
530	16	3.3	2846	22	AAH41292	CDNA encoding huma	603	16	3.3	7957	23	ABL28428	Drosophila melanog
531	16	3.3	2963	21	AAA49197	Human EF-chiral ca	604	16	3.3	7969	22	AAS46680	Tumour suppressor
c 532	16	3.3	2967	23	ABLI10022	Drosophila melanog	605	16	3.3	8307	23	ABL23161	Drosophila melanog
c 533	16	3.3	2971	22	AAH16177	Human cDNA sequenc	606	16	3.3	8542	23	ABL01872	Partial rice pyruv
c 534	16	3.3	2978	22	AAT59540	Human polynucleoti	607	16	3.3	8626	16	AAQ98237	Drosophila melanog
c 535	16	3.3	3001	21	AAH51765	Chromosome 13q31-q	608	16	3.3	9182	22	ABL04532	Human reproductive
c 536	16	3.3	3031	21	AAA64722	C. trachomatis LcV	c 609	16	3.3	9183	22	AAI04447	Human reproductive
c 537	16	3.3	3031	22	AAH56225	Chlamydia trachoma	c 610	16	3.3	9339	22	AAI04697	Human immune/haema
c 538	16	3.3	3034	22	AAH54843	S. epidermidis gen	c 611	16	3.3	9375	22	AAK84948	Human immune/haema
c 539	16	3.3	3072	22	AAK69732	Human immune/haema	c 612	16	3.3	9731	22	AAI04943	Human reproductive
c 540	16	3.3	3101	22	AAT59541	Human polynucleoti	c 613	16	3.3	9947	23	ABL09494	Drosophila melanog
c 541	16	3.3	3126	21	AAA36741	Original F-MuV/H-M	c 614	16	3.3	10301	22	AAK89494	Human immune/haema
c 542	16	3.3	3126	21	AAA36742	F-MuV/H-MV nucleot	c 615	16	3.3	10679	22	AAK89493	Human digestive sy
c 543	16	3.3	3126	22	AAH54548	S. epidermidis gen	c 616	16	3.3	10719	23	ABLI2106	Drosophila melanog
c 544	16	3.3	3144	22	AAH13942	Human cDNA sequenc	617	16	3.3	10785	22	ABA07367	Human pancreatic c
c 545	16	3.3	3149	22	AAI61108	Human polynucleoti	618	16	3.3	10785	22	AAS30060	Human lung antigen
c 546	16	3.3	3181	22	AAH27594	Human EF-chiral ca	619	16	3.3	10785	22	AAK65411	Human immune/haema
c 547	16	3.3	3203	20	AAH20283	Borrelia burgdorfe	620	16	3.3	10785	22	AAK91098	Human digestive sy
c 548	16	3.3	3257	20	AAH61632	B. burgdorferi ant	c 621	16	3.3	10855	24	ABL33488	Human immune syste
c 549	16	3.3	3273	17	AAT18868	Human survival mot	622	16	3.3	11310	23	ABLI14400	Drosophila melanog
c 550	16	3.3	3279	14	AAQ49397	TMF gene, Homo sa	623	16	3.3	11597	23	ABL23160	Drosophila melanog
c 551	16	3.3	3282	24	ABK09761	Human ovarian tumo	624	16	3.3	12507	24	ABL32299	Human immune syste
c 552	16	3.3	3350	13	AAQ29361	Ocean pout DNA seq	c 625	16	3.3	13021	22	AAI16553	Human novel protei
c 553	16	3.3	3354	20	AAH61631	B. burgdorferi ant	c 626	16	3.3	13021	22	AAS35084	DNA #34 encoding h
c 554	16	3.3	3569	23	ABLI19880	Drosophila melanog	c 627	16	3.3	13222	22	AAH25109	Nucleotide sequenc
c 555	16	3.3	3655	23	ABLI04023	Drosophila melanog	628	16	3.3	13315	22	ABA07371	Human pancreatic c
c 556	16	3.3	3734	22	AAS33201	DNA encoding human	629	16	3.3	13315	22	AAS30064	Human lung antigen
c 557	16	3.3	3754	18	AAV74869	Staphylococcus aur	630	16	3.3	13315	22	AAK65415	Human immune/haema
c 558	16	3.3	3756	23	ABLI11758	Drosophila melanog	631	16	3.3	13315	22	AAK91102	Human digestive sy
c 559	16	3.3	3774	22	AAH54262	S. epidermidis gen	632	16	3.3	13332	22	ABA15106	Human nervous syst
c 560	16	3.3	3786	21	AAH58265	Corn cellulose syn	633	16	3.3	13920	23	ABLI07110	Drosophila melanog
c 561	16	3.3	3787	22	ABA01228	Putative TBP inter	634	16	3.3	14537	22	AAH46355	Tumour suppressor
c 562	16	3.3	3813	21	AAH299509	DNA encoding a mai	635	16	3.3	15366	23	ABL21564	Drosophila melanog
c 563	16	3.3	3813	21	AAH299524	DNA encoding a mai	c 636	16	3.3	15384	22	AAF55095	Nucleotide sequenc
c 564	16	3.3	3900	22	AAH54813	S. epidermidis gen	c 637	16	3.3	15384	22	AAF55096	Nucleotide sequenc
c 565	16	3.3	3974	23	ABLI21565	Drosophila melanog	c 638	16	3.3	15500	22	ABA15840	Human nervous syst
c 566	16	3.3	4063	22	AAH22657	Human cDNA encodin	639	16	3.3	15500	22	AAS36609	Human cardiovascular
c 567	16	3.3	4203	20	AAH64063	Zea mays promoter	640	16	3.3	15587	24	AAS61238	Human gene regulat
c 568	16	3.3	4207	22	ABA17738	Human nervous syst	641	16	3.3	15674	24	AAS61238	Human immune syste
c 569	16	3.3	4208	22	ABA17737	Human nervous syst	642	16	3.3	15674	24	ABL34476	Human metastasis a
c 570	16	3.3	4208	22	ABA17739	Human nervous syst	643	16	3.3	15714	22	AAS36855	Human cardiovascular
c 571	16	3.3	4287	23	ABL23481	Drosophila melanog	644	16	3.3	17131	21	AAZ60888	DNA encoding a hum
c 572	16	3.3	4525	23	ABLI2092	Drosophila melanog	645	16	3.3	17499	23	ABL21344	Drosophila melanog
c 573	16	3.3	4583	22	AAH67070	Human immune/haema	646	16	3.3	17500	23	ABLI13076	Drosophila melanog
c 574	16	3.3	4593	21	AAH64794	C. trachomatis pmp	647	16	3.3	20261	22	ABA07368	Human pancreatic c
c 575	16	3.3	4593	22	AAH57036	Chlamydia trachoma	648	16	3.3	20261	22	AAS30061	Human lung antigen
c 576	16	3.3	4593	22	AAH56257	Chlamydia trachoma	649	16	3.3	20261	22	AAK65412	Human immune/haema
c 577	16	3.3	4734	23	ABLI15322	Drosophila melanog	650	16	3.3	20261	22	AAK91099	Human digestive sy
c 578	16	3.3	4968	23	ABLI13204	Drosophila melanog	651	16	3.3	21354	22	AAH46815	Tumour suppressor
c 579	16	3.3	5183	22	AAH36788	Human musculoskele	c 652	16	3.3	28860	23	ABL09806	Drosophila melanog
c 580	16	3.3	5243	19	AAH65691	Fowlpox Virus vect	c 653	16	3.3	29521	22	AAH32517	Human genomic DNA
c 581	16	3.3	5275	20	AAI10632	Splice variant ZAP	c 654	16	3.3	29543	22	AAS32516	Human reproductive
c 582	16	3.3	5474	24	AAH33271	Human immune syste	c 655	16	3.3	32012	22	AAI05864	Human immune/haema
c 583	16	3.3	5641	22	AAH73449	Human immune/haema	656	16	3.3	32145	22	AAK68491	Human immune/haema
c 584	16	3.3	5804	18	AAH74560	Staphylococcus aur	657	16	3.3	32145	22	AAH68575	Human immune/haema
c 585	16	3.3	5834	21	AAH35024	Human adenosine re	c 658	16	3.3	33780	22	AAH24652	Nucleotide sequenc
c 586	16	3.3	5836	21	AAH21146	Human low adenosin	659	16	3.3	38342	22	AAS46746	Tumour suppressor
c 587	16	3.3	5999	23	ABLI2246	Drosophila melanog	660	16	3.3	61020	22	AAH46787	Tumour suppressor
c 588	16	3.3	6013	24	AAS61323	Human gene regulat	c 661	16	3.3	76574	23	ABLI03438	Drosophila melanog
c 589	16	3.3	6073	24	ABLI33543	Human immune syste	662	16	3.3	113309	20	AAH20250	Borrelia burgdorfe
c 590	16	3.3	6195	23	ABLI14426	Drosophila melanog	663	16	3.3	113515	24	ABL34174	Human immune syste
c 591	16	3.3	6260	23	ABLI02590	Drosophila melanog	c 664	16	3.3	133894	17	AAT13635	AcNPV genomic DNA
c 592	16	3.3	6299	23	ABLI04022	Drosophila melanog	665	16	3.3	160271	22	AAH85750	Bipolar affective
593	16	3.3	6362	23	ABLI19982	Drosophila melanog	666	16	3.3	160271	22	AAH85756	Human chromosome 1

667	16	3.3	160271	22	AAS04858	Human chromosome 1	740	15	3.1	289	22	AAI61705	Soybean 318013 reg
668	16	3.3	160271	22	AAS04864	Human chromosome 1	741	15	3.1	289	22	AAI61706	Soybean 318013 reg
669	16	3.3	160271	22	AAS06667	Human chromosome 1	742	15	3.1	289	22	AAI61706	Human secreted pro
670	16	3.3	160271	22	AAH40997	160kb fragment of	743	15	3.1	298	21	AAC31958	Human gene express
671	16	3.3	160271	22	AAH23794	Human chromosome 1	c 744	15	3.1	300	20	AAZ13124	Human gene express
672	16	3.3	160271	22	AAH23794	Human chromosome 1	745	15	3.1	300	20	AAZ12829	Human gene express
c 673	16	3.3	168575	22	AAH21613	Nucleotide sequenc	746	15	3.1	300	21	AAC00634	Human secreted pro
c 674	16	3.3	168575	22	AAH21613	Human hyporetin r	747	15	3.1	303	20	AAH40439	Human secreted pro
c 675	16	3.3	265118	22	AAH41227	Pyrococcus abyss	c 748	15	3.1	313	20	AAZ24564	Human lung tumor a
c 676	16	3.3	269223	22	AAH28554	Genomic fragment #	749	15	3.1	313	20	AAZ24564	Human lung cancer-
c 677	16	3.3	319608	21	AAH51601	Human chromosome 1	c 750	15	3.1	313	21	AAH65803	EST clone FG525.
c 678	16	3.3	319608	22	AAH51601	Human chromosome 1	751	15	3.1	313	21	AAH65803	Human gene signatu
c 679	16	3.3	349980	22	AAH66431	Human schizophre	752	15	3.1	313	21	AAH66431	Probe for DNA enco
c 680	16	3.3	349980	22	AAH66431	Pyrococcus abyss	753	15	3.1	313	21	AAH66431	Nucleotide sequenc
c 681	16	3.3	465237	24	ABA90193	C glutamicum codin	754	15	3.1	313	21	AAH66431	Human musculoskele
c 682	16	3.3	580073	18	AAH58840	Human oestrogen re	755	15	3.1	313	21	AAH66431	Drosophila melanog
c 683	15	3.1	15	16	AAH94022	Mycoplasma genital	756	15	3.1	313	21	AAH66431	Human polynucleoti
c 684	15	3.1	15	20	AAH81367	SH gene primer NH2	757	15	3.1	313	21	AAH66431	Enterococcus faeca
c 685	15	3.1	15	20	AAH81368	PCR primer used to	758	15	3.1	313	21	AAH66431	Human secreted pro
c 686	15	3.1	20	20	AAH81375	Human thioredoxin	759	15	3.1	313	21	AAH66431	Human immune/haema
c 687	15	3.1	27	20	AAH81375	PCR primer used to	c 760	15	3.1	313	21	AAH66431	EST clone BA79. H
c 688	15	3.1	41	22	AAH69965	Human ribosome S7	761	15	3.1	313	21	AAH66431	Human EST-derived
c 689	15	3.1	48	22	AAH63971	Human TRF1 TANK2 b	762	15	3.1	313	21	AAH66431	Novel cDNA encodin
c 690	15	3.1	60	21	AAH63971	Human secreted pro	763	15	3.1	313	21	AAH66431	Human brain Expres
c 691	15	3.1	87	21	AAH63971	Human secreted pro	764	15	3.1	313	21	AAH66431	Human polynucleoti
c 692	15	3.1	110	21	AAH63971	BDA-generated regi	765	15	3.1	313	21	AAH66431	Human polynucleoti
c 693	15	3.1	114	14	AAH63971	Human single nucle	766	15	3.1	313	21	AAH66431	Novel human polynu
c 694	15	3.1	127	20	AAH63971	Human breast cance	767	15	3.1	313	21	AAH66431	Human breast cance
c 695	15	3.1	127	20	AAH63971	Human breast cance	768	15	3.1	313	21	AAH66431	Human nervous syst
c 696	15	3.1	144	19	AAH63971	Human biallelic po	769	15	3.1	313	21	AAH66431	Human breast cance
c 697	15	3.1	153	24	AAH63971	Lung small cell ca	770	15	3.1	313	21	AAH66431	Human gene signatu
c 698	15	3.1	160	22	AAH63971	Human breast cance	771	15	3.1	313	21	AAH66431	Human breast cance
c 699	15	3.1	162	22	AAH63971	Human foetal liver	772	15	3.1	313	21	AAH66431	Human secreted pro
c 700	15	3.1	162	22	AAH63971	Human foetal liver	773	15	3.1	313	21	AAH66431	Human secreted pro
c 701	15	3.1	162	22	AAH63971	Human brain expres	774	15	3.1	313	21	AAH66431	S. epidermidis ope
c 702	15	3.1	163	22	AAH63971	Human bone marrow	775	15	3.1	313	21	AAH66431	S. epidermidis ope
c 703	15	3.1	163	22	AAH63971	Probe #19160 used	776	15	3.1	313	21	AAH66431	Human foetal liver
c 704	15	3.1	163	22	AAH63971	Osteoarthritis tis	777	15	3.1	313	21	AAH66431	Probe #6402 for ge
c 705	15	3.1	163	22	AAH63971	Human immune/haema	778	15	3.1	313	21	AAH66431	Human brain expres
c 706	15	3.1	163	22	AAH63971	Human secreted pro	779	15	3.1	313	21	AAH66431	Human bone marrow
c 707	15	3.1	163	22	AAH63971	DNA encoding novel	780	15	3.1	313	21	AAH66431	Probe #6271 for ge
c 708	15	3.1	163	22	AAH63971	DNA encoding novel	781	15	3.1	313	21	AAH66431	Probe #7605 used t
c 709	15	3.1	163	22	AAH63971	Human nervous syst	782	15	3.1	313	21	AAH66431	Human neurogulin g
c 710	15	3.1	163	22	AAH63971	Human secreted pro	783	15	3.1	313	21	AAH66431	Human nervous syst
c 711	15	3.1	163	22	AAH63971	Human secreted pro	784	15	3.1	313	21	AAH66431	Human polynucleoti
c 712	15	3.1	163	22	AAH63971	Human biallelic po	785	15	3.1	313	21	AAH66431	Human polynucleoti
c 713	15	3.1	163	22	AAH63971	Human breast cell	786	15	3.1	313	21	AAH66431	Novel human polynu
c 714	15	3.1	163	22	AAH63971	Human foetal liver	787	15	3.1	313	21	AAH66431	Human secreted pro
c 715	15	3.1	163	22	AAH63971	Probe #14440 for g	788	15	3.1	313	21	AAH66431	Human 5' EST isola
c 716	15	3.1	163	22	AAH63971	Human bone marrow	789	15	3.1	313	21	AAH66431	DNA encoding a hum
c 717	15	3.1	163	22	AAH63971	Probe #13841 for g	790	15	3.1	313	21	AAH66431	Genomic sequence #
c 718	15	3.1	163	22	AAH63971	Probe #17904 used	791	15	3.1	313	21	AAH66431	Human digestive sy
c 719	15	3.1	163	22	AAH63971	Probe #9501 used t	792	15	3.1	313	21	AAH66431	Probe #5102 for ge
c 720	15	3.1	163	22	AAH63971	Human breast cell	793	15	3.1	313	21	AAH66431	Human polynucleoti
c 721	15	3.1	163	22	AAH63971	Human foetal liver	794	15	3.1	313	21	AAH66431	Human bone marrow
c 722	15	3.1	163	22	AAH63971	Probe #11430 for g	795	15	3.1	313	21	AAH66431	Human bone marrow
c 723	15	3.1	163	22	AAH63971	Human brain expres	796	15	3.1	313	21	AAH66431	Probe #4647 for ge
c 724	15	3.1	163	22	AAH63971	Human bone marrow	797	15	3.1	313	21	AAH66431	Probe #4769 used t
c 725	15	3.1	163	22	AAH63971	Human genome fragm	798	15	3.1	313	21	AAH66431	Probe #4511 used t
c 726	15	3.1	163	22	AAH63971	Human gene signatu	799	15	3.1	313	21	AAH66431	DNA encoding novel
c 727	15	3.1	163	22	AAH63971	Human secreted pro	800	15	3.1	313	21	AAH66431	Human immune/haema
c 728	15	3.1	163	22	AAH63971	Human secreted pro	801	15	3.1	313	21	AAH66431	Human prostate tum
c 729	15	3.1	163	22	AAH63971	Cat flea head and	802	15	3.1	313	21	AAH66431	Human colon cancer
c 730	15	3.1	163	22	AAH63971	Cat flea head and	803	15	3.1	313	21	AAH66431	Novel human polynu
c 731	15	3.1	163	22	AAH63971	Human breast cance	804	15	3.1	313	21	AAH66431	Human immune/haema
c 732	15	3.1	163	22	AAH63971	EST clone FJ70. H	805	15	3.1	313	21	AAH66431	Human immune/haema
c 733	15	3.1	163	22	AAH63971	Single nucleotide	806	15	3.1	313	21	AAH66431	Enterococcus faeca
c 734	15	3.1	163	22	AAH63971	Probe m198. Synth	807	15	3.1	313	21	AAH66431	Zea mays DNA fragm
c 735	15	3.1	163	22	AAH63971	Human ovarian and	808	15	3.1	313	21	AAH66431	
c 736	15	3.1	163	22	AAH63971	Human reproductive	809	15	3.1	313	21	AAH66431	
c 737	15	3.1	163	22	AAH63971	Human gene signatu	810	15	3.1	313	21	AAH66431	
c 738	15	3.1	163	22	AAH63971	Human secreted pro	811	15	3.1	313	21	AAH66431	
c 739	15	3.1	163	22	AAH63971	EST clone H01176.	812	15	3.1	313	21	AAH66431	

813	15	3.1	432	22	AAF66597	Novel human polynu	886	15	3.1	580	20	AAZ09021	Differentiation In
814	15	3.1	434	22	ABA43324	Human foetal cell	c 887	15	3.1	581	21	AAF09240	Fusarium venenatum
815	15	3.1	434	22	ABA53767	Human foetal liver	c 888	15	3.1	586	22	AAH29657	Drosophila melanog
816	15	3.1	434	22	ABA23514	Probe #1980 for ge	889	15	3.1	591	22	AAH09474	Human cDNA clone (
817	15	3.1	434	22	AAI12062	Probe #1995 for ge	890	15	3.1	594	22	ABA60763	Human foetal liver
818	15	3.1	434	22	AAI33396	Probe #2082 used t	891	15	3.1	594	22	ABA28813	Probe #7279 for ge
819	15	3.1	434	22	AAI01984	Probe #1975 used t	892	15	3.1	594	22	AAK09049	Human brain expres
820	15	3.1	436	20	AAV90509	EST clone DW665.	893	15	3.1	594	22	AAK34940	Human bone marrow
821	15	3.1	443	21	AAK59994	Human secreted pro	894	15	3.1	594	22	AAI40656	Probe #9342 used t
822	15	3.1	443	22	AAH88197	Human polynucleoti	895	15	3.1	594	22	AAH10872	Human cDNA clone (
823	15	3.1	443	22	AAH98725	Human EST-derived	c 896	15	3.1	594	24	AAH62881	Human G protein-co
824	15	3.1	444	22	AAI87083	Human polynucleoti	c 897	15	3.1	598	21	AAH79254	Human lung tumour-
825	15	3.1	445	22	AAH68101	Human lung tumour	c 898	15	3.1	598	23	AAD23330	Human lung tumour-
826	15	3.1	447	21	AAZ51090	zea mays Rad6 prot	899	15	3.1	600	19	AAV26007	Bacteriophage DNA
827	15	3.1	447	22	AAK86750	DNA encoding a Can	c 900	15	3.1	600	22	AAK11852	Human brain expres
828	15	3.1	447	22	AAK23431	Candida albicans e	901	15	3.1	600	22	AAK55306	Human brain thiore
829	15	3.1	448	22	AAI81871	Human polynucleoti	c 902	15	3.1	602	21	AAZ80136	Human colon cancer
830	15	3.1	451	23	AAK574824	DNA encoding novel	c 903	15	3.1	607	21	AAK35255	Arabidopsis thalia
831	15	3.1	452	22	ABA57711	Human foetal liver	c 904	15	3.1	608	22	AAH12915	Human cDNA clone (
832	15	3.1	452	22	AAI16622	Human breast cancer	c 905	15	3.1	617	21	AAH16165	Human colon cancer
833	15	3.1	452	22	AAK05772	Human brain expres	c 906	15	3.1	618	22	AAH11934	Human cDNA clone (
834	15	3.1	452	22	AAK31596	Human bone marrow	c 907	15	3.1	630	22	AAH07045	Human cDNA clone (
835	15	3.1	452	22	AAI37289	Probe #5975 used t	c 908	15	3.1	635	22	AAH69296	Human immune/haema
836	15	3.1	453	24	ABK16175	Human lung tumour	909	15	3.1	637	18	AAH84066	DNA encoding a Sta
837	15	3.1	460	22	ABA42863	Human breast cell	910	15	3.1	639	22	AAH53051	S. epidermidis ope
838	15	3.1	460	22	ABA53286	Human foetal liver	c 911	15	3.1	642	24	AAK97007	Corn DNA for APT2
839	15	3.1	460	22	ABA23059	Probe #1525 for ge	912	15	3.1	643	21	AAK98968	Human pancreatic c
840	15	3.1	460	22	AAK39558	DNA encoding nove	913	15	3.1	644	21	AAK51570	Arabidopsis thalia
841	15	3.1	460	22	AAK01544	Human brain expres	914	15	3.1	645	21	AAK53175	Arabidopsis thalia
842	15	3.1	460	22	AAK26989	Human bone marrow	915	15	3.1	646	21	AAK39800	Arabidopsis thalia
843	15	3.1	460	22	AAK88897	Human digestive sy	916	15	3.1	651	21	AAK33007	Arabidopsis thalia
844	15	3.1	462	22	AAI36085	Human musculoskele	917	15	3.1	655	21	AAK42004	Human secreted exp
845	15	3.1	463	22	ABA54340	Human foetal liver	c 918	15	3.1	655	22	AAK57941	Human immune/haema
846	15	3.1	463	22	AAI12643	Probe #2576 for ge	c 919	15	3.1	660	21	AAK13181	Aspergillus oryzae
847	15	3.1	469	22	AAK89469	Human digestive sy	920	15	3.1	661	22	AAK36689	Human musculoskele
848	15	3.1	469	22	AAH29331	Drosophila melanog	921	15	3.1	664	22	AAK88919	Human digestive sy
849	15	3.1	470	22	AAH93301	Phospholium falcipa	922	15	3.1	664	22	AAI57617	Human colorectal c
850	15	3.1	473	22	AAK31276	Human bone marrow	c 923	15	3.1	664	23	ABL03785	Drosophila melanog
851	15	3.1	474	22	AAH87814	Peppermint plant o	c 924	15	3.1	693	21	AAK253665	Neisseria meningit
852	15	3.1	476	22	ABA57451	Human foetal liver	c 925	15	3.1	693	22	AAK71551	Human immune/haema
853	15	3.1	476	22	ABA26952	Probe #5418 for ge	c 926	15	3.1	694	21	AAK01638	Human colon cancer
854	15	3.1	476	22	AAK05489	Human brain expres	c 927	15	3.1	699	21	AAK53664	Neisseria gonorrhoe
855	15	3.1	476	22	AAK31090	Human bone marrow	c 928	15	3.1	699	21	AAK53666	Neisseria meningit
856	15	3.1	476	22	AAI36999	Probe #5685 used t	c 929	15	3.1	699	21	AAK53667	Neisseria gonorrhoe
857	15	3.1	478	22	AAI91262	Human polynucleoti	c 930	15	3.1	699	21	AAK53668	Neisseria meningit
858	15	3.1	478	23	AAK82617	DNA encoding novel	c 931	15	3.1	699	21	AAK53669	Neisseria meningit
859	15	3.1	481	22	ABA42474	Human breast cell	c 932	15	3.1	705	21	AAK34442	Arabidopsis thalia
860	15	3.1	481	22	ABA52904	Human foetal liver	933	15	3.1	707	22	AAI97846	Human neuroblastom
861	15	3.1	481	22	ABA22685	Probe #1151 for ge	934	15	3.1	709	22	AAI24902	Human breast cancer
862	15	3.1	481	22	AAK01152	Human brain expres	c 935	15	3.1	719	21	AAK78408	Human secreted pro
863	15	3.1	481	22	AAK26614	Human bone marrow	936	15	3.1	720	19	AAV57265	Clone R2.1 from mu
864	15	3.1	481	22	AAI11242	Probe #1175 for ge	c 937	15	3.1	723	21	AAK34885	Arabidopsis thalia
865	15	3.1	481	22	AAI32507	Probe #1193 used t	c 938	15	3.1	734	22	AAH07888	Human cDNA clone (
866	15	3.1	481	22	AAI01158	Probe #1149 used t	c 939	15	3.1	736	22	AAH04586	Human cDNA clone (
867	15	3.1	489	17	AAK34476	Neurite cDNA clone	c 940	15	3.1	737	21	AAK77438	Human ORFX ORF2993
868	15	3.1	489	20	AAZ09873	Human neurite cDNA	c 941	15	3.1	737	22	AAI94916	Human neuroblastom
869	15	3.1	490	22	AAI23236	Human breast cancer	c 942	15	3.1	741	22	AAH06089	Human cDNA clone (
870	15	3.1	491	22	AAH10670	Human cDNA clone (	c 943	15	3.1	747	21	AAK16535	Human colon cancer
871	15	3.1	492	22	AAH12488	Human cDNA clone (	944	15	3.1	751	21	AAK43827	Mouse secreted exp
872	15	3.1	505	22	AAK92608	Human cDNA 3'-end	c 945	15	3.1	752	20	AAK20434	Human secreted pro
873	15	3.1	520	22	AAI86602	Human polynucleoti	c 946	15	3.1	752	22	AAH32952	Human colon cancer
874	15	3.1	528	20	AAK84705	Human metastatic m	c 947	15	3.1	754	20	AAZ15610	Human gene express
875	15	3.1	534	22	ABA61780	Human foetal liver	c 948	15	3.1	754	20	AAZ15588	Human gene express
876	15	3.1	534	22	AAI20615	Human breast cancer	c 949	15	3.1	755	20	AAZ15590	Human gene express
877	15	3.1	534	22	AAI41699	Probe #10385 used	c 950	15	3.1	755	20	AAZ15589	Human gene express
878	15	3.1	534	23	AAK55814	Streptococcus pneu	951	15	3.1	756	22	AAH33954	Human colon cancer
879	15	3.1	541	21	AAA44053	Human secreted exp	952	15	3.1	758	20	AAZ15984	Human gene express
880	15	3.1	541	22	ABA12507	Human nervous syst	953	15	3.1	763	21	AAAF09113	Fusarium venenatum
881	15	3.1	545	22	AAK93437	Umbilical vein end	c 954	15	3.1	766	22	AAH94026	Human foetal cDNA,
882	15	3.1	550	21	AAK94970	Cat flea hindgut a	955	15	3.1	783	22	AAH03436	Human cDNA clone (
883	15	3.1	553	21	AAK54988	Arabidopsis thalia	c 956	15	3.1	787	20	AAZ17095	Human gene express
884	15	3.1	560	21	AAK75790	Human ORFX ORF1345	c 957	15	3.1	787	20	AAZ17096	Human gene express
885	15	3.1	563	19	AAK14583	H. pylori GHPO 167	c 958	15	3.1	791	20	AAZ17080	Human gene express

c 959	15	3.1	791	20	AAZ17099
c 960	15	3.1	791	21	AAH01670
c 961	15	3.1	794	22	AAH03478
c 962	15	3.1	797	22	AAK92128
c 963	15	3.1	797	22	AAK93392
c 964	15	3.1	810	22	AAI94452
c 965	15	3.1	810	22	AAI95919
c 966	15	3.1	825	22	AAI92614
c 967	15	3.1	828	22	AAH03692
c 968	15	3.1	828	22	AAH08444
c 969	15	3.1	830	22	AAI17249
c 970	15	3.1	833	23	AAH86336
c 971	15	3.1	837	22	ABA19160
c 972	15	3.1	851	21	AACT7917
c 973	15	3.1	851	22	AAH33210
c 974	15	3.1	852	21	AAH38561
c 975	15	3.1	853	21	AAH39867
c 976	15	3.1	854	22	AAH06956
c 977	15	3.1	859	22	AAI20030
c 978	15	3.1	860	22	AAH03300
c 979	15	3.1	867	22	AAH06703
c 980	15	3.1	867	22	ABA06865
c 981	15	3.1	875	23	AAH866339
c 982	15	3.1	884	21	AAH96504
c 983	15	3.1	884	22	AAH91928
c 984	15	3.1	890	22	AAH99176
c 985	15	3.1	917	22	AAH98958
c 986	15	3.1	920	21	AAH96889
c 987	15	3.1	939	22	AAH32032
c 988	15	3.1	942	22	AAH98890
c 989	15	3.1	942	22	AAI10302
c 990	15	3.1	943	21	AAZ99420
c 991	15	3.1	945	22	AAZ23439
c 992	15	3.1	953	22	AAI19154
c 993	15	3.1	954	23	AAH83540
c 994	15	3.1	975	22	AAH91905
c 995	15	3.1	979	23	ABL14641
c 996	15	3.1	993	21	AAH37259
c 997	15	3.1	1019	22	AAH44366
c 998	15	3.1	1023	22	AAI19153
c 999	15	3.1	1026	21	AAH67627
c 1000	15	3.1	1033	21	AAH42022

## ALIGNMENTS

RESULT 1  
AAT00524  
ID AAT00524 standard; cDNA; 489 bp.  
XX  
AC AAT00524:

DT 02-FEB-1996 (first entry)

DE Simian interleukin-15 precursor.

**KW** Interleukin-15; epithelium-derived T-cell factor; T lymphocyte; ss.

OS *Cebus apella*.

Key	Location/Qualifiers
CDS	1..489
FT	/tag= a
FT	/note= "claimed"
FT	145..489
FT	/tag= b
FT	/note= "claimed"
misc_feature	

PN W09527722-A.

19-OCT-1995.

PF 06-APR-1994; 94WO-US03793.  
XX  
PR 06-APR-1994; 94WO-US03793.  
XX  
PA (IMMV) IMMUNEX CORP.

PT Isolated DNA encoding polypeptide with mammalian IL-15 activity - which  
PT stimulates proliferation and differentiation of T cells, used for  
PT treating carcinoma(s), melanomas, etc. and viral infections

PS Claim 28; Page 26; 48pp; English.

A simian species of IL-15 (sIL-15) was purified and analysed by SDS-PAGE. Bioassay of unstained gel slices indicated IL-15 activity was assoc. with proteins having mol. wts in the range of 15-17 kDa. The N-terminus of the 15-17 kDa was sequenced. The results indicated the identity of the first 33 AAs of AAR83309. Subsequent sequencing of a cDNA clone obtd. from a simian library provided a sequence encoding the polypeptide AAR83436. AAR83436 comprises a relatively short 48 AA leader sequence and a mature polypeptide AAR83309. The sequence of the N-terminal 31 AAs of AAR83309 was used to design synthetic PCR primers for the amplification of IL-15-specific DNA sequences. The first 6 AAs of the N-terminus were used to design one primer, a degenerate mixture coding for all possible codon usages - AAT00528. The AA sequences of the simian mature N-terminus 26-31 were used to design a second primer, a degenerate mixture coding for a complement of all possible codon usages of AAs 26-31, omitting posn. 3 of Val (AAT00529, AAT00530). Polyadenylated RNAs from CV-1/EBNA cells were used as templates. A 92 bp DNA fragment was used as a hybridisn. probe to screen a portion of a plasmid library contg. cDNA inserts prepd. from CV-1/EBNA polyadenylated RNA. This resulted in the isolation of clone C85.sIL-15 that has an ORF given in AAT00524. AAR83309 is the active polypeptide & AAR83436 is the precursor polypeptide.

Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other;

Query Match	100.0%	Score 489;	DB 16;	Length 489;
Best Local Similarity	100.0%	Pred. No. 5.1e-231;		
Matches 489;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

QY	1	ATGAGAAATTTTCGAAACCAACACATTTTGAGAAGATATTTCCATCCAGTCGTACCTGTGTTTACTT	60
Db	1	atgagaatttcgaaccacatttgagaagatttccatccagtgcctacctgtgtttactt	60
QY	61	CTAAGAGTCATTTTCTAACTGAAGCTTGGCATTCATGTCTTCAATTTTGGCGTGTTCAGT	120
Db	61	ctaaagagtcattttcttaactgaagctggcatcattgtcttcattttgggctgttccagt	120
QY	121	GCAGGGCTCCCTFAAACAGAGCAACTGGTGAATGTAATAGTCATTTTGAAAAAATT	180
Db	121	gcagg9ctccctcaaacagagccaaactgg9tgaa9tgaatgaatttgaaaaaatt	180
QY	181	GAAGATCTTATTCAATCTATGCATATTGATGCTACTTTATATACAGAAAGTCATGTTCAAC	240
Db	181	gaagatcttattcaatctatgcatttga9tgcattttatatcacagaagtgatgttcaac	240
QY	241	CCGAGTTGCAGGTTACAGCAATGAAGTGGTCTTCTCTTGAGTTGCAAGTATATTTACAT	300
Db	241	ccagttgcagg9taaacagcaatgaagtgcttctctcttggag9tgcgaagtattttccat	300
QY	301	GAGTCCGGAGATACAGATATTCATGATACAGTAGAANAATCTTATCATCTCTACCAACACAC	360
Db	301	gag9tccggagatcacagatatttca9cacag9tagaanaatttatcatctctagcaaacac	360
QY	361	ATCTTGTCCTTCTAATGGGAATATACAGAATCTGGATGCAAAAGATGTGAGGAACATGAG	420

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Db 361 atctgtcttcaatgggaataacagactggaatgcaagaatgtgagaactagag 420
QY 421 GAAAAAATAATTAAGAATTTTGGAGAGTTTGTACATATTGTCCAAATGTTCAATCAAC 480
Db 421 gaaaaaataattaaagaatttttgagagttttgtacatatgtccaaatgttcatcaac 480
QY 481 ACTTCTTGA 489
Db 481 acttcttga 489

RESULT 2
AAQ84583
ID AAQ84583 standard; cDNA; 489 BP.
XX
AC AAQ84583;
XX
DT 04-SEP-1995 (first entry)
XX
DE Simlan IL-15 clone C85.sIL-15.
XX
KW Interleukin-15; IL-15; sIL-15; T-cell growth factor;
KW African green monkey; CV-1; antitumor; virucide; ss.
XX
OS Cercopithecus aethiops.
XX
FH Key Location/Qualifiers
FT CDS 1..489
FT /tag= a
FT /product= IL-15 precursor
FT sig_peptide 1..144
FT /tag= b
FT mat_peptide 145..486
FT /tag= c
FT /product= mature IL-15
XX
XX ZA9402636-A.
XX
XX 28-DEC-1994.
PD
XX 18-APR-1994; 94ZA-0002636.
PF
XX 18-APR-1994; 94ZA-0002636.
PR
XX (IMMV ) IMMUNEX CORP.
PA
XX
XX Anderson DM, Eisenman JR, Fung V, Grabstein KH;
PI Rauch C;
XX
XX WPI: 1995-082473/11.
DR P-PSDB; AAR66926.
XX
XX New purified interleukin-15 - which induces T cell proliferation
PT and differentiation, used for the treatment of tumours and viral
PT infection
XX
XX Disclosure; Page 26; 47pp; English.
PS
XX
XX cDNA generated from PMA-stimulated CV-1/EBNA cells was amplified
CC by PCR using primers based on the N-terminal sequence of simlan
CC interleukin-15 (sIL-15). A probe based on an isolated clone was used
CC to screen a plasmid library containing cDNA inserts prepared from
CC CV-1/EBNA poly-A RNA. Clone C85.sIL-15 was isolated that has the
CC ORF given in AAQ84583.
XX
XX Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other;
SQ

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Query Match 100.0%; Score 489; DB 16; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-231;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGAGAAATTCGAACACACATTTTGAGAGTATTTCATCCAGTCTACCTGTTGTTACTT 60
Db 1 a g a g a a t t c g a a c c a c a t t t g a g a a g c a t t t c c a t c c a g t g c c a c c t g t t c a c t t 60
QY 61 CTAAAGAGTCATTTTCTAACTGAAGCTGGCATTTCATGCTCTTCAATTTTGGGCTGTTTCAGT 120
Db 61 c t a a g a g a g t c a t t t t c t a a c t g a a g c t g g c a t t c a t g t c t c a t t t t g g g c t g t t c a g t 120
QY 121 GCAGGGCTCCCTAAACACAGAACGCCAACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTT 180
Db 121 g c a g g g c t c c c t a a a c a c a g a a g c c a a c t g g t g a a t g t a a a g t a t t t g a a a a a a t t 180
QY 181 GAAGATCTTATTCATCTATGCAATATTGATATTGCTACTTTTATATACAGAAAGTGATGTTCAAC 240
Db 181 g a a g a t c t t a t t c a a t c t a t g c a t a t t g a t g c t a c t t t a t a t a c a g a a a g t g a t g t t c a c 240
QY 241 CCCAGTTGCAAGGTAACAGCAATGAAGTGCTTTCTCTTGAGTTGCAAGTTATTTACATCAT 300
Db 241 c c c a g t t g c a a g g t a a c a g c a a t g a a g t g c t t t c t c t t g g a g t t g c a a g t a t t t c a c a t 300
QY 301 GAGTCGGGAGATACAGATATTTCATGATACAGTAGAGAAAATCTTATCATCTCTAGCAACAAC 360
Db 301 g a g t c g g g a g a t a c a g a t a t t t c a t g a t a c a g t a g a a a t c t t a t c a t c c t a g c a a a c a c 360
QY 361 ATCTTGCTCTTAATGGGAATATAACAGAAATCTGGATGCAAGAAATGTGAGGAAC TAGAG 420
Db 361 a t c t t g c t c t t a a t g g g a a t a t a a c a g a a t c t g g a t c g g a a g a a t g t g a g g a a c t a g a g 420
QY 421 GAAAAAATATTAAAGAATTTTTCGAGAGTTTGTACATATTGTCCTCAAAATGTTTCATCAAC 480
Db 421 g a a a a a a t a t t a a a g a a t t t t t g c a g a g t t t g t a c a t a t t g t c c a a a t g t t c a a c a c 480
QY 481 ACTTCTTGA 489
Db 481 acttcttga 489

RESULT 3
AAT49456
ID AAT49456 standard; cDNA; 489 BP.
XX
AC AAT49456;
XX
DT 11-MAR-1997 (first entry)
XX
DE Human epithelium derived T cell factor cDNA.
XX
KW hETF; human IMTLH bone marrow stromal cell line; T-cell; B-cell;
KW lymphocyte; proliferation; differentiation; gastrointestinal;
KW HIV infection; human immunodeficiency virus; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FT CDS 1..489
FT /tag= a
FT mat_peptide 145..486
FT /tag= b
FT /product= hETF
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XX US5574138-A.
PN
XX 12-NOV-1996.
PD
XX 08-MAR-1993; 93US-0031399.
PF
XX 22-FEB-1995; 95US-0393305.
PR
XX 08-MAR-1993; 93US-0031399.
PR
XX 22-APR-1994; 94US-0233606.
PR
XX (IMMV ) IMMUNEX CORP.
XX
XX Anderson DM, Eisenman JR, Fung V, Grabstein KH;
PI

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QY 241 CCCAGTTGCAAGGTAAACAGCAATGAAGTCTTTCTTCTTGAGCTTGCAAGCTTATTTTCACAT 300  
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Db 241 cccagttgcaaggttaacagcaaatgaagtctttcttcttggagttgcaagttatttcacat 300  
QY 301 GAGTCCGGAGATACAGATATTCATGATACAGTAGAGAAATCTTTATCATCTCCTAGCAACAAC 360  
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Db 301 gagtccggagatacagatatctatgatcacagttagaaaattcttatcatctctagcaacaac 360  
QY 361 ATCTTGCTCTCTTAATGGGAATATAACAGAACTCTGGATGCAAGAATGTGAGGAACATAGAG 420  
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Db 361 atcttgctctcttaatgggaataataacagaatctggtatgcaagaatgtgaggaactagag 420  
QY 421 GAAAAAATATTAAGGAATTTTTCAGAGCTTTTGTACATATTTGTCCAAATGTTTCATCAAC 480  
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Db 421 gaaaaaatattaaagaatttttcagagttttgtacatatgttccaaaattgttcatcaac 480  
QY 481 ACTTCTTTGA 489  
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Db 481 acttcttga 489

RESULT 5  
AAV02874 standard; cDNA; 489 BP.  
AC AAT36634;  
XX AAT36634;  
DT 17-NOV-1996 (first entry)  
XX Simian interleukin-15 cDNA.  
DE Interleukin-15; antagonist; mutein; graft versus host disease;  
KW allograft; T-cell growth factor; ss.  
XX Unspecified simian.  
OS WO9626274-A1.  
PN 29-AUG-1996.  
XX 21-FEB-1996; 96WO-US02520.  
PF 22-FEB-1995; 95US-0392317.  
PR (IMV ) IMMUNEX CORP.  
XX Grabstein KH, Paxton RJ, Pettit DK;  
PI WPI; 1996-402367/40.  
DR P-PSDB; AAR98526.  
XX Antagonists of interleukin-15 - are used to treat patients having  
PT symptoms of graft-versus-host disease and for prolonging allo:graft  
PT survival  
XX Disclosure; Page 24; 32pp; English.  
PS A cDNA clone (AAT36634) codes for simian interleukin-15 (IL-15)  
CC (AAR98526), a T-cell growth factor. Muteins of simian IL-15 or  
CC human IL-15 (see also AAR98527) are useful as antagonists of IL-15  
CC and can be prep'd. by PCR-mediated mutagenesis of the encoding  
CC sequences. Preferred muteins have amino acid substitutions at  
CC Asp56 and/or Gln156 of the IL-15 protein that prevent signal  
CC transduction. They are useful for treating graft-versus-host  
CC disease and for prolonging allograft survival.  
XX Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other;  
SQ

Query Match 100.08; Score 489; DB 17; Length 489;  
Best Local Similarity 100.08; Pred. No. 5.le-231;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCAGAAATTCGAAACACACATTTGAGAAGTATTTCCATCCAGTCTACCTGTCTTACTTT 60  
|||||  
Db 1 atgagaatttcgaaccacacatttgagaagtatttccatccagtgctacctgtgttactt 60  
QY 61 CTAAGAGATCATTTTCTAACTGAAGCTGGCATTCATGTCTTCAATTTTGGGCTGTTTCAGT 120  
|||||  
Db 61 ctaagagatcatttttctaactgaagctggcattcagtccttcattttgggctgtttcagt 120  
QY 121 GAGGGCTCCCTAAACACAGAAGCCAACTGGGTGAATGTATTAAGTGATTTGAAAAAATT 180  
|||||  
Db 121 gcagggctccctaaacacagaagccaaactgggtgaatgtaataagtattttgaaaaaatt 180  
QY 181 GAAGATCTTATCAATCTATGCATATTTGATGCTACTTTTATATACAGAAAGTGATGTTCC 240  
|||||  
Db 181 gaagatcttattcaactctatgcatattgctgctactttatatcacagaagtgatgttcc 240  
QY 241 CCCAGTTGCAAGGTAACAGCAATGAAGTCTTTCTTCTTGAGTTGCAAGTTATTTTCACAT 300  
|||||  
Db 241 cccagttgcaaggttaacagcaaatgaagtgtcttctcttgagttgcaagttatttcacat 300  
QY 301 GAGTCCGGAGATACAGATATTTCAATGATACAGTAGAGAAATCTTTATCATCTCCTAGCAACAAC 360  
|||||  
Db 301 gagtccggagatacagatatctatgatcacagttagaaaattcttatcatctctagcaacaac 360  
QY 361 ATCTTGCTCTCTTAATGGGAATATAACAGAACTCTGGATGCAAGAATGTGAGGAACATAGAG 420  
|||||  
Db 361 atcttgctctcttaatgggaataataacagaatctggtatgcaagaatgtgaggaactagag 420  
QY 421 GAAAAAATATTAAGGAATTTTTCAGAGCTTTTGTACATATTTGCCAAATGTTTCATCAAC 480  
|||||  
Db 421 gaaaaaatattaaagaatttttcagagttttgtacatatgttccaaaattgttcatcaac 480  
QY 481 ACTTCTTTGA 489  
|||||  
Db 481 acttcttga 489

RESULT 6  
AAV02874 standard; DNA; 489 BP.  
ID AAV02874 standard; DNA; 489 BP.  
XX AC AAV02874;  
XX AC AAV02874;  
DT 08-MAY-1998 (first entry)  
XX Human epithelium derived T-cell factor DNA.  
DE Epithelium derived T-cell factor; ETF; human; gastrointestinal disease;  
KW B-cell stimulation; epithelium; villi; CD8+; CD4+; T-cell stimulation;  
KW treatment; prevention; ss.  
XX Homo sapiens.  
OS Key Location/Qualifiers  
FH 1..489  
FT CDS /tag= a  
FT /product= ETF  
FT sig\_peptide 1..144  
FT /tag= b  
FT mat\_peptide 145..486  
FT /tag= c  
FT /product= ETF  
FT /note= "Epithelium-derived T-cell factor"  
XX US5707616-A.  
PN  
XX  
PD 13-JAN-1998.  
XX  
PF 04-OCT-1996; 96US-0726817.  
XX  
XX 22-FEB-1995; 95US-0393305.  
PR 08-MAR-1993; 93US-0031399.  
PR

```
PR 22-APR-1994; 94US-0233606.
XX (IMMV ) IMMUNEX CORP.
XX
XX Anderson DM, Eisenman JR, Fung V, Grabstein KH;
PI Rauch C;
XX
XX WPI: 1998-100295/09.
XX P-PSDB; AAW39187.
XX
XX Treatment or prevention of gastrointestinal diseases - by
PT administering epithelium-derived T-cell factor polypeptide
PT
XX Claim 1C; Column 37-40; 34pp; English.
XX
XX This sequence encodes a human epithelium-derived T-cell factor (ETF)
CC which is used in a method for treating or preventing gastrointestinal
CC disease. These polypeptides have particular application in the treatment
CC of gastrointestinal disorders associated with disruption of the
CC gastrointestinal epithelium or villi such as chemotherapy- and
CC radiation-therapy induced enteritis (gut toxicity), mucositis, peptic
CC ulcer disease, gastroenteritis and colitis, villus atrophic disorders,
CC malignancy and inflammatory bowel disease. ETF polypeptides may also be
CC useful in the treatment of human immunodeficiency virus (HIV) and
CC HIV-associated disease due to their ability to stimulate CD4+ and CD8+
CC cells. Biologically active ETF may be used to treat a variety of other
CC diseases or conditions where T-cell or B cell stimulation is desired.
XX
XX Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other;
SQ

Query Match 100.0%; Score 489; DB 19; Length 489;
Best Local Similarity 100.0%; Pred. No. 5.1e-231;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTTCCAAACCCACATTTTGAGAGTATTTCATCCAGTGTCTGTTTACTTT 60
DB 1 atgagaatttcgaaccacatttgagaagtatttcacatccagtgctacctgtgttactt 60
QY 61 CTAAAGAGTCATTTTCTAACTGAAGCTGGCATTCATGTCTTTCATTTTGGCTGTTCAGT 120
DB 61 ctaagagtcattttctaactgaagtcgaagtcattcattgtcttcatcttggcgctgttca 120
QY 121 GCAGGGCTCCCTAAACAGACGCCAACCTGGGTGAATGTAAATGAAGTATTTGAAAAAATT 180
DB 121 gcagggtctccctaaacagacgccaaactgggtgaatgtaataagtgatttgaaaaaatt 180
QY 181 GAAGATCTTTATTCATCTATGTCATATTGATGCTACTTTATATACAGAAAGTGTTCAC 240
DB 181 gaagatctttatctcatctatgcatattgatgctactttatacacggaagtgatgttca 240
QY 241 CCCAGTTCGAAGGTAACAGCAATGAAGTGCTTTCTCTTGGAGTTGCAAGTTATTTTCACAT 300
DB 241 cccagttgcaaggttaacagcaatgaagtgctttctcttggagttgcaagttatttca 300
QY 301 GAGTCGGAGATACAGATATTTCATGATACAGTAGAGAAATCTTATCATCTCAGCAACAAC 360
DB 301 gagtcggagatcacagatttcattgatcacagttagaaaaatttatcatctcctagca 360
QY 361 ATCTGTCTTCTTAATGGGAATATAACAGAAATCTGGATGCAAGAAATGTGAGGAAGTAGAG 420
DB 361 atctgtcttcttaa199gaataatacagaatcttgatgcaagaagaatgtgaggaaactag 420
QY 421 GAAAAAATATTAAAGAAATTTTTCGAGAGTTTTTGACATATTGTCCAAATGTTTCATCAAC 480
DB 421 gaaaaaattataaagaatttttgcagagttttgtacatattgtccaaatgttcatcaac 480
QY 481 ACTTCTTGA 489
DB 481 acttcttga 489

RESULT 7
```







QY 445 CAGAGTTTGTACATATTGTCCAAATGTTTCATCAACACTTCTTGA 489  
|||||  
Db 301 cagagttttgtacatattgtccaaatgttcatcaacacttcttga 345

## RESULT 12

AAF57025  
ID AAF57025 standard; cDNA; 345 BP.

XX AAF57025;

XX 14-MAY-2001 (first entry)

DE Human ETF (hETF) mature polypeptide encoding cDNA.

XX Epithelium-derived T-cell factor; ETF; simian; human; enteritis;  
KW gastrointestinal disease; mucositis; peptic ulcer; cytostatic;  
KW villus atrophic disorder; inflammatory bowel disease; antiinflammatory;  
KW anti-HIV; antiviral; T-lymphocyte stimulator; ss.

XX Homo sapiens.

XX Key Location/Qualifiers  
FH CDS 1..345  
FT /\*tag= a  
FT /product= "mature hETF"  
XX

PN US6184359-B1.

XX 06-FEB-2001.

XX 09-NOV-1998; 98US-0189193.

XX 22-FEB-1995; 95US-0393305.

PR 04-OCT-1996; 96US-0725969.

PR 08-MAR-1993; 93US-0031399.

PR 22-APR-1994; 94US-0233606.

XX (IMMV ) IMMUNEX CORP.

XX Grabstein KH, Anderson DM, Eisenman JR, Fung V, Rauch C;

XX WPI; 2001-217801/22.

DR P-PSDB; AAB62015.

XX New antibodies that specifically binds epithelium-derived T-cell factor

PT polypeptide useful for e.g. treating or preventing gastrointestinal

PT diseases, HIV and HIV-associated diseases, augmenting destruction of

PT tumour cells -

XX Disclosure; Fig 2; 35pp; English.

XX The invention relates to simian and human epithelium-derived T-cell  
CC factor (ETF) polypeptides. Antibodies that specifically bind to the ETF  
CC polypeptides are used for treating or preventing gastrointestinal  
CC diseases, such as chemotherapy and radiation therapy-induced enteritis  
CC and mucositis, peptic ulcer disease, villus atrophic disorders and  
CC inflammatory bowel disease; for increasing tolerated doses for radiation  
CC therapy and chemotherapy agents which are limited by gastrointestinal  
CC toxicity; and for treating HIV and HIV-associated diseases. The  
CC antibodies are further used to treat a variety of other diseases or  
CC conditions where it is desired to stimulate proliferation of  
CC T-lymphocytes and B lymphocytes, or the secretion of immunoglobulin B  
CC LAK or NK lytic activity, or to augment the destruction of tumour cells  
CC or cells infected with virus. The present sequence represents a cDNA  
CC encoding the human ETF (hETF) mature polypeptide.

XX Sequence 345 BP; 124 A; 50 C; 64 G; 107 T; 0 other;

## Query Match

70.6%; Score 345; DB 22; Length 345;

Best Local Similarity 100.0%; Pred. No. 4.5e-160;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 AACTGGGTGAATGTAATAAGTATTTGAAAAAATTCGAAGATCTTATTCAATCTATGTCAT 204  
|||||  
Db 1 aactgggtgaatgtaataagattttgaaaaaattggaagatcttattcattccatcgcacat 60

QY 205 ATTGATGCTACTTTATATACAGAAAGTGATGTTTCAACCCAGTTGCAAGGTAACAGCAATG 264  
|||||  
Db 61 attgatgctactttattatatacagaaagtgatgttcacccagttgcaaggtaacagcaatg 120

QY 265 AAGTGTCTTCTCTTGGAGTTGCAAGTTATTTCACATGAGTCCGAGATACAGATATTTCAT 324  
|||||  
Db 121 aagtgtcttctcttggagttgcaagttatttccatgagtcaggagagatagatattcat 180

QY 325 GATACAGTACAAAATCTTATCATCCTAGCAAAACACATCTTGCTTCTTAATGGCAATATA 384  
|||||  
Db 181 gatacagtagaaatcttcatcctcctagcaaacacatcttcttcttaattggaatata 240

QY 385 ACAGAAATCTGGATGCAAGAATGTGAGAACTAGAGAGAAAAAATAATTAAGAATTTTGG 444  
|||||  
Db 241 acagaatctggatgcaagaatgtgaggaactagagagaaaaataatttttg 300

QY 445 CAGAGTTTGTACATATTGTCCAAATGTTTCATCAACACTTCTTGA 489  
|||||

Db 301 cagagttttgtacatattgtccaaatgttcatcaacacttcttga 345

## RESULT 13

AAT00526

ID AAT00526 standard; cDNA; 489 BP.

XX AAT00526;

XX 02-FEB-1996 (first entry)

DE Human interleukin-15 precursor.

XX Interleukin-15; epithelium-derived T-cell factor; T lymphocyte; ss.

XX Homo sapiens.

XX Key Location/Qualifiers  
FH CDS 1..489  
FT /\*tag= a  
FT /note= "claimed"

FT misc\_feature 145..489

FT /\*tag= b  
FT /note= "claimed"

XX WO9527722-A.

XX 19-OCT-1995.

XX 06-APR-1994; 94WO-US03793.

XX 06-APR-1994; 94WO-US03793.

XX (IMMV ) IMMUNEX CORP.

XX Anderson DM, Eisenman JR, Fung V, Grabstein KH;

XX Rauch C;

XX WPI; 1995-373556/48.

DR P-PSDB; AAR83438.

XX Isolated DNA encoding polypeptide with mammalian IL-15 activity - which  
PT stimulates proliferation and differentiation of T cells, used for  
PT treating carcinoma(s), melanomas, etc. and viral infections  
XX Claim 36; Page 28-29; 48pp; English.

XX A simian species of IL-15 (sIL-15) was purified and its AA

sequence and cDNA sequence analysed (see AAR83309, AAR83436, AAT00524, AAT00525). Both the simian and the human ORFs encode a precursor polypeptide (AAR83436, AAR83438). The precursor polypeptides each comprise a 48-AA leader sequence and a sequence encoding mature simian or human IL-15 polypeptides. The active simian and human IL-15 polypeptides are disclosed in AAR83309 & AAR83310 respectively. The invention also comprises other mammalian IL-15, including human IL-15, that hybridise to probes defined by AAR83438. A plasmid contg. a recombinant clone of human IL-15 cDNA was deposited with ATCC on Feb. 19 1993 under ATCC 69245. The deposit was named I41-hETF. AAR83435 is a mammalian mature IL-15 polypeptide. It is a generic sequence which encompasses both AAR83309 (simian) and AAR83310 (human) IL-15 mature polypeptides.

XX  
SQ Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 21.9%; Score 107; DB 16; Length 489;  
Best Local Similarity 99.4%; Pred. No. 7.8e-43;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTGCTCTTCATTTTGGCTGTTTCAGTGCAGGG 126  
|||||  
Db 67 agtcatttttctaactgaagctggcattgctcttcattttggctgtttcagtgcaagg 126  
|||||  
QY 127 CTCCTAAAACAGACCAACTGGTGAATGTAATAGTGATTGAAAAAATTGAAGAT 186  
|||  
Db 127 ctctctaaaacagacccaactgggtgaatgtaataagtattgaaaaaattgaagat 186  
|||||  
QY 187 CTTATTCAATCTATGATATGATGCTACTTTATATAC 224  
|||||  
Db 187 cttattcaatctatgatattgatgtactttatatac 224  
|||||

RESULT 14  
AAQ84584  
ID AAQ84584 standard; cDNA; 489 BP.  
XX  
AC AAQ84584;  
XX  
DT 04-SEP-1995 (first entry)  
XX  
DE Human IL-15 clone I41.hETF.  
XX  
KW Interleukin-15; IL-15; hIL-15; T-cell growth factor;  
KW antitumor; virucide; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..489  
FT /\*tag= a  
FT /product= IL-15 precursor  
FT sig\_peptide 1..144  
FT /\*tag= b  
FT mat\_peptide 145..486  
FT /\*tag= c  
FT /product= mature IL-15  
XX  
PN ZA9402636-A.  
XX  
PD 28-DEC-1994.  
XX  
PF 18-APR-1994; 94ZA-0002636.  
XX  
PR 18-APR-1994; 94ZA-0002636.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;  
PI Rauch C;  
XX  
DR WPI; 1995-082473/11.

DR P-PSDB; AAR66927.  
XX  
PT New purified interleukin-15 - which induces T cell proliferation and differentiation, used for the treatment of tumours and viral infection  
XX  
PS Disclosure; Page 28-29; 47pp; English.  
XX  
CC A siL-15 probe was prepared from isolated simian interleukin-15 cDNA and used to screen a cDNA library generated from the IMTLH cell line derived from human bone marrow stromal cells. Clone I41.hETF encoded human IL-15.  
XX  
SQ Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 21.9%; Score 107; DB 16; Length 489;  
Best Local Similarity 99.4%; Pred. No. 7.8e-43;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTGCTCTTCATTTTGGCTGTTTCAGTGCAGGG 126  
|||||  
Db 67 agtcatttttctaactgaagctggcattgctcttcattttggctgtttcagtgcaagg 126  
|||||  
QY 127 CTCCTAAAACAGACCAACTGGTGAATGTAATAGTGATTGAAAAAATTGAAGAT 186  
|||  
Db 127 ctctctaaaacagacccaactgggtgaatgtaataagtattgaaaaaattgaagat 186  
|||||  
QY 187 CTTATTCAATCTATGATATGATGCTACTTTATATAC 224  
|||||  
Db 187 cttattcaatctatgatattgatgtactttatatac 224  
|||||

RESULT 15  
AAT49455  
ID AAT49455 standard; cDNA; 489 BP.  
XX  
AC AAT49455;  
XX  
DT 11-MAR-1997 (first entry)  
XX  
DE Simian epithelium derived T cell factor cDNA.  
XX  
KW sETF; African green monkey; CV1/EBNA cell; T-cell; B-cell;  
KW lymphocyte; proliferation; differentiation; gastrointestinal;  
KW HIV infection; human immunodeficiency virus; ss.  
XX  
OS Cercopithecus aethiops.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..489  
FT /\*tag= a  
FT mat\_peptide 145..486  
FT /\*tag= b  
FT /product= sETF  
XX  
PN US5574138-A.  
XX  
PD 12-NOV-1996.  
XX  
PF 08-MAR-1993; 93US-0031399.  
XX  
PR 22-FEB-1995; 95US-0393305.  
PR 08-MAR-1993; 93US-0031399.  
PR 22-APR-1994; 94US-0233606.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;  
PI Rauch C;  
XX  
DR WPI; 1996-517923/51.  
DR P-PSDB; AAW09098 AND AAW09099.

XX New epithelium derived T cell factor - induces proliferation of T  
PT and B cells, stimulates destruction of tumour and virus-infected  
PT cells and protects against toxicity, partic. for treating intestinal  
PT disease and HIV infection  
XX  
XX Claim 1; Fig 1; 35pp; English.  
XX  
XX The simian ETF (epithelium derived T cell factor) was isolated from  
CC African green monkey CV1/EBNA cell conditioned medium. The N-  
CC terminal sequence of the purified sETF was determined and then PCR  
CC primers were designed based on the sequence information. A 92 bp  
CC fragment was amplified from CV1/EBNA DNA and was used as a probe to  
CC screen a CV1/EBNA cDNA library for the full-length sETF coding  
CC sequence (i.e. the present sequence). Mature sETF induces  
CC proliferation and/or differentiation of precursor or mature T cells  
CC and is useful for promoting long-term in vitro culture of  
CC T-lymphocytes and T-cell lines. It is used for treating  
CC gastrointestinal diseases including peptic ulcer, colitis and  
CC malignancy and for treating HIV infection.  
XX  
XX Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;  
SQ

Query Match 21.9%; Score 107; DB 17; Length 489;  
Best Local Similarity 99.4%; Pred. No. 7.8e-43;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126  
|||||  
Db 67 agtcatttttctaactgaagctggcattcatgtcttcatttttgggctgtttcagtcaggg 126  
|||||

QY 127 CTCCTTAAACAGACGCAACTGGTGAATGTAATAGTCAATTTGAAAAAATTGAAGAT 186  
|||||  
Db 127 cttcctaaacagacagccaaactgggtgaatgtaataagtgatttgaaaaaattgaagat 186  
|||||

QY 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224  
|||||  
Db 187 cttattcaatctatgcattattgatgctactttatatac 224  
|||||

RESULT 16  
AAT42243  
ID AAT42243 standard; DNA; 489 BP.  
XX  
XX AAT42243;  
XX  
XX 05-FEB-1997 (first entry)  
XX Human epithelium-derived T cell factor gene.  
XX  
XX Epithelium-derived T-cell factor; simian; human; culture; proliferation;  
KW epithelial cell; differentiation; T-lymphocyte; African green monkey;  
KW primer; PCR; polymerase chain reaction; amplification; probe; ss.  
XX  
XX Homo sapiens.  
XX  
XX key Location/Qualifiers  
FH sig\_peptide 1..144  
FT /\*tag= a  
FT mat\_peptide 145..486  
FT /\*tag= b  
XX  
XX US5552303-A.  
XX  
XX 03-SEP-1996.  
XX  
XX 08-MAR-1993; 93US-0031399.  
XX  
XX 08-MAR-1993; 93US-0031399.  
XX  
XX (IMMV ) IMMUNEX CORP.

PI Anderson D, Eisenman J, Fung V, Grabstein K, Rauch C;  
XX WPI; 1996-412063/41.  
DR P-PSDB; AAW07255.  
XX  
XX New isolated simian and human epithelium-derived T-cell factors -  
PT which stimulate the proliferation and/or differentiation of  
PT T-lymphocytes and T-cell lines  
XX  
XX Claim 21; Column 23-24; 22pp; English.  
XX  
XX This is the nucleotide sequence encoding a human epithelium-derived  
CC T-cell factor (ETF). The gene was obtained using a 1.37 kb fragment of  
CC the corresp. African green monkey gene (AAT42243) as a probe to screen a  
CC cDNA library constructed from RNA derived from the IMTLH cell line.  
CC This cell line is derived by stable transformation of a human bone  
CC marrow stromal cell culture with pSV3neo. From a pool of about 1000 cDNA  
CC clones, one clone 141.hETF contained this sequence. ETF is a protein of  
CC 15-17 kD which is expressed by epithelial cells and stimulates  
CC proliferation and/or differentiation of precursor and/or mature T cells.  
CC The protein is therefore useful for promoting long term in vivo culture  
CC of T-lymphocytes and T-cell lines.  
XX  
XX Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;  
SQ

Query Match 21.9%; Score 107; DB 17; Length 489;  
Best Local Similarity 99.4%; Pred. No. 7.8e-43;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126  
|||||  
Db 67 agtcatttttctaactgaagctggcattcatgtcttcatttttgggctgtttcagtcaggg 126  
|||||

QY 127 CTCCTTAAACAGACGCAACTGGTGAATGTAATAGTCAATTTGAAAAAATTGAAGAT 186  
|||||  
Db 127 cttcctaaacagacagccaaactgggtgaatgtaataagtgatttgaaaaaattgaagat 186  
|||||

QY 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224  
|||||  
Db 187 cttattcaatctatgcattattgatgctactttatatac 224  
|||||

RESULT 17  
AAT36635  
ID AAT36635 standard; cDNA; 489 BP.  
XX  
XX AAT36635;  
XX  
XX 17-NOV-1996 (first entry)  
XX Human interleukin-15 cDNA.  
XX  
XX Interleukin-15; antagonist; mutein; graft versus host disease;  
KW allograft; T-cell growth factor; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO9626274-A1.  
XX  
XX 29-AUG-1996.  
XX  
XX 21-FEB-1996; 96WO-US02520.  
XX  
XX 22-FEB-1995; 95US-0392317.  
XX  
XX (IMMV ) IMMUNEX CORP.  
XX  
XX Grabstein KH, Paxton RJ, Pettit DK;  
PI WPI; 1996-402367/40.  
DR P-PSDB; AAR98527.  
XX

PT Antagonists of interleukin-15 - are used to treat patients having  
PT symptoms of graft-versus-host disease and for prolonging allo-graft  
PT survival

PS Disclosure; Page 25; 32pp; English.

XX A CDNA clone (AAT36635) codes for human interleukin-15 (IL-15)  
CC (AAR98527), a T-cell growth factor. Muteins of human IL-15 or  
CC simian IL-15 (see also AAR98526) are useful as antagonists of IL-15  
CC and can be pred. by PCR-mediated mutagenesis of the encoding  
CC sequences. Preferred muteins have amino acid substitutions at  
CC Asp56 and/or Gln156 of the IL-15 protein that prevent signal  
CC transduction. They are useful for treating graft-versus-host  
CC disease and for prolonging allograft survival.

XX Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 21.9%; Score 107; DB 17; Length 489;  
Best Local Similarity 99.4%; Pred. No. 7.8e-43;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCATCTCTTCAATTTGGCTGTTTCAGTGCAGGG 126  
DB |||||||  
DB 67 agtcaatttctaactgaagctggcattcatcttcttcattttggcgctgtttcagtgcaagg 126  
QY 127 CTCCTAAAACAGAACGCAACTGGTCAATGTAATGAAGTGTATTTGAAAAAATTGAAGAT 186  
DB || |||||||  
DB 127 ctctctaaacagacgaagcaactgggtgaatgtaataagtgatttggaaaaaattgaagat 186  
QY 187 CTTATTCATCTATGATATGATGCTACTTTATATAC 224  
DB |||||||  
DB 187 cttattcaactctatgcattatgtatgctactttatatac 224

RESULT 18

AAT97227  
ID AAT97227 standard; DNA; 489 BP.

XX AAT97227;

XX 07-MAY-1998 (first entry)

XX Wild-type Interleukin-15 (IL-15) encoding DNA.

XX Interleukin-15; IL-15; mutant; human; treatment; autoimmune disease;  
KW psoriasis; multiple sclerosis; rheumatic arthritis; immune response;  
KW type 1 diabetes; AIDS; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..489

FT /tag= a

FT /product= "interleukin-15"

FT 1..144

FT /tag= b

FT 145..486

FT /tag= c

FT 445..447

FT /tag= d

FT /note= "the codon CAG encoding Gln can be substituted  
FT by a codon encoding Asp"

FT 466..468

FT /tag= e

FT /note= "the codon CAA encoding Gln can be substituted  
FT by a codon encoding Asp"

XX WO9741232-A1.

XX 06-NOV-1997.

XX 25-APR-1997; 97WO-US06931.

XX 26-APR-1996; 96US-0016634.  
XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

XX Maslinski W, Strom T;  
XX WPI; 1997-549734/50.  
DR P-PSDB; AAW37369.

XX Mutant interleukin 15 polypeptide(s) - used for treating auto-immune  
PT diseases e.g psoriasis, multiple sclerosis etc.  
XX Disclosure; Pages 54-55; 86pp; English.

XX This DNA encodes a wild-type interleukin-15 (IL-15) polypeptide. This  
CC wild-type sequence can be mutated at codon positions 149 and 156 to  
CC create a mutant IL-15 polypeptide. The mutant polypeptide is at least  
CC 90% identical to wild-type IL-15 and is capable of inhibiting at least  
CC one of the cellular events that normally occurs when wild-type IL-15  
CC specifically binds to a cell surface receptor. The mutant IL-15 is used  
CC for suppressing the immune response in a patient. It can be used for  
CC treating autoimmune diseases such as rheumatic arthritis, type 1 diabetes  
CC or a rheumatic disease selected from systemic lupus erythematosus (SLE),  
CC Sjogren's syndrome, scleroderma, mixed connective tissue disease,  
CC dermatomyositis, polymyositis, Reiter's syndrome and Behcet's disease.  
CC It can also be used to treat Hashimoto's thyroiditis, Grave's disease,  
CC multiple sclerosis, myasthenia gravis, encephalomyelitis, a variety of  
CC pemphigus, psoriasis, inflammatory bowel disease, AIDS and vascular  
CC injury. The mutant IL-15 can also be used for reducing the viability of  
CC a cell that expresses a IL-15 receptor. It can also be used to diagnose  
CC a disease treatable with an IL-15 antagonist.

XX Sequence 489 BP; 159 A; 80 C; 95 G; 155 T; 0 other;

Query Match 21.9%; Score 107; DB 18; Length 489;  
Best Local Similarity 99.4%; Pred. No. 7.8e-43;

Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCATCTCTTCAATTTGGCTGTTTCAGTGCAGGG 126  
DB |||||||  
DB 67 agtcaatttctaactgaagctggcattcatcttcttcattttggcgctgtttcagtgcaagg 126  
QY 127 CTCCTAAAACAGAACGCAACTGGTCAATGTAATGAAGTGTATTTGAAAAAATTGAAGAT 186  
DB || |||||||  
DB 127 ctctctaaacagacgaagcaactgggtgaatgtaataagtgatttggaaaaaattgaagat 186  
QY 187 CTTATTCATCTATGATATGATGCTACTTTATATAC 224  
DB |||||||  
DB 187 cttattcaactctatgcattatgtatgctactttatatac 224

RESULT 19

AAT97228

ID AAT97228 standard; DNA; 489 BP.

XX AAT97228;

XX 07-MAY-1998 (first entry)

XX Mutant interleukin-15 (IL-15) encoding DNA.

XX Interleukin-15; IL-15; mutant; human; treatment; autoimmune disease;  
KW psoriasis; multiple sclerosis; rheumatic arthritis; immune response;  
KW type 1 diabetes; AIDS; ss.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

FT CDS 1..489

FT /tag= a

```
FT sig_peptide /product= "mutant IL-15 polypeptide"
FT 1..144 /tag= b
FT mat_peptide /tag= c
FT 145..486 /tag= d
FT mutation /note= "wild-type codon CAG encoding Gln is mutated
FT /tag= e
FT mutation 455..468 /tag= e
FT /note= "wild-type codon CAA encoding Gln is mutated
FT /tag= e
FT mutation 469..486 /tag= e
FT /note= "wild-type codon CAG encoding Gln is mutated
FT /tag= e
FT mutation 487..499 /tag= e
FT /note= "wild-type codon CAG encoding Gln is mutated
FT /tag= e
PN WO9741232-A1.
XX 06-NOV-1997.
XX 25-APR-1997; 97WO-US06931.
XX 26-APR-1996; 96US-0016634.
XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX Maslinski W, Strom T;
XX WPI: 1997-549734/50.
XX P-PSDB; AAW37370.
XX Mutant interleukin 15 polypeptide(s) - used for treating auto-immune
XX diseases e.g psoriasis, multiple sclerosis etc.
XX Disclosure; Pages 56-57; 86pp; English.
XX This DNA encodes a mutant interleukin-15 (IL-15) polypeptide. The
XX wild-type IL-15 sequence was mutated at codon positions 149 and 156 to
XX create this mutant IL-15 polypeptide. This mutant polypeptide is at least
XX 90% identical to wild-type IL-15 and is capable of inhibiting at least
XX one of the cellular events that normally occurs when wild-type IL-15
XX specifically binds to a cell surface receptor. The mutant IL-15 is used
XX for suppressing the immune response in a patient. It can be used for
XX treating autoimmune diseases such as rheumatic arthritis, type I diabetes
XX or a rheumatic disease selected from systemic lupus erythematosus (SLE),
XX Sjogren's syndrome, scleroderma, mixed connective tissue disease,
XX dermatomyositis, polymyositis, Reiter's syndrome and Behcet's disease.
XX It can also be used to treat Hashimoto's thyroiditis, Grave's disease,
XX multiple sclerosis, myasthenia gravis, encephalomyelitis, a variety of
XX pemphigus, psoriasis, inflammatory bowel disease, AIDS and vascular
XX injury. The mutant IL-15 can also be used for reducing the viability of
XX a cell that expresses a IL-15 receptor. It can also be used to diagnose
XX a disease treatable with an IL-15 antagonist.
XX Sequence 489 BP; 158 A; 80 C; 96 G; 155 T; 0 other;

Query Match 21.9%; Score 107; DB 18; Length 489;
Best Local Similarity 99.4%; Pred. No. 7.8e-43;
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126
DB 67 agtcattttctaaactgaagctggcatctgctcttcattttgggctgtttcagtgcaagg 126
QY 127 CTCCTCTAAACAGAGCAAGCTGGTGAATGTAATGTAAGTGTATTTGAAAAAATTTGAAGAT 186
DB 127 ctctctaaaacagagcaagccaactgggtgaatgtaataagtgatttgaaaaaattgaagat 186
QY 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224
DB 187 cttattcaatctatgcattatgctactttatatac 224

RESULT 20
```

```
AAT58404
ID AAT58404 standard; cDNA; 489 BP.
XX
AC AAT58404;
XX
DT 18-MAR-1997 (first entry)
DE Interleukin-15 coding sequence.
XX
KW IL-15; interleukin-15; T-cell growth factor; proliferation; stimulate;
KW muscle growth; differentiation; hypertrophy; treat; atrophy; wasting;
KW skeletal; cardiac; muscle; congestive heart failure; diabetes-associated;
KW glucose-intolerance; dyslipidaemia; rhabdomyosarcoma; dystrophy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..489
FT /tag= a
FT /product= IL-15
XX
XX WO9637223-A1.
XX 28-NOV-1996.
XX 07-MAY-1996; 96WO-US06423.
XX 24-MAY-1995; 95US-0535733.
XX (IMMV ) IMMUNEX CORP.
XX Grabstein KH, Quinlan LS, Trout AB;
XX WPI: 1997-020939/02.
XX P-PSDB; AAW01658.
XX Muscle trophic compsn. contg. Interleukin 15 - for treating, e.g.
XX congestive heart failure, muscle wasting etc.
XX Disclosure; Page 12; 22pp; English.
XX This sequence encodes human interleukin-15 (IL-15) (see AAW01658), a
XX known T-cell growth factor that can support proliferation of an
XX IL-2-dependent cell line, CTL-L-2. Compsns. contg. IL-15 to stimulate
XX muscle growth, differentiation or hypertrophy are claimed. The
XX stimulation of muscle growth is useful for treating atrophy, or wasting,
XX in particular, skeletal and cardiac muscle atrophy. The compsns. further
XX comprises a steroid, growth hormone and insulin-like growth factor.
XX Congestive heart failure, muscle wasting and diabetes-associated
XX glucose-intolerance or dyslipidaemia, rhabdomyosarcoma and muscular
XX dystrophy can all be treated by such compsns..
XX Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 21.9%; Score 107; DB 18; Length 489;
Best Local Similarity 99.4%; Pred. No. 7.8e-43;
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126
DB 67 agtcattttctaaactgaagctggcatctgctcttcattttgggctgtttcagtgcaagg 126
QY 127 CTCCTCTAAACAGAGCAAGCTGGTGAATGTAATGTAAGTGTATTTGAAAAAATTTGAAGAT 186
DB 127 ctctctaaaacagagcaagccaactgggtgaatgtaataagtgatttgaaaaaattgaagat 186
QY 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224
DB 187 cttattcaatctatgcattatgctactttatatac 224

RESULT 21
```

RESULT	22
AAV02873	
ID	AAV02873 standard; DNA; 489 BP.
AC	AAV02873;
XX	
XX	
XX	08-MAY-1998 (first entry)
XX	
XX	Simian epithelium derived T-cell factor DNA.
XX	
KW	Epithelium derived T-cell factor; ETF; simian; gastrointestinal disease;
KW	B-cell stimulation; epithelium; villi; CD4+; CD8+; T-cell stimulation;
KW	treatment; prevention; ss.
XX	
XX	Simian.
XX	
XX	Key
XX	Location/Qualifiers
FT	1..489
FT	/*tag= a
FT	1..48
FT	/*tag= b
FT	49..486
FT	/*tag= c
FT	/product= ETF
FT	/note= "Epithelium-derived T-cell factor"
XX	
XX	US5707616-A.
XX	
XX	13-JAN-1998.
XX	
XX	04-OCT-1996; 96US-0726817.
XX	
XX	22-FEB-1995; 95US-0393305.
PR	08-MAR-1993; 93US-0031399.
PR	22-APR-1994; 94US-0233606.
XX	
XX	(IMMV ) IMMUNEX CORP.
PA	
XX	Anderson DM, Eisenman JR, Fung V, Grabstein KH;
PI	Rauch C;
XX	
XX	WPI; 1998-100295/09.
DR	P-PSDB; AAW39185.
XX	
XX	Treatment or prevention of gastrointestinal diseases - by
PT	administering epithelium-derived T-cell factor polypeptide
XX	
XX	Claim 1C; Column 35-36; 34pp; English.
XX	
CC	This sequence encodes a simian epithelium-derived T-cell factor (ETF)
CC	which is used in a method for treating or preventing gastrointestinal
CC	disease. These polypeptides have particular application in the treatment
CC	of gastrointestinal disorders associated with disruption of the
CC	gastrointestinal epithelium or villi such as chemotherapy- and
CC	radiation-therapy induced enteritis (gut toxicity), mucositis, peptic
CC	ulcer disease, gastroenteritis and colitis, villus atrophic disorders,
CC	malnutrition and inflammatory bowel disease. ETF polypeptides may also be
CC	useful in the treatment of human immunodeficiency virus (HIV) and
CC	HIV-associated disease due to their ability to stimulate CD4+ and CD8+
CC	cells. Biologically active ETF may be used to treat a variety of other
CC	diseases or conditions where T-cell or B cell stimulation is desired.
XX	
XX	Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;
SQ	
Query Match 21.9%; Score 107; DB 19; Length 489;	
Best Local Similarity 99.4%; Pred. No. 7.8e-43;	
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps	
QY	67 AGTCATTTCCTACTGAAGCTGGCATTTCATGCTTCATTTTGGCGCTTTCAGTGCAGG 126
Db	67 agtcatttcttaactgaagctggcattcattgcttcatttggctgtttcagcgagg 126









```

ID AAA58044 standard; cDNA to mRNA; 1202 BP.
XX
AC AAA58044;
XX
DT 10-OCT-2000 (first entry)
DE Human interleukin-15 (IL-15) cDNA copy of mRNA.
XX
KW Human interleukin-15; IL-15; antisense therapy; expression inhibition;
KW T-cell mediated immune response; autoimmune disorder;
KW inflammatory polyarthropathy; rheumatoid arthritis; transplant rejection;
KW graft versus host disease; lupus erythematosus; asthma;
KW inflammatory bowel disease; gene therapy; immunosuppressive;
KW antiinflammatory; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH 5'UTR 1..316
FT /*tag= a
FT CDS 317..805
FT /*tag= b
FT /*product= "Human IL-15"
FT 3'UTR 806..1202
FT /*tag= c
XX
PN WO200028019-A2.
XX
PD 18-MAY-2000.
XX
XX 04-NOV-1999; 99WO-IL00589.
XX
XX 05-NOV-1998; 98IL-0126919.
XX
XX (UYNE ) UNIV BEN-GURION NEGEV RES & DEV.
XX (MORR-) MOR RES APPL LTD.
XX
XX Douvdevani A, Chaimovitz C;
XX WPI; 2000-376536/32.
XX
XX Antisense oligomer useful for alleviating inflammatory polyarthropathy
XX associated with organ and cell transplant rejection, inhibits
XX production of interleukin-15 by hybridizing to its mRNA -
XX
XX Disclosure; Fig 1; 29pp; English.
XX
XX The invention relates to antisense oligonucleotides (AAA58045, AAA58047-
XX AAA58057) capable of inhibiting the expression of human interleukin-15
XX (IL-15) by hybridizing to IL-15 mRNA (AAA58044). IL-15 is a member of
XX the short chain, 4 alpha helix bundle cytokine family and is a potent
XX T-cell growth factor and activator. IL-15 acts as a stimulator of
XX various T-cell mediated pathological immune responses, such as
XX autoimmune disorders (e.g., rheumatoid arthritis, graft versus host
XX disease and organ transplant rejection), and has a proinflammatory role
XX in rheumatoid arthritis synovitis. The antisense oligonucleotides are
XX useful for inhibiting IL-15 production and are thus useful for
XX alleviating inflammatory polyarthropathy associated with rheumatoid
XX arthritis, organ transplant rejection (e.g., kidney transplant
XX rejection), cell transplant rejections (e.g., asthma, lupus erythematosus and
XX inflammatory bowel disease. The present sequence represents a cDNA copy
XX of human IL-15 mRNA.
XX
SQ Sequence 1202 BP; 355 A; 219 C; 249 G; 379 T; 0 other;

Query Match 21.98; Score 107; DB 21; Length 1202;
Best Local Similarity 99.48; Pred. No. 7.7e+43;
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 67 AGTCATTTCCTAACTGAAGCTGGCATTTCATGTTGGGTGTTTCAGTGCAGGG 126
Db 383 agtcaatttttaactgaagctggcatttcatttcatttggcgtgttcagtcaggg 442
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QY 127 CTCCTAAACAGAGCCAACTGGTGAATGTAATAGTGAATTTGAAAAAATTGAAGAT 186
Db 443 ctctctaaacagagaagcccaactgggtgaatgtaataagtgatttgaaaaaattgaagat 502
QY 187 CTTATTCAATCTATGTCATATTGATGCTACTTTATATAC 224
Db 503 cttattcaattctatgcattatgatgctactttatatac 540

RESULT 31
ID AAA35220
XX AAA35220 standard; DNA; 1202 BP.
XX
AC AAA35220;
XX
DT 28-JUL-2000 (first entry)
DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:94.
XX
XX Homo sapiens.
XX WO200009525-A2.
XX
XX 24-FEB-2000.
XX
XX 03-AUG-1999; 99WO-US17712.
XX
XX 03-AUG-1998; 98US-0095212.
XX (UVEC-) UNIV EAST CAROLINA.
XX
XX Nyce JW;
XX WPI; 2000-205971/18.
XX
XX New antisense oligonucleotides useful for treating e.g. pulmonary
XX vasoconstriction, inflammation, allergies, asthma, hypertension,
XX bronchitis, emphysema, respiratory distress syndrome, ischemia or
XX cancers -
XX
XX Disclosure; Page 1260; 1343pp; English.
XX
XX The present invention describes a new composition comprising an
XX antisense oligonucleotide (ON) with low adenosine (up to 15%), which
XX targets nucleic acids involved in bronchoconstriction, allergies, and/or
XX inflammation. The ON can have antiinflammatory, antiallergic,
XX antisthmatic, cytostatic and analgesic activities. The compositions are
XX useful for the treatment of diseases associated with inflammation,
XX impaired airways, including lung disease and diseases whose secondary
XX effects afflict the lungs of a subject. They can be used for treating
XX e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
XX asthma, impeded respiration, respiratory distress syndrome, pain, cystic
XX fibrosis, pulmonary hypertension, emphysema, chronic obstructive
XX pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
XX carcinomas, and cancers which may metastasize to the lungs, including
XX breast and prostate cancer. The reduction of the adenosine content of
XX the ONs reduces side effects. The A-containing ONs break down with the
XX release of deoxyadenosine which activates adenosine receptors causing
XX bronchoconstriction and inflammation. AAA32313 to AAA35512 represent the
XX nucleotide sequences given in the sequence listing from the present
XX invention, which correspond to SEQ ID NO:1 to 2815, and then the last
XX 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
XX differ from the previously named sequences. SEQ ID NO:11 to 1680
```



CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
 CC immunosuppressive, antisthmatic, hypotensive and cytostatic activities.  
 CC The antisense oligonucleotides and (I) can be used to down-regulate the  
 CC expression and or activity of target polypeptides associated with  
 CC lung/respiratory disorders and malignancies, such as stimulating and  
 CC activating peptide factors and transmitters, transcription factors,  
 CC immunoglobulins and antibodies, antibody receptors, cytokines and  
 CC chemokines, endogenously produced specific and non-specific enzymes,  
 CC binding proteins, adhesion molecules and their receptors, cytokine and  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and non-nervous system  
 CC receptors, CNS and peripheral nervous and non-nervous system peptide  
 CC transmitters, defensins, growth factors, vasoactive peptides and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisense oligonucleotides may be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)  
 CC and/or surfactant hypoproduction which are associated with a disease or  
 CC condition selected from pulmonary vasoconstriction, inflammation,  
 CC allergies, asthma, impeded respiration, respiratory distress syndrome  
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
 CC fragments and antisense oligonucleotides used in the exemplification of  
 CC the present invention.  
 XX  
 SQ Sequence 17904 BP; 6014 A; 2945 C; 3330 G; 5615 T; 0 other;

Query Match 21.9%; Score 107; DB 21; Length 17904;  
 Best Local Similarity 99.4%; Pred. No. 7.4e-43;  
 Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 67 AGTCATTTTCTAAGTCGATTCATCTCTTTCATTTTGGCGTGTTCAGTGAGGG 126  
 Db 1631 agtcatctttaaactgaagtcgcatctgtcttcatttttggtgttcagtcgagg 1690  
 QY 127 CTCCTAAACAGAGCAACTGGTGAATGTAATAGTGTATTTGAAAAATTTGAAGAT 186  
 Db 1691 ctctctaaacagagccaaactgggtgaatgaatgaattgaaaaaattgaagat 1750  
 QY 187 CTTATTCATCTATGCATATTGATGCTTATATATAC 224  
 Db 1751 cttattcaatctgcatattgactgactttatatac 1788

RESULT 34  
 AAF21341  
 ID AAF21341 standard; DNA; 1248 BP.  
 XX  
 AC AAF21341;  
 XX  
 DT 14-MAR-2001 (first entry)  
 XX  
 DE Human low adenosine antisense oligonucleotide related sequence #2908.  
 KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
 KW human; airway disorder; bronchoconstriction; lung inflammation;  
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 KW immunosuppressive; antisthmatic; analgesic; hypotensive; cytostatic;  
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 KW cancer; ss.  
 OS Homo sapiens.  
 XX  
 PN WO200062736-A2.  
 XX  
 PD 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US08020.  
 PF  
 XX 06-APR-1999; 99US-0127958.  
 PR  
 XX (UYEC-) UNIV EAST CAROLINA.  
 PA (NYCE/) NYCE J W.  
 PA  
 XX NYCE JW;  
 PI  
 XX WPI; 2000-679539/66.  
 DR  
 XX Low adenosine (A) content antisense oligonucleotides which do not  
 PT trigger adenosine receptors during metabolism, useful e.g. for treating  
 PT cancers and respiratory obstructions -  
 PT  
 XX Disclosure: Page 1344; 1592pp; English.  
 PS  
 XX The present invention describes low adenosine (A) content antisense  
 CC oligonucleotides and compositions (I) comprising them. In the antisense  
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
 CC immunosuppressive, antisthmatic, hypotensive and cytostatic activities.  
 CC The antisense oligonucleotides and (I) can be used to down-regulate the  
 CC expression and or activity of target polypeptides associated with  
 CC lung/respiratory disorders and malignancies, such as stimulating and  
 CC activating peptide factors and transmitters, transcription factors,  
 CC immunoglobulins and antibodies, antibody receptors, cytokines and  
 CC chemokines, endogenously produced specific and non-specific enzymes,  
 CC binding proteins, adhesion molecules and their receptors, cytokine and  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and non-nervous system  
 CC receptors, CNS and peripheral nervous and non-nervous system peptide  
 CC transmitters, defensins, growth factors, vasoactive peptides and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisense oligonucleotides may be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)  
 CC and/or surfactant hypoproduction which are associated with a disease or  
 CC condition selected from pulmonary vasoconstriction, inflammation,  
 CC allergies, asthma, impeded respiration, respiratory distress syndrome  
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
 CC fragments and antisense oligonucleotides used in the exemplification of  
 CC the present invention.  
 XX  
 SQ Sequence 1248 BP; 397 A; 209 C; 223 G; 419 T; 0 other;

Query Match 19.4%; Score 95; DB 21; Length 1248;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-37;  
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 130 CCTAAACAGAGCAACTGGTGAATGTAATAGTGTATTTGAAAAATTTGAAGATCTT 189  
 Db 567 cctaaacagagccaaactgggtgaatgaatgaattgaaaaaattgaagatcct 626  
 QY 190 ATTCAATCTATGCATATTGATGCTTATATATAC 224  
 Db 627 attcaatctgcatattgactgactttatatac 661  
 RESULT 35  
 AAA35219  
 ID AAA35219 standard; DNA; 1248 BP.  
 XX  
 AC AAA35219;  
 XX  
 DT 28-JUL-2000 (first entry)  
 XX  
 DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:93.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;  
 KW phosphorothioate; impaired respiration; inflammation; allergy;  
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200009525-A2.  
 XX  
 PD 24-FEB-2000.  
 XX  
 PF 03-AUG-1999; 99WO-US17712.  
 XX  
 XX 03-AUG-1999; 98US-0095212.  
 PR  
 XX (UYEC-) UNIV EAST CAROLINA.  
 PA  
 XX Nyce JW;  
 PI  
 XX WPI; 2000-205971/18.  
 DR  
 XX  
 XX New antisense oligonucleotides useful for treating e.g. pulmonary  
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
 PT cancers -  
 XX  
 PS Disclosure: Page 1260; 1343pp; English.  
 XX  
 CC The present invention describes a new composition comprising an  
 CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which  
 CC targets nucleic acids involved in bronchoconstriction, allergies, and/or  
 CC inflammation. The ON can have antiinflammatory, antiallergic,  
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
 CC useful for the treatment of diseases associated with inflammation,  
 CC impaired airways, including lung disease and diseases whose secondary  
 CC effects afflict the lungs of a subject. They can be used for treating  
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,  
 CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic  
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
 CC carcinomas, and cancers which may metastasize to the lungs, including  
 CC breast and prostate cancer. The reduction of the adenosine content of  
 CC the ONs reduces side effects. The A-containing ONs break down with the  
 CC release of deoxyadenosine which activates adenosine receptors causing  
 CC bronchoconstriction and inflammation. The A-containing ONs break down with the  
 CC nucleotide sequences given in the sequence listing from the present  
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last  
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences  
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680  
 CC (AAA32323 to AAA33992) are specifically claimed ONs from the present  
 CC invention. N.B. Sequences given in the disclosure of the present  
 CC invention do not match up with their corresponding SEQ ID NO: sequences  
 CC given in the sequence listing.  
 XX  
 SQ Sequence 1248 BP; 397 A; 209 C; 223 G; 419 T; 0 other;  
 Query Match 19.4%; Score 95; DB 21; Length 1248;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-37;  
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 130 CCTAAACAGAGCCCACTGGGTGAATGTAATAAGTATTGAAAAAATGAAGATCTT 189  
 Db 567 cctaaacagagcccaactgggtgaatgtaataagtgattgaaaaaattgaagatctt 626  
 QY 190 ATTCAATCTATGCATATTGCTACTTTATATAC 224  
 Db 627 attcaatctatgcataattgctactttatatac 661

RESULT 36  
 AAZ37358  
 ID AAZ37358 standard; DNA; 1248 BP.  
 XX  
 AC AAZ37358;  
 XX  
 DT 04-FEB-2000 (first entry)  
 XX  
 DE Human Interleukin-15 coding sequence.  
 XX  
 KW Interleukin-15; IL-15; antisense inhibitor; untranslated region; 5'UTR;  
 KW 3'UTR; human; infection; inflammation; tumour; therapy; diagnosis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5985663-A.  
 XX  
 PD 16-NOV-1999.  
 XX  
 PF 25-NOV-1998; 98US-0200141.  
 XX  
 PR 25-NOV-1998; 98US-0200141.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Bennett CF, Cowser LM;  
 XX  
 DR WPI; 2000-022283/02.  
 DR P-PSDB; AAY54825.  
 XX  
 XX Antisense compound useful for inhibiting human interleukin-15  
 PT expression useful for treating diseases associated with interleukin-15  
 PT expression -  
 XX  
 PS Example 13; Column 43-44; 31pp; English.  
 XX  
 CC This sequence encodes the human interleukin-15. The invention relates to  
 CC antisense compounds that are targeted to a 5' or 3' untranslated region  
 CC (5'UTR or 3'UTR) of a nucleic acid molecule encoding human interleukin-15  
 CC (IL-15), and inhibit the expression of human IL-15. The antisense  
 CC inhibitors are useful for inhibiting expression of IL-15 in human  
 CC cells or tissues in vitro, for treating humans or other animals suspected  
 CC of having or being prone to a disease associated with IL-15 expression,  
 CC e.g. infections, inflammation or tumours. The inhibitors can also be used  
 CC for research or diagnostic purposes. Using antisense compounds  
 CC specifically and effectively inhibits IL-15 function.  
 XX  
 SQ Sequence 1248 BP; 397 A; 209 C; 223 G; 419 T; 0 other;  
 Query Match 19.4%; Score 95; DB 21; Length 1248;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-37;  
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 130 CCTAAACAGAGCCCACTGGGTGAATGTAATAAGTATTGAAAAAATGAAGATCTT 189  
 Db 567 cctaaacagagcccaactgggtgaatgtaataagtgattgaaaaaattgaagatctt 626  
 QY 190 ATTCAATCTATGCATATTGCTACTTTATATAC 224  
 Db 627 attcaatctatgcataattgctactttatatac 661  
 RESULT 37  
 AAA35223  
 ID AAA35223 standard; DNA; 17844 BP.  
 XX  
 AC AAA35223;  
 XX  
 DT 28-JUL-2000 (first entry)  
 XX



The present invention describes a new composition comprising an antisenescence oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischemic conditions, pulmonary vasoconstriction, allergies, asthma, impaired respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive



DR WPI; 2000-679539/66.  
XX Low adenosine (A) content antisense oligonucleotides which do not  
PT trigger adenosine receptors during metabolism, useful e.g. for treating  
PT cancers and respiratory obstructions -  
XX  
XX  
PS Disclosure; Page 1345-1348; 1592pp; English.  
XX  
CC The present invention describes low adenosine (A) content antisense  
CC oligonucleotides and compositions (I) comprising them. In the antisense  
CC oligonucleotides the A is replaced by a 'universal' or alternative base.  
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.  
CC The antisense oligonucleotides and (I) can be used to down-regulate the  
CC expression and/or activity of target polypeptides associated with the  
CC lung/respiratory disorders and malignancies, such as stimulating and  
CC activating peptide factors and transmitters, transcription factors and  
CC immunoglobulins and antibodies, antibody receptors, cytokines and  
CC chemokines, endogenously produced specific and non-specific enzymes,  
CC binding proteins, adhesion molecules and their receptors, cytokine and  
CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
CC nervous system (CNS) and peripheral nervous and non-nervous system  
CC receptors, CNS and peripheral nervous and non-nervous system peptide  
CC transmitters, defensins, growth factors, vasoactive peptides and  
CC receptors, binding proteins and malignancy associated proteins. The  
CC antisense oligonucleotides may be used in this way to treat disorders  
CC including respiratory obstruction (especially pulmonary obstruction  
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)  
CC and/or surfactant hypoproduction which are associated with a disease or  
CC condition selected from pulmonary vasoconstriction, inflammation,  
CC allergies, asthma, impeded respiration, respiratory distress syndrome  
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
CC hyperinflation, emphysema, chronic obstructive pulmonary disease (COPD),  
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
CC fragments and antisense oligonucleotides used in the exemplification of  
CC the present invention.  
XX  
XX Sequence 14968 BP; 5108 A; 2436 C; 2758 G; 4666 T; 0 other;  
SQ

Query Match 14.7%; Score 72; DB 21; Length 14968;  
Best Local Similarity 100.0%; Pred. No. 1.3e-25;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 418 GAGCAAAAATATTAAAGAAATTTTCGAGAGTTTGTACATATGTCCAAATGTTTCATC 477  
Db 13533 gaggaataaataataaagaattttgacagagttttgtacatatattgccaaatgttcac 13592  
QY 478 AACACTTCTTGA 489  
Db 13593 aacacttcttga 13604  
RESULT 43  
ID AAA35221  
XX AAA35221 standard; DNA; 14968 BP.  
XX  
XX AAA35221;  
XX  
XX 28-JUL-2000 (first entry)  
XX Human adenosine receptor related polynucleotide 2nd SEQ ID NO:95.  
XX  
XX Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphorothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiasthmatic; cytostatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
XX

OS Homo sapiens.  
XX WO200009525-A2.  
XX  
XX 24-FEB-2000.  
XX  
XX 03-AUG-1999; 99WO-US17712.  
XX  
XX 03-AUG-1998; 98US-0095212.  
XX  
XX (UYEC-) UNIV EAST CAROLINA.  
XX  
XX Nyce JW;  
XX WPI; 2000-205971/18.  
XX New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers -  
XX  
XX Disclosure; Page 1260-1264; 1343pp; English.  
XX  
XX The present invention describes a new composition comprising an  
CC antisense oligonucleotide (ON) with low adenosine (up to 13%), which  
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,  
CC asthma, impeded respiration, respiratory distress syndrome, emphysema,  
CC pulmonary hypertension, emphysema, and cancers such as leukemias, lymphomas,  
CC carcinomas, and cancers which may metastasize to the lungs, including  
CC the release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last  
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences  
CC differ from the previously named sequences. SEQ ID NO:11 to 1680  
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present  
CC invention. N.B. Sequences given in the disclosure of the present  
CC invention do not match up with their corresponding SEQ ID NO: sequences  
CC given in the sequence listing.  
XX  
XX Sequence 14968 BP; 5109 A; 2436 C; 2757 G; 4666 T; 0 other;  
SQ

Query Match 14.7%; Score 72; DB 21; Length 14968;  
Best Local Similarity 100.0%; Pred. No. 1.3e-25;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 418 GAGCAAAAATATTAAAGAAATTTTCGAGAGTTTGTACATATGTCCAAATGTTTCATC 477  
Db 13533 gaggaataaataataaagaattttgacagagttttgtacatatattgccaaatgttcac 13592  
QY 478 AACACTTCTTGA 489  
Db 13593 aacacttcttga 13604  
RESULT 44  
ID AAD14464  
XX AAD14464 standard; DNA; 14968 BP.  
XX  
XX AAD14464;  
XX  
XX 15-NOV-2001 (first entry)  
XX

DE Human IL-15 gene allele.  
 XX Human; interleukin 15; IL-15; gene therapy; chromosome 4q31; infection;  
 KW drug screening; anthropological lineage; paternity testing; HIV;  
 KW Human Immunodeficiency Virus; forensic application; T-cell leukaemia; ds.  
 XX  
 OS Homo sapiens.

XX Key Location/Qualifiers  
 FH CDS 347..13604  
 FT /\*tag= a  
 FT /product= "Human IL-15 protein"  
 FT 1..346  
 FT /\*tag= b  
 FT /cons\_splice= (5'site:NO, 3'site:NO)  
 FT /number= 1  
 FT /\*tag= c  
 FT /number= 1  
 FT 358..1350  
 FT /\*tag= d  
 FT /cons\_splice= (5'site:NO, 3'site:NO)  
 FT /number= 2  
 FT 1351..1448  
 FT /\*tag= e  
 FT /number= 2  
 FT 1449..2806  
 FT /\*tag= f  
 FT /cons\_splice= (5'site:NO, 3'site:NO)  
 FT /number= 3  
 FT 2807..2892  
 FT /\*tag= g  
 FT /number= 3  
 FT 2893..8695  
 FT /\*tag= h  
 FT /number= 4  
 FT 8696..8740  
 FT /\*tag= i  
 FT /number= 4  
 FT 8741..10602  
 FT /\*tag= j  
 FT /number= 5  
 FT 10603..10739  
 FT /\*tag= k  
 FT /number= 5  
 FT 10740..13492  
 FT /\*tag= l  
 FT /number= 6  
 FT /cons\_splice= (5'site:NO, 3'site:NO)  
 FT 13493..13604  
 FT /\*tag= m  
 FT /number= 6  
 FT 13605..14968  
 FT /\*tag= n  
 FT /number= 7  
 FT /cons\_splice= (5'site:NO, 3'site:NO)  
 FT replace (101, T)  
 FT /\*tag= o  
 FT replace (191, C)  
 FT /\*tag= p  
 FT replace (192, C)  
 FT /\*tag= q  
 FT replace (267, T)  
 FT /\*tag= r  
 FT replace (333, T)  
 FT /\*tag= s  
 FT replace (367, A)  
 FT /\*tag= t  
 FT replace (431, T)  
 FT /\*tag= u  
 FT replace (504, C)  
 FT /\*tag= v  
 FT replace (1536, A)

FT variation /\*tag= w  
 FT replace (8866, A)  
 FT /\*tag= x  
 FT variation replace (10504, G)  
 FT /\*tag= y  
 XX WO200158914-A2.  
 XX PN  
 XX 16-AUG-2001.  
 PD  
 XX 08-FEB-2001; 2001WO-US04130.  
 PF  
 XX 08-FEB-2000; 2000US-0181059.  
 PR  
 XX (GENA-) GENAISSANCE PHARM INC.  
 PA  
 XX Anastasio AE, Chew A, Denton RR, Nandabalan K, Stephens JC;  
 PI  
 XX WPI; 2001-522460/57.  
 DR  
 XX P-PSDB; AAE08576.  
 DR  
 XX Novel polynucleotides comprising one of 11, PSI-PS11, single nucleotide  
 PT polymorphisms in human interleukin-15 gene, and useful for treating  
 PT disorders affected by expression of function of interleukin-15 isogene  
 PT  
 XX  
 XX Claim 19; Fig 1; 78pp; English.  
 PS  
 XX The present sequence is human interleukin-15 (IL-15) gene allele located  
 CC on chromosome 4q31. The polymorphic variants of IL-15 genes are useful  
 CC for studying the expression and function of IL-15 and expressing  
 CC IL-15 protein for use in useful for screening for candidate drugs to  
 CC treat diseases related to IL-15 activity. Genotyping or haplotyping an  
 CC individual at the novel IL-15 polymorphic sites are useful for studying  
 CC population diversity, anthropological lineage, the significance of  
 CC diversity and lineage of the phenotypic level, paternity testing,  
 CC forensic applications and for identifying associations between IL-15  
 CC genetic variation and a trait such as level of drug response or  
 CC susceptibility to disease. Identifying an association between a genotype  
 CC or haplotype and a trait, is useful for developing diagnostic tests and  
 CC therapeutic treatments for infections, human immunodeficiency virus and  
 CC T-cell leukaemia. The identification of an association between a clinical  
 CC response and a genotype or haplotype (or haplotype pair) for the IL-15  
 CC gene may be the basis for designing a diagnostic method to determine  
 CC those individuals who will or will not respond to the treatment, or  
 CC alternatively, will respond at a lower level and thus may require more  
 CC treatment, i.e. a greater dose of a drug. The genotyping or haplotyping  
 CC methods are also useful for developing drugs targeting IL-15. The  
 CC genotyping and haplotyping methods are also useful in designing clinical  
 CC trials. IL-15 DNA is useful for therapeutic purposes for treating  
 CC disorders affected by expression of function of novel IL-15 isogene and  
 CC also in gene therapy. Expression of an IL-15 isogene may be turned off  
 CC by transforming a targetted organ, tissue or cell population of an  
 CC expression vector that expresses high levels of untranslatable mRNA for  
 CC the isogene.  
 XX  
 SQ Sequence 14968 BP; 5108 A; 2436 C; 2758 G; 4666 T; 0 other;

Query Match 14.7%; Score 72; DB 22; Length 14968;  
 Best Local Similarity 100.0%; Pred. NO. 1.3e-25;  
 Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 418 GAGGAAAAATATTAAGAATTTTTCAGAGTTTTTGTACATATGTCGAATGTCATC 477  
 |||||  
 Db 13533 gaggaataataaagaattttgcagagttttgacatatgtccaaatgtcatc 13592  
 Qy 478 AACACTTCTTGA 489  
 |||||  
 Db 13593 aacactttttga 13604

RESULT 45

AA015838  
ID AAD15838 standard; DNA; 14968 BP.  
XX  
AC AAD15838;  
XX  
DT 15-NOV-2001 (first entry)  
XX  
DE Human interleukin 15 (IL-15) gene.  
XX  
KW Human; interleukin 15; IL-15; gene therapy; chromosome 4q31; infection;  
KW drug screening; anthropological lineage; paternity testing; HIV;  
KW Human Immunodeficiency Virus; forensic application; T-cell leukaemia; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 101  
FT /\*tag= a  
FT /\*note= "This degenerate base represents polymorphic site"  
FT 191  
FT misc\_feature b  
FT /\*tag= b  
FT /\*note= "This degenerate base represents polymorphic site"  
FT 192  
FT misc\_feature c  
FT /\*tag= c  
FT /\*note= "This degenerate base represents polymorphic site"  
FT 267  
FT misc\_feature d  
FT /\*tag= d  
FT /\*note= "This degenerate base represents polymorphic site"  
FT 333  
FT misc\_feature e  
FT /\*tag= e  
FT /\*note= "This degenerate base represents polymorphic site"  
FT 367  
FT misc\_feature f  
FT /\*tag= f  
FT /\*note= "This degenerate base represents polymorphic site"  
FT 431  
FT misc\_feature g  
FT /\*tag= g  
FT /\*note= "This degenerate base represents polymorphic site"  
FT 504  
FT misc\_feature h  
FT /\*tag= h  
FT /\*note= "This degenerate base represents polymorphic site"  
FT 1536  
FT misc\_feature i  
FT /\*tag= i  
FT /\*note= "This degenerate base represents polymorphic site"  
FT 8866  
FT misc\_feature j  
FT /\*tag= j  
FT /\*note= "This degenerate base represents polymorphic site"  
FT 10504  
FT misc\_feature k  
FT /\*tag= k  
FT /\*note= "This degenerate base represents polymorphic site"  
XX  
PN WO200158914-A2.  
XX  
PD 16-AUG-2001.  
XX  
PF 08-FEB-2001; 2001WO-US04130.  
XX  
PR 08-FEB-2000; 2000US-0181059.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Anastasio AE, Chew A, Denton RR, Nandabalan K, Stephens JC;  
XX  
DR WPI; 2001-522460/57.  
XX  
PT Novel polynucleotides comprising one of 11, PSI-PS11, single nucleotide  
PT polymorphisms in human interleukin-15 gene, and useful for treating  
PT disorders affected by expression of function of interleukin-15 isogene  
PT .  
XX  
PS Disclosure; Page 73-78; 78pp; English.  
XX  
CC The present sequence is human interleukin-15 (IL-15) gene located  
CC on chromosome 4q31. The polymorphic variants of IL-15 genes are useful

CC for studying the expression and function of IL-15 and expressing  
CC IL-15 protein for use in useful for screening for candidate drugs to  
CC treat diseases related to IL-15 activity. Genotyping or haplotyping an  
CC individual at the novel IL-15 polymorphic sites are useful for studying  
CC population diversity, anthropological lineage, the significance of  
CC diversity and lineage of the phenotypic level, paternity testing,  
CC forensic applications and for identifying associations between IL-15  
CC genetic variation and a trait such as level of drug response or  
CC susceptibility to disease. Identifying an association between a genotype  
CC or haplotype and a trait, is useful for developing diagnostic tests and  
CC therapeutic treatments for infections, human immunodeficiency virus and  
CC T-cell leukaemia. The identification of an association between a clinical  
CC response and a genotype or haplotype (or haplotype pair) for the IL-15  
CC gene may be the basis for designing a diagnostic method to determine  
CC those individuals who will or will not respond to the treatment, or  
CC alternatively, will respond at a lower level and thus may require more  
CC treatment, i.e. a greater dose of a drug. The genotyping or haplotyping  
CC methods are also useful for developing drugs targeting IL-15. The  
CC genotyping and haplotyping methods are also useful in designing clinical  
CC trials. IL-15 DNA is useful for therapeutic purposes for treating  
CC disorders affected by expression of function of novel IL-15 isogene and  
CC also in gene therapy. Expression of an IL-15 isogene may be turned off  
CC by transforming a targeted organ, tissue or cell population of an  
CC expression vector that expresses high levels of untranslatable mRNA for  
CC the isogene.  
XX  
SQ Sequence 14968 BP; 5107 A; 2432 C; 2755 G; 4663 T; 11 other;  
  
Query Match 14.7%; Score 72; DB 22; Length 14968;  
Best Local Similarity 100.0%; Pred. No. 1.3e-25;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 418 GAGGAAAAAATTAATTAAGATTTTGCAGAGTTTGTACATATGTCACAAATGTTTCATC 477  
|||||  
DB 13533 gaggaataaataaagaattttgcagagttttgtacattatgtccaaatgttcac 13592  
|||||  
QY 478 AACACTTCTGA 489  
|||||  
DB 13593 aacacttcttga 13604  
  
RESULT 46  
AAL25950/c  
ID AAL25950 standard; CDNA; 384 BP.  
XX  
AC AAL25950;  
XX  
DT 07-DEC-2001 (first entry)  
XX  
DE Human breast cancer expressed polynucleotide 18407.  
XX  
KW Human; breast cancer; cell marker; cytostatic; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200151628-A2.  
XX  
PD 19-JUL-2001.  
XX  
PF 10-JAN-2001; 2001WO-US00798.  
XX  
PR 14-JAN-2000; 2000US-0176077.  
PR 14-MAR-2000; 2000US-0189167.  
PR 24-MAR-2000; 2000US-0192099.  
PR 29-MAR-2000; 2000US-0193480.  
PR 15-MAY-2000; 2000US-0205230.  
PR 09-JUN-2000; 2000US-0211315.  
PR 25-JUL-2000; 2000US-0220534.  
XX  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
PI Lillie J, Xu Y, Wang Y, Steinmann K;

```
XX WPI; 2001-451856/48.
DR
XX New peptide useful as a marker for the diagnosis of breast cancer -
PT
XX Claim 1; Page 3400; 3695pp; English.
XX
XX The invention relates to human breast cancer expressed polynucleotides
CC (AAL07544-AAL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterising treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.
XX
XX Sequence 384 BP; 126 A; 63 C; 67 G; 127 T; 1 other;
SQ
Query Match 5.9%; Score 29; DB 22; Length 384;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 461 TTGTCCAAATGTTTCATCAACACTTCTTGA 489
Db 275 TTGTCCAAATGTTTCATCAACACTTCTTGA 247
|||||
RESULT 47
AAL19115/c
ID AAL19115 standard; cDNA; 474 BP.
XX
XX AAL19115;
XX
XX 07-DEC-2001 (first entry)
XX
XX Human breast cancer expressed polynucleotide 11572.
XX
XX Human; breast cancer; cell marker; cytostatic; ss.
XX
XX Homo sapiens.
XX
XX WO200151628-A2.
XX
XX 19-JUL-2001.
XX
XX 10-JAN-2001; 2001WO-US00798.
XX
XX 14-JAN-2000; 2000US-0176077.
XX
XX 14-MAR-2000; 2000US-0189167.
XX
XX 24-MAR-2000; 2000US-0192099.
XX
XX 29-MAR-2000; 2000US-0193480.
XX
XX 15-MAY-2000; 2000US-0205230.
XX
XX 09-JUN-2000; 2000US-0211315.
XX
XX 25-JUL-2000; 2000US-0220534.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lillie J, Xu Y, Wang Y, Steinmann K;
XX
XX WPI; 2001-451856/48.
XX
XX New peptide useful as a marker for the diagnosis of breast cancer -
PT
XX Claim 1; Page 2067; 3695pp; English.
XX
XX The invention relates to human breast cancer expressed polynucleotides
CC (AAL07544-AAL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterising treating and
```

```
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.
XX
XX Sequence 474 BP; 155 A; 76 C; 87 G; 155 T; 1 other;
SQ
Query Match 5.9%; Score 29; DB 22; Length 474;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 461 TTGTCCAAATGTTTCATCAACACTTCTTGA 489
Db 279 TTGTCCAAATGTTTCATCAACACTTCTTGA 251
|||||
RESULT 48
AAL08205/c
ID AAL08205 standard; cDNA; 506 BP.
XX
XX AAL08205;
XX
XX 07-DEC-2001 (first entry)
XX
XX Human breast cancer expressed polynucleotide 662.
XX
XX Human; breast cancer; cell marker; cytostatic; ss.
XX
XX Homo sapiens.
XX
XX WO200151628-A2.
XX
XX 19-JUL-2001.
XX
XX 10-JAN-2001; 2001WO-US00798.
XX
XX 14-JAN-2000; 2000US-0176077.
XX
XX 14-MAR-2000; 2000US-0189167.
XX
XX 24-MAR-2000; 2000US-0192099.
XX
XX 29-MAR-2000; 2000US-0193480.
XX
XX 15-MAY-2000; 2000US-0205230.
XX
XX 09-JUN-2000; 2000US-0211315.
XX
XX 25-JUL-2000; 2000US-0220534.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lillie J, Xu Y, Wang Y, Steinmann K;
XX
XX WPI; 2001-451856/48.
XX
XX New peptide useful as a marker for the diagnosis of breast cancer -
PT
XX Claim 1; Page 198; 3695pp; English.
XX
XX The invention relates to human breast cancer expressed polynucleotides
CC (AAL07544-AAL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterising treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.
XX
XX Sequence 506 BP; 155 A; 87 C; 106 G; 155 T; 3 other;
SQ
Query Match 5.9%; Score 29; DB 22; Length 506;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 461 TTGTCCAAATGTTTCATCAACACTTCTTGA 489
|||||
```

Db 315 TTGTCCAAATGTTTCATCAACACTTCTTGA 287

RESULT 49  
AAZ88711/C  
ID AAZ88711 standard; cDNA; 30 BP.  
XX  
AC AAZ88711;  
XX  
XX 11-MAY-2000 (first entry)  
XX  
DE Human IL-15 targetted antisense oligonucleotide HCL-103.  
XX  
KW IL-15; interleukin 15; human; anti-IL15; anti-inflammatory; hepatotropic;  
KW anti-arthritis; neuroprotective; antiproliferative; antiulcer; antisense;  
KW gene therapy; macrophage; inflammatory disorder; bowel disease; primer;  
KW arthritis; cirrhosis; multiple sclerosis; chronic liver disease;  
KW ulcerative colitis; cell proliferative disorder; treatment; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200001851-A1.  
XX  
PD 13-JAN-2000.  
XX  
PF 07-JUL-1999; 99WO-US15499.  
XX  
PR 07-JUL-1998; 98US-0091873.  
XX  
PA (HISM ) HISAMITSU PHARM CO LTD.  
XX  
PI Veerapanane D, Hamanaka S, Hiroyuki K, Nozawa I;  
XX  
DR WPI; 2000-171026/15.  
XX  
PT Novel antisense oligonucleotides targeted to interleukin-15 used to  
PT treat inflammatory diseases and cell proliferative diseases such as  
PT inflammatory bowel disease and chronic liver disease -  
XX  
PS Claim 12; Fig 2; 52pp; English.  
XX  
CC This invention describes novel antisense oligonucleotides of 8-40  
CC nucleic acids, targeted to interleukin-15 (IL-15). The products of the  
CC invention have anti-IL15, anti-inflammatory, hepatotropic,  
CC anti-arthritis, neuroprotective, antiproliferative and antiulcer activity  
CC and can be used for gene therapy. The antisense oligonucleotides are used  
CC to inhibit interleukin-15 (IL-15) expression and production, and prevent  
CC the recruitment and activation of macrophages. They are used to treat  
CC diseases associated with an increased expression of IL-15. Such diseases  
CC include inflammatory disorders, such as inflammatory bowel disease,  
CC ulcerative colitis and cell proliferative disorders. The treatment may  
CC be in vivo or ex vivo. The antisense oligonucleotides of the invention  
CC are specific for interleukin-15 (IL-15), and can be delivered  
CC exogenously or can be expressed from DNA or RNA vectors. AAZ88709-288723  
CC represent the antisense oligonucleotides disclosed in the method of the  
CC invention.  
XX  
SQ Sequence 30 BP; 8 A; 6 C; 4 G; 12 T; 0 other;

Query Match 5.5%; Score 27; DB 21; Length 30;  
Best Local Similarity 100.0%; Pred. No. 0.0021;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAATTCGAAACACATTGAGA 27  
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Db 27 ATGAGAATTCGAAACACATTGAGA 1

RESULT 50  
AAZ88714/C  
ID AAZ88714 standard; cDNA; 25 BP.

XX AAZ88714;  
AC  
XX  
DT 11-MAY-2000 (first entry)  
XX  
DE Human IL-15 targetted antisense oligonucleotide HCL-106.  
XX  
XX  
KW IL-15; interleukin 15; human; anti-IL15; anti-inflammatory; hepatotropic;  
KW anti-arthritis; neuroprotective; antiproliferative; antiulcer; antisense;  
KW gene therapy; macrophage; inflammatory disorder; bowel disease; primer;  
KW arthritis; cirrhosis; multiple sclerosis; chronic liver disease;  
KW ulcerative colitis; cell proliferative disorder; treatment; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200001851-A1.  
XX  
PD 13-JAN-2000.  
XX  
PF 07-JUL-1999; 99WO-US15499.  
XX  
PR 07-JUL-1998; 98US-0091873.  
XX  
PA (HISM ) HISAMITSU PHARM CO LTD.  
XX  
PI Veerapanane D, Hamanaka S, Hiroyuki K, Nozawa I;  
XX  
DR WPI; 2000-171026/15.  
XX  
PT Novel antisense oligonucleotides targeted to interleukin-15 used to  
PT treat inflammatory diseases and cell proliferative diseases such as  
PT inflammatory bowel disease and chronic liver disease -  
XX  
PS Claim 12; Fig 2; 52pp; English.  
XX  
CC This invention describes novel antisense oligonucleotides of 8-40  
CC nucleic acids, targeted to interleukin-15 (IL-15). The products of the  
CC invention have anti-IL15, anti-inflammatory, hepatotropic,  
CC anti-arthritis, neuroprotective, antiproliferative and antiulcer activity  
CC and can be used for gene therapy. The antisense oligonucleotides are used  
CC to inhibit interleukin-15 (IL-15) expression and production, and prevent  
CC the recruitment and activation of macrophages. They are used to treat  
CC diseases associated with an increased expression of IL-15. Such diseases  
CC include inflammatory disorders, such as inflammatory bowel disease,  
CC ulcerative colitis and cell proliferative disorders. The treatment may  
CC be in vivo or ex vivo. The antisense oligonucleotides of the invention  
CC are specific for interleukin-15 (IL-15), and can be delivered  
CC exogenously or can be expressed from DNA or RNA vectors. AAZ88709-288723  
CC represent the antisense oligonucleotides disclosed in the method of the  
CC invention.  
XX  
SQ Sequence 25 BP; 6 A; 6 C; 6 G; 7 T; 0 other;

Query Match 4.7%; Score 23; DB 21; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 AGTGATGTTTACCCCGAGTTGCAA 251  
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Db 25 AGTGATGTTTACCCCGAGTTGCAA 3

Search completed: August 6, 2002, 21:37:53  
Job time: 4702 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 6, 2002, 21:32:10 ; Search time 1856.14 Seconds  
(without alignments)  
5513.095 Million cell updates/sec

Title: US-09-724-841-4  
Perfect score: 489  
Sequence: 1 ATGAGATTTCGAACACACA.....TGTTCACTCAACTTCTTGA 489

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 12

Total number of hits satisfying chosen parameters: 262374

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_on.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_on.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htgo\_inv.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
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1 489 100.0 489 6 AR004267  
2 489 100.0 489 6 AR024348  
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6 489 100.0 489 6 AR122867  
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8 489 100.0 489 6 AX006785  
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10 489 100.0 489 6 I28850  
11 489 100.0 489 6 I79220  
12 489 100.0 1275 9 CAU03099  
13 423 86.5 492 9 AB000555  
14 423 86.5 559 9 MMU19843  
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17 345 70.6 345 6 I28857  
18 345 70.6 345 6 I79227  
19 107 21.9 453 9 HSL15MR  
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49 80 16.4 345 6 I28856  
50 80 16.4 345 6 I79226  
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62 24 4.9 489 4 AF108148  
63 23 4.7 30 6 AX353399  
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67 21 4.3 21 6 AR103279  
68 21 4.3 36 6 AR024357  
69 21 4.3 36 6 AR122054  
70 21 4.3 36 6 AR122876  
71 21 4.3 36 6 AR125113  
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c 78	21	4.3	69	6	AR125112	AR125112 Sequence	c 151	19	3.9	94973	9	AL645819	AL645819 Human DNA
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c 80	21	4.3	38199	3	AC009745	AC009745 Drosophill	c 153	19	3.9	102223	9	AC022432	AC022432 Homo sapi
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c 89	21	4.3	179947	2	AC009786	AC009786 Homo sapi	c 162	19	3.9	131732	10	AF259071	AF259071 Mus muscu
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c 102	20	4.1	54585	2	AC100191	AC100191 Mus muscu	c 174	19	3.9	150391	2	AC011764	AC011764 Drosophill
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c 104	20	4.1	66817	9	AC005201	AC005201 Homo sapi	c 176	19	3.9	153210	2	AC104574	AC104574 Homo sapi
c 105	20	4.1	69200	2	AC034294	AC034294 Homo sapi	c 177	19	3.9	153693	2	AC010373	AC010373 Homo sapi
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c 113	20	4.1	162922	2	AC011281	AC011281 Homo sapi	c 185	19	3.9	161812	9	HS197017	AL008629 Human DNA
c 114	20	4.1	163660	2	AC046165	AC046165 Homo sapi	c 186	19	3.9	162345	3	AC006415	AC006415 Drosophill
c 115	20	4.1	163807	2	AC018934	AC018934 Homo sapi	c 187	19	3.9	165901	10	MM437P9	AL049866 Mus muscu
c 116	20	4.1	163807	2	AC018934	AC018934 Homo sapi	c 188	19	3.9	166384	2	AC074113	AC074113 Homo sapi
c 117	20	4.1	164868	9	AC016045	AC016045 Homo sapi	c 189	19	3.9	166701	9	AC005747	AC005747 Homo sapi
c 118	20	4.1	165027	3	CEY48C3A	AL117203 Caenorhab	c 190	19	3.9	167949	9	AC087821	AC087821 Homo sapi
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c 125	20	4.1	208035	2	AC006520	AC006520 Mus muscu	c 197	19	3.9	175578	2	AC087435	AC087435 Homo sapi
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c 128	19	3.9	25	6	AR094646	AF223391 Homo sapi	c 200	19	3.9	177037	9	AL163542	AL163542 Human DNA
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c 131	19	3.9	3080	8	KLMBP1	BD008808 Antagonis	c 203	19	3.9	178793	2	AC097015	AC097015 Homo sapi
c 132	19	3.9	8964	6	AX251976	X74159 K.lactis MB	c 204	19	3.9	179589	2	AC018860	AC018860 Homo sapi
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c 135	19	3.9	8964	6	AX349013	AX346436 Sequence	c 207	19	3.9	185074	2	AC093526	AC093526 Homo sapi
c 136	19	3.9	11681	1	AE007746	AX349013 Sequence	c 208	19	3.9	185764	2	AC025289	AC025289 Homo sapi
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c 140	19	3.9	48086	9	HS1041B16	AB012161 Mus muscu	c 212	19	3.9	187880	2	AC108716	AC108716 Homo sapi
c 141	19	3.9	52891	2	AC107919	AL031223 Human DNA	c 213	19	3.9	188782	9	AC023150	AC023150 Homo sapi
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c 145	19	3.9	68702	9	AL445193	Z72004 Human DNA s	c 217	19	3.9	193852	2	AC016544	AC016544 Homo sapi
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248	18	3	7	18	6	AR087041	Sequence	AR087041	18	3	7	9972	6	AR093385	Sequence
249	18	3	7	18	6	AR087045	Sequence	AR087045	18	3	7	9972	6	AR093385	Sequence
250	18	3	7	18	6	AR087046	Sequence	AR087046	18	3	7	9972	6	AR093385	Sequence
251	18	3	7	20	6	AX024725	Sequence	AX024725	18	3	7	9972	6	AR093385	Sequence

366	18	3.7	70802	2	AC024426	AC024426 Homo sapi	c 439	18	3.7	131933	9	AL590311	AL590311 Human DNA
c 367	18	3.7	71319	2	AC009670	AC009670 Homo sapi	440	18	3.7	132114	9	AC026772	AC026772 Homo sapi
368	18	3.7	71522	8	AB006703	AB006703 Arabidops	c 441	18	3.7	134924	2	AC104458	AC104458 Homo sapi
c 369	18	3.7	72751	9	AC090112	Pan trogl	c 442	18	3.7	134959	30	AL139218	AL139218 Human DNA
370	18	3.7	73005	2	AC084076	AC084076 Homo sapi	c 443	18	3.7	135060	9	AL354659	AL354659 Human DNA
371	18	3.7	73334	6	AX347027	Sequence	c 444	18	3.7	136506	9	AC010462	AC010462 Homo sapi
c 372	18	3.7	73334	6	AX356494	Sequence	c 445	18	3.7	137571	2	AC079539	AC079539 Mus muscu
c 373	18	3.7	73862	2	AC106138	Rattus no	c 446	18	3.7	138373	2	AC011380	AC011380 Homo sapi
c 374	18	3.7	74586	2	AC060793	AC060793 Homo sapi	447	18	3.7	139260	9	AC066587	AC066587 Homo sapi
c 375	18	3.7	74982	2	AC067958	AC067958 Homo sapi	448	18	3.7	141469	9	AL139811	AL139811 Human DNA
c 376	18	3.7	77839	2	AC106608	Rattus no	449	18	3.7	141738	9	AC011824	AC011824 Homo sapi
c 377	18	3.7	79666	9	AL136969	Human DNA	450	18	3.7	141833	9	AL442063	AL442063 Human DNA
c 378	18	3.7	80770	8	AB005240	Arabidops	c 451	18	3.7	142396	9	AL157407	AL157407 Human DNA
c 379	18	3.7	81172	2	AC036240	Homo sapi	c 452	18	3.7	142549	2	AP004271	AP004271 Oryza sat
c 380	18	3.7	82512	9	HUM13K623	AC000061 Human BAC	c 453	18	3.7	142640	9	AC006399	AC006399 Homo sapi
c 381	18	3.7	84300	9	HSJ104817	AL121961 Human DNA	454	18	3.7	142908	2	AL513172	AL513172 Homo sapi
c 382	18	3.7	85195	9	AL136093	Human DNA	c 455	18	3.7	142990	2	AC104383	AC104383 Homo sapi
c 383	18	3.7	87871	8	ATF4C12	AL392145 Arabidops	c 456	18	3.7	143606	2	AC073488	AC073488 Homo sapi
c 384	18	3.7	90693	9	AC005592	AC005592 Homo sapi	457	18	3.7	144257	2	AC068131	AC068131 Homo sapi
c 385	18	3.7	91202	2	AC007609	AC007609 Homo sapi	c 458	18	3.7	145291	2	AC011799	AC011799 Homo sapi
c 386	18	3.7	92019	9	AL450320	Human DNA	459	18	3.7	145384	2	AC092995	AC092995 Homo sapi
c 387	18	3.7	92693	9	AL157766	Human DNA	460	18	3.7	145668	2	AC092272	AC092272 Homo sapi
c 388	18	3.7	95097	9	AC022202	Homo sapi	c 461	18	3.7	146112	2	AC105682	AC105682 Rattus no
c 389	18	3.7	95554	2	AC093284	AC093284 Homo sapi	462	18	3.7	146602	9	CNS05TD5	AL356015 Human chr
c 390	18	3.7	96067	9	AP000953	AP000953 Homo sapi	463	18	3.7	146727	2	AC107467	AC107467 Rattus no
c 391	18	3.7	99123	8	AF069716	Arabidops	464	18	3.7	146836	9	AC019317	AC019317 Homo sapi
c 392	18	3.7	99589	2	AC093299	AC093299 Homo sapi	c 465	18	3.7	146903	2	AC024410	AC024410 Homo sapi
c 393	18	3.7	99819	2	AC079761	AC079761 Homo sapi	466	18	3.7	146918	2	AC099498	AC099498 Homo sapi
c 394	18	3.7	100888	9	AL591104	Human DNA	467	18	3.7	146994	9	AL137245	AL137245 Human DNA
c 395	18	3.7	101458	2	AP000680	AP000680 Homo sapi	c 468	18	3.7	147423	9	AC099487	AC099487 Homo sapi
c 396	18	3.7	101719	2	AL357495	AL357495 Homo sapi	469	18	3.7	148018	2	HSJ7613A2	AL121990 Homo sapi
c 397	18	3.7	101946	2	AL365320	AL365320 Homo sapi	470	18	3.7	148109	2	AC018918	AC018918 Homo sapi
c 398	18	3.7	102343	2	AC106551	AC106551 Rattus no	c 471	18	3.7	148202	2	AC026493	AC026493 Homo sapi
c 399	18	3.7	103370	9	AL161656	Human DNA	c 472	18	3.7	149002	2	AL445484	AL445484 Homo sapi
c 400	18	3.7	103916	9	AC004225	AC004225 Homo sapi	473	18	3.7	149064	2	AC106432	AC106432 Rattus no
c 401	18	3.7	104844	9	HSJ1057J7	AL109936 Human DNA	c 474	18	3.7	150149	4	AC091119	AC091119 Canis fam
c 402	18	3.7	107330	9	AC019178	AC019178 Homo sapi	c 475	18	3.7	150312	9	CNS01RIJ	AL163613 Human chr
c 403	18	3.7	107705	3	AC024826	AC024826 Caenorhab	c 476	18	3.7	150519	2	AC097847	AC097847 Rattus no
c 404	18	3.7	107705	3	AC024826	AC024826 Caenorhab	c 477	18	3.7	151171	2	AC020775	AC020775 Homo sapi
c 405	18	3.7	108182	3	AC009308	AC009308 Homo sapi	c 478	18	3.7	151348	9	AC087713	AC087713 Homo sapi
c 406	18	3.7	108924	3	AC005889	AC005889 Drosophil	c 479	18	3.7	151498	9	AC099331	AC099331 Homo sapi
c 407	18	3.7	109333	2	AC105893	AC105893 Rattus no	480	18	3.7	151651	2	AC011633	AC011633 Homo sapi
c 408	18	3.7	109333	2	AC105893	AC105893 Rattus no	c 481	18	3.7	151881	9	AC008629	AC008629 Homo sapi
c 409	18	3.7	109602	2	AP004613	AP004613 Oryza sat	c 482	18	3.7	151987	2	AP004339	AP004339 Oryza sat
c 410	18	3.7	110000	10	AE008686_0	AE008686 Mus muscu	c 483	18	3.7	152387	2	AC099672	AC099672 Homo sapi
c 411	18	3.7	110696	2	AC097150	AC097150 Rattus no	c 484	18	3.7	152432	2	AC025746	AC025746 Homo sapi
c 412	18	3.7	111414	2	AC020265	AC020265 Drosophil	c 485	18	3.7	152878	3	CEX18D10A	AL034393 Caenorhab
c 413	18	3.7	112709	2	AP003758	AP003758 Oryza sat	486	18	3.7	153297	2	AC027558	AC027558 Homo sapi
c 414	18	3.7	113250	9	AC004900	AC004900 Homo sapi	487	18	3.7	153310	2	AC100724	AC100724 Mus muscu
c 415	18	3.7	113596	2	AC105357	AC105357 Homo sapi	488	18	3.7	153741	9	AC012511	AC012511 Homo sapi
c 416	18	3.7	113609	2	AC011368	AC011368 Homo sapi	c 489	18	3.7	153764	9	AL355350	AL355350 Human DNA
c 417	18	3.7	114041	2	AP001868	AP001868 Homo sapi	c 490	18	3.7	153860	2	AC016301	AC016301 Homo sapi
c 418	18	3.7	114519	9	AL157813	AL157813 Human DNA	491	18	3.7	154090	9	AC025577	AC025577 Homo sapi
c 419	18	3.7	114791	9	HSJ850E9	AL121758 Human DNA	492	18	3.7	154289	2	AC027714	AC027714 Homo sapi
c 420	18	3.7	116526	9	AC013243	AC013243 Rattus no	c 493	18	3.7	154588	9	AL355871	AL355871 Human DNA
c 421	18	3.7	117083	9	AC021264	AC021264 Homo sapi	494	18	3.7	154649	2	AC064854	AC064854 Homo sapi
c 422	18	3.7	117979	2	AC098538	AC098538 Rattus no	c 495	18	3.7	155349	9	AL162257	AL162257 Homo sapi
c 423	18	3.7	118360	8	AF166114	AF166114 Mesostigm	496	18	3.7	155416	9	AL160286	AL160286 Human DNA
c 424	18	3.7	121157	2	AC094303	AC094303 Rattus no	497	18	3.7	155439	9	AC008626	AC008626 Homo sapi
c 425	18	3.7	121552	8	ATF12E4	AL162751 Arabidops	498	18	3.7	155603	2	AC088517	AC088517 Homo sapi
c 426	18	3.7	123218	2	AC094197	AC094197 Rattus no	c 499	18	3.7	155813	2	AC019350	AC019350 Homo sapi
c 427	18	3.7	123241	2	AC022090	AC022090 Homo sapi	500	18	3.7	155825	2	AC023503	AC023503 Homo sapi
c 428	18	3.7	123331	9	AC005164	AC005164 Homo sapi	c 501	18	3.7	156184	2	AC041018	AC041018 Homo sapi
c 429	18	3.7	125413	2	AC026607	AC026607 Homo sapi	c 502	18	3.7	156335	3	AC008219	AC008219 Drosophil
c 430	18	3.7	125837	9	AC016553	AC016553 Homo sapi	c 503	18	3.7	156353	9	AC091381	AC091381 Papio cyn
c 431	18	3.7	126910	9	AC005856	AC005856 Homo sapi	c 504	18	3.7	156585	2	AC012109	AC012109 Homo sapi
c 432	18	3.7	128500	9	AC069426	AC069426 Homo sapi	c 505	18	3.7	156623	2	AC095104	AC095104 Rattus no
c 433	18	3.7	128632	2	AC079622	AC079622 Homo sapi	c 506	18	3.7	157308	2	AC079351	AC079351 Homo sapi
c 434	18	3.7	129108	9	AC011482	AC011482 Homo sapi	c 507	18	3.7	157533	9	AL354709	AL354709 Human DNA
c 435	18	3.7	129451	2	AC073783	AC073783 Mus muscu	c 508	18	3.7	157750	2	AC006097	AC006097 Homo sapi
c 436	18	3.7	130117	9	AC004907	AC004907 Homo sapi	509	18	3.7	157832	2	AC011653	AC011653 Homo sapi
c 437	18	3.7	131321	2	AC080160	AC080160 Mus muscu	c 510	18	3.7	158151	9	CNS05TDT	AL357094 Human chr
c 438	18	3.7	131570	2	AC022411	AC022411 Homo sapi	c 511	18	3.7	158288	2	AC092770	AC092770 Homo sapi

c 512	18	3.7 158426	2	AC094845	AC094845 Rattus no	585	18	3.7 170962	2	AL389927	Homo sapi
c 513	18	3.7 158591	9	AL139277	Human DNA	c 586	18	3.7 171069	2	AP003845	Oryza sat
c 514	18	3.7 159759	2	AC096247	Rattus no	587	18	3.7 171249	9	AC010975	Homo sapi
c 515	18	3.7 159769	2	AC007337	Homo sapi	588	18	3.7 171697	2	AC093548	Drosophill
c 516	18	3.7 160087	2	AC007131	Homo sapi	589	18	3.7 172794	2	AC096201	Rattus no
c 517	18	3.7 160271	2	AC016199	Homo sapi	590	18	3.7 173508	9	AC006385	Homo sapi
c 518	18	3.7 160429	2	AC078981	Homo sapi	c 591	18	3.7 173644	8	AC093568	Oryza sat
c 519	18	3.7 160492	9	AP001884	AP001884 Homo sapi	c 592	18	3.7 174264	10	AL591373	Mouse DNA
c 520	18	3.7 160572	2	AC092249	AC092249 Canis fam	c 593	18	3.7 174469	9	AC022882	Homo sapi
c 521	18	3.7 160701	2	AP004618	AP004618 Oryza sat	c 594	18	3.7 174576	2	AC105180	Homo sapi
c 522	18	3.7 160708	2	AC068406	AC068406 Homo sapi	595	18	3.7 174631	2	AC105180	Homo sapi
c 523	18	3.7 161422	2	AC108686	AC108686 Homo sapi	596	18	3.7 174640	2	AC069059	Homo sapi
c 524	18	3.7 161549	9	AC073174	AC073174 Homo sapi	597	18	3.7 174640	2	AC017044	Homo sapi
c 525	18	3.7 161757	2	AC044901	AC044901 Homo sapi	598	18	3.7 174642	2	AC091769	Homo sapi
c 526	18	3.7 161855	2	AC067769	AC067769 Homo sapi	c 599	18	3.7 174963	2	AC022145	Homo sapi
c 527	18	3.7 161855	2	AC067769	AC067769 Homo sapi	c 600	18	3.7 175182	2	AC105559	Rattus no
c 528	18	3.7 161855	2	AC067769	AC067769 Homo sapi	c 601	18	3.7 175588	9	AC027119	Homo sapi
c 529	18	3.7 161871	10	AC005938	AC005938 Mus muscu	602	18	3.7 175594	9	AL162503	Human DNA
c 530	18	3.7 161962	2	AC091883	AC091883 Homo sapi	603	18	3.7 176034	9	CNS01DX5	Human chr
c 531	18	3.7 162023	2	AC084033	AC084033 Homo sapi	604	18	3.7 176292	9	AP002407	Homo sapi
c 532	18	3.7 162681	9	AC087835	AC087835 Pan trogl	c 605	18	3.7 176405	2	AC027399	Homo sapi
c 533	18	3.7 162809	2	AC011379	AC011379 Homo sapi	606	18	3.7 176406	2	AC108019	Homo sapi
c 534	18	3.7 162859	4	AC089993	AC089993 Bos tauru	607	18	3.7 176476	2	AC096094	Rattus no
c 535	18	3.7 163031	9	AC024947	AC024947 Homo sapi	608	18	3.7 176689	9	AL162414	Human DNA
c 536	18	3.7 163228	2	AC090939	AC090939 Homo sapi	609	18	3.7 177019	9	AC022833	Homo sapi
c 537	18	3.7 163673	2	AC027598	AC027598 Homo sapi	c 610	18	3.7 177300	9	AC096741	Homo sapi
c 538	18	3.7 163712	2	AC099568	AC099568 Homo sapi	c 611	18	3.7 178161	8	AC084320	Oryza sat
c 539	18	3.7 163861	9	AL356772	AL356772 Human DNA	c 612	18	3.7 178188	2	AC087341	Homo sapi
c 540	18	3.7 163881	9	AC007436	AC007436 Homo sapi	613	18	3.7 178530	2	AC010773	Homo sapi
c 541	18	3.7 163889	2	AC004958	AC004958 Homo sapi	c 614	18	3.7 178628	2	AL450996	Homo sapi
c 542	18	3.7 164364	2	AC099332	AC099332 Homo sapi	c 615	18	3.7 178640	2	AC069170	Homo sapi
c 543	18	3.7 164481	2	AC034152	AC034152 Homo sapi	c 616	18	3.7 178984	2	AC069170	Homo sapi
c 544	18	3.7 165199	9	AC003973	AC003973 Homo sapi	c 617	18	3.7 179002	2	AC084023	Oryza sat
c 545	18	3.7 165199	9	AC003973	AC003973 Homo sapi	c 618	18	3.7 179209	2	AC088931	Homo sapi
c 546	18	3.7 165208	2	AC098770	AC098770 Rattus no	c 619	18	3.7 179258	2	AC091549	Homo sapi
c 547	18	3.7 165262	2	AP003181	AP003181 Homo sapi	c 620	18	3.7 179401	2	AC083562	Homo sapi
c 548	18	3.7 165496	2	AC097242	AC097242 Rattus no	c 621	18	3.7 179401	2	AC083805	Homo sapi
c 549	18	3.7 165533	2	AC094484	AC094484 Rattus no	c 622	18	3.7 179465	2	AC027024	Homo sapi
c 550	18	3.7 165794	2	AC096508	AC096508 Homo sapi	c 623	18	3.7 179525	2	AC094760	Homo sapi
c 551	18	3.7 165904	2	AL158148	AL158148 Homo sapi	c 624	18	3.7 179528	9	AC026189	Homo sapi
c 552	18	3.7 165931	30	AC010954	AC010954 Homo sapi	c 625	18	3.7 180401	9	AC007489	Homo sapi
c 553	18	3.7 166197	2	AC073552	AC073552 Homo sapi	c 626	18	3.7 180510	9	AC022415	Homo sapi
c 554	18	3.7 166307	2	OSJN01012	OSJN01012 Homo sapi	c 627	18	3.7 180630	3	AC007975	Homo sapi
c 555	18	3.7 166357	9	AC026307	AC026307 Homo sapi	c 628	18	3.7 180787	2	AC097811	Drosophill
c 556	18	3.7 166504	9	AC008275	AC008275 Homo sapi	c 629	18	3.7 181570	2	AC068738	Homo sapi
c 557	18	3.7 166508	2	AL513343	AL513343 Homo sapi	c 630	18	3.7 181570	2	AC068738	Homo sapi
c 558	18	3.7 166567	2	AC097102	AC097102 Homo sapi	c 631	18	3.7 181745	9	AC008179	Homo sapi
c 559	18	3.7 166772	2	AC098691	AC098691 Homo sapi	c 632	18	3.7 181904	2	AC027623	Homo sapi
c 560	18	3.7 167077	2	AC091093	AC091093 Homo sapi	c 633	18	3.7 182026	2	AC011313	Homo sapi
c 561	18	3.7 167108	9	CNS01RHA	CNS01RHA Homo sapi	c 634	18	3.7 182860	9	AC068700	Homo sapi
c 562	18	3.7 167437	2	AC023068	AC023068 Human chr	c 635	18	3.7 183833	9	AL161646	Human DNA
c 563	18	3.7 167462	2	AC103496	AC103496 Homo sapi	c 636	18	3.7 185087	2	AL627386	Mus muscu
c 564	18	3.7 167623	2	AC073450	AC073450 Rattus no	c 637	18	3.7 185281	2	AC011214	Homo sapi
c 565	18	3.7 167857	9	AL138778	AL138778 Homo sapi	c 638	18	3.7 185636	2	AC027109	Homo sapi
c 566	18	3.7 167887	2	AC026066	AC026066 Homo sapi	c 639	18	3.7 185721	2	AC027109	Homo sapi
c 567	18	3.7 168128	2	AC024729	AC024729 Homo sapi	c 640	18	3.7 185850	9	AL357394	Human DNA
c 568	18	3.7 168373	9	AL391683	AL391683 Homo sapi	c 641	18	3.7 186164	2	AC106411	Homo sapi
c 569	18	3.7 168644	9	AC004544	AC004544 Homo sapi	c 642	18	3.7 186531	9	AC024606	Homo sapi
c 570	18	3.7 169072	2	AC069525	AC069525 Homo sapi	c 643	18	3.7 186660	2	AC026107	Homo sapi
c 571	18	3.7 169075	2	AC093276	AC093276 Homo sapi	c 644	18	3.7 186865	2	AC095269	Rattus no
c 572	18	3.7 169566	2	AC073579	AC073579 Homo sapi	c 645	18	3.7 186881	2	AL646048	Mus muscu
c 573	18	3.7 169730	3	AC010006	AC010006 Homo sapi	c 646	18	3.7 187266	2	AC073984	Homo sapi
c 574	18	3.7 169821	2	AC025490	AC025490 Homo sapi	c 647	18	3.7 187418	9	AC090580	Homo sapi
c 575	18	3.7 169867	2	AC094703	AC094703 Rattus no	c 648	18	3.7 187960	9	AP000866	Homo sapi
c 576	18	3.7 170057	3	AC009197	AC009197 Drosophill	c 649	18	3.7 188205	9	AC003986	Homo sapi
c 577	18	3.7 170101	2	AC090160	AC090160 Homo sapi	c 650	18	3.7 188349	9	AL390197	Human DNA
c 578	18	3.7 170101	14	ASU18466	U18466 African swi	c 651	18	3.7 189006	2	AP001456	Rattus no
c 579	18	3.7 170202	2	AL161934	AL161934 Homo sapi	c 652	18	3.7 189621	2	AL589681	Homo sapi
c 580	18	3.7 170222	2	AC106499	AC106499 Rattus no	c 653	18	3.7 189670	2	AC041047	Homo sapi
c 581	18	3.7 170460	3	AC010012	AC010012 Drosophill	c 654	18	3.7 189681	9	AC018822	Homo sapi
c 582	18	3.7 170658	2	AC025838	AC025838 Homo sapi	c 655	18	3.7 189981	9	AC018503	Homo sapi
c 583	18	3.7 170846	9	AC068121	AC068121 Homo sapi	c 656	18	3.7 191161	9	AC018503	Homo sapi
c 584	18	3.7 170944	2	AC094217	AC094217 Rattus no	c 657	18	3.7 191284	2	AL109362	Homo sapi
								3.7 191373	10	AP001295	Mus muscu

c 658	18	3. 7	191502	2	AC098735	AC098735	Mus muscu	c 731	18	3. 7	299301	2	AC098584	AC098584	Homo sapi
c 659	18	3. 7	191699	2	AC031977	AC031977	Homo sapi	c 732	18	3. 7	308600	3	AC023053	AC023053	Homo sapi
c 660	18	3. 7	191734	2	AC016560	AC016560	Homo sapi	c 733	18	3. 7	308638	3	AE003474	AE003474	Drosophil
c 661	18	3. 7	191734	2	AC016560	AC016560	Homo sapi	c 734	18	3. 7	314150	1	CJ11168X1	CJ11168X1	Campyloba
c 662	18	3. 7	191962	2	AC048342	AC048342	Homo sapi	c 735	18	3. 7	331909	2	AP001684	AP001684	Homo sapi
c 663	18	3. 7	192296	9	AL009654	AL009654	Human DNA	c 736	18	3. 7	331909	2	AP001684	AP001684	Homo sapi
c 664	18	3. 7	192296	9	AL162723	AL162723	Human DNA	c 737	18	3. 7	340000	9	AX282123	AX282123	Sequence
c 665	18	3. 7	192780	2	AC011978	AC011978	Homo sapi	c 738	18	3. 7	349980	6	AX282125	AX282125	Sequence
c 666	18	3. 7	192994	2	AL672051	AL672051	Mus muscu	c 739	18	3. 7	349980	6	AX282125	AX282125	Sequence
c 667	18	3. 7	193309	2	AL672051	AL672051	Mus muscu	c 740	17	3. 5	144	11	G44141	G44141	WTAF-3781-S
c 668	18	3. 7	193632	9	AC093458	AC093458	Homo sapi	c 741	17	3. 5	148	11	GI9043	GI9043	cow STS BMS
c 669	18	3. 7	193713	2	AC095007	AC095007	Rattus no	c 742	17	3. 5	183	10	HAMHGC05	HAMHGC05	Syrian hams
c 670	18	3. 7	194332	2	AC023140	AC023140	Homo sapi	c 743	17	3. 5	230	9	HSCOA504	HSCOA504	Human 3-hyd
c 671	18	3. 7	194575	2	AC098597	AC098597	Homo sapi	c 744	17	3. 5	259	9	HSOBR130	HSOBR130	Human OBR g
c 672	18	3. 7	194874	2	AC080090	AC080090	Homo sapi	c 745	17	3. 5	280	3	DPVA37M1	DPVA37M1	D.plni sate
c 673	18	3. 7	195007	9	CNS06C81	AL391749	Human chr	c 746	17	3. 5	311	9	HS179XD10	HS179XD10	H. sapiens
c 674	18	3. 7	195089	2	AC100875	AL100875	Homo sapi	c 747	17	3. 5	311	9	AF047279	AF047279	Homo sapi
c 675	18	3. 7	195153	2	AL499616	AL499616	Homo sapi	c 748	17	3. 5	311	9	AF052775	AF052775	Homo sapi
c 676	18	3. 7	196355	9	AC099557	AC099557	Homo sapi	c 749	17	3. 5	311	9	AF052776	AF052776	Homo sapi
c 677	18	3. 7	196431	2	CNS01DD5	AL133162	Homo sapi	c 750	17	3. 5	311	9	AF052778	AF052778	Homo sapi
c 678	18	3. 7	196550	9	AC020734	AC020734	Homo sapi	c 751	17	3. 5	313	1	U93694	U93694	Borrellia bu
c 679	18	3. 7	196946	2	AL645470	AL645470	Mus muscu	c 752	17	3. 5	346	1	ECOGPTB	ECOGPTB	E.coli gpt
c 680	18	3. 7	197650	2	AL391243	AL391243	Homo sapi	c 753	17	3. 5	354	1	ECPEPD	ECPEPD	E.coli pepd
c 681	18	3. 7	197828	2	AC034169	AC034169	Homo sapi	c 754	17	3. 5	392	6	AX310126	AX310126	Sequence
c 682	18	3. 7	198088	9	AC078957	AC078957	Homo sapi	c 755	17	3. 5	406	10	PHDLTRC	PHDLTRC	Phodopus su
c 683	18	3. 7	198431	2	AL669895	AL669895	Mus muscu	c 756	17	3. 5	457	3	DMU24572	DMU24572	Drosophila
c 684	18	3. 7	198480	2	AC025077	AC025077	Homo sapi	c 757	17	3. 5	470	11	HS65516S	HS65516S	H. sapiens
c 685	18	3. 7	198812	9	AC023480	AC023480	Homo sapi	c 758	17	3. 5	500	11	G33279	G33279	human STS S
c 686	18	3. 7	199981	2	AC079007	AC079007	Homo sapi	c 759	17	3. 5	521	1	ECOGPTD	ECOGPTD	E.coli gpt
c 687	18	3. 7	200439	2	AC099614	AC099614	Mus muscu	c 760	17	3. 5	521	1	ECOGPTD	ECOGPTD	E.coli gpt
c 688	18	3. 7	201132	2	AC099614	AC099614	Mus muscu	c 761	17	3. 5	700	9	HSXNP21	HSXNP21	Homo sapien
c 689	18	3. 7	201176	2	AC092058	AC092058	Homo sapi	c 762	17	3. 5	758	8	SNU03077	SNU03077	Stephanodis
c 690	18	3. 7	202375	2	AC109798	AC109798	Bos tauri	c 763	17	3. 5	759	8	SNU03077	SNU03077	Stephanodis
c 691	18	3. 7	202583	2	AC096585	AC096585	Homo sapi	c 764	17	3. 5	765	8	SNU03076	SNU03076	Stephanodis
c 692	18	3. 7	203020	2	AC092832	AC092832	Homo sapi	c 765	17	3. 5	765	8	SNU03074	SNU03074	Stephanodis
c 693	18	3. 7	203084	2	AC067854	AC067854	Homo sapi	c 766	17	3. 5	790	9	HLPR115	HLPR115	Human lept1
c 694	18	3. 7	204310	2	AL512273	AL512273	Homo sapi	c 767	17	3. 5	815	8	AB040439	AB040439	Medicago
c 695	18	3. 7	207705	2	AL590630	AL590630	Mus muscu	c 768	17	3. 5	895	11	RP282357	RP282357	R.prowazeki
c 696	18	3. 7	208410	2	AL670360	AL670360	Mus muscu	c 769	17	3. 5	908	11	CNS06171	CNS06171	T3 end of
c 697	18	3. 7	208506	2	AP003530	AP003530	Homo sapi	c 770	17	3. 5	937	14	S77150	S77150	[3' LTR] [d
c 698	18	3. 7	209287	9	AF020277	AF020277	Homo sapi	c 771	17	3. 5	959	33	AC061410	AC061410	Giardia 1
c 699	18	3. 7	209925	9	AF020223	AF020223	Human gen	c 772	17	3. 5	961	33	AC043620	AC043620	Giardia 1
c 700	18	3. 7	210115	9	AL442127	AL442127	Human DNA	c 773	17	3. 5	962	1	BBU04282	BBU04282	Borrellia bu
c 701	18	3. 7	210786	2	AC095106	AC095106	Rattus no	c 774	17	3. 5	978	33	AC070198	AC070198	Giardia 1
c 702	18	3. 7	211230	2	AC012540	AC012540	Mus muscu	c 775	17	3. 5	996	33	AC028235	AC028235	Giardia 1
c 703	18	3. 7	211301	2	AC100752	AC100752	Mus muscu	c 776	17	3. 5	1011	6	AX224521	AX224521	Sequence 3
c 704	18	3. 7	211305	9	AC099975	AC099975	Homo sapi	c 777	17	3. 5	1011	11	CNS06K3L	CNS06K3L	Caenorhab
c 705	18	3. 7	211458	2	AC095183	AC095183	Rattus no	c 778	17	3. 5	1055	2	AC006711	AC006711	Caenorhab
c 706	18	3. 7	212172	9	AC073531	AC073531	Homo sapi	c 779	17	3. 5	1056	5	XL066288	XL066288	Xenopus lae
c 707	18	3. 7	213379	2	AC094767	AC094767	Rattus no	c 780	17	3. 5	1057	1	ECGPT1	ECGPT1	E.coli xant
c 708	18	3. 7	214442	2	AC103314	AC103314	Rattus no	c 781	17	3. 5	1057	15	ECGPT	ECGPT	E.coli gpt
c 709	18	3. 7	217532	2	AL645543	AL645543	Mus muscu	c 782	17	3. 5	1063	1	ECOGPTC	ECOGPTC	E.coli gpt
c 710	18	3. 7	218548	9	AL158035	AL158035	Human DNA	c 783	17	3. 5	1063	8	GSU30348	GSU30348	Gracilario
c 711	18	3. 7	218774	2	AC079182	AC079182	Mus muscu	c 784	17	3. 5	1126	8	AF036339	AF036339	Euphorbia
c 712	18	3. 7	219635	2	AL390207	AL390207	Homo sapi	c 785	17	3. 5	1133	6	AR105733	AR105733	Sequence
c 713	18	3. 7	220491	2	AL445206	AL445206	Homo sapi	c 786	17	3. 5	1133	6	AR105734	AR105734	Sequence 2
c 714	18	3. 7	223847	3	AE003776	AE003776	Drosophil	c 787	17	3. 5	1133	6	IL4088	IL4088	Sequence 2
c 715	18	3. 7	225879	3	AE003776	AE003776	Drosophil	c 788	17	3. 5	1133	6	IL4089	IL4089	Sequence 3
c 716	18	3. 7	234176	2	AC098280	AC098280	Rattus no	c 789	17	3. 5	1150	4	BTA18308	BTA18308	Bos taurus
c 717	18	3. 7	235659	2	AC098876	AC098876	Mus muscu	c 790	17	3. 5	1209	6	IL4108	IL4108	Sequence 22
c 718	18	3. 7	238741	2	AC068894	AC068894	Homo sapi	c 791	17	3. 5	1209	6	IL4108	IL4108	Sequence 22
c 719	18	3. 7	240065	2	AC093481	AC093481	Mus muscu	c 792	17	3. 5	1214	1	AF378156	AF378156	Mycoplasma
c 720	18	3. 7	243167	2	AC095680	AC095680	Rattus no	c 793	17	3. 5	1237	3	AF378156	AF378156	Mycoplasma
c 721	18	3. 7	244530	2	AC097044	AC097044	Rattus no	c 794	17	3. 5	1336	1	ECGPT2	ECGPT2	E. coli xan
c 722	18	3. 7	246050	1	AL627274	AL627274	Salmonell	c 795	17	3. 5	1448	6	I20877	I20877	Sequence 1
c 723	18	3. 7	252920	9	AC002366	AC002366	Human xp2	c 796	17	3. 5	1465	10	MMMDRIA03	MMMDRIA03	Mus muscu
c 724	18	3. 7	267547	3	AE003623	AE003623	Drosophil	c 797	17	3. 5	1542	9	HSU12789	HSU12789	Human clone
c 725	18	3. 7	275272	2	AC097195	AC097195	Rattus no	c 798	17	3. 5	1565	14	AF251407	AF251407	Influenza
c 726	18	3. 7	284207	2	AC103329	AC103329	Rattus no	c 799	17	3. 5	1565	14	AF251423	AF251423	Influenza
c 727	18	3. 7	293431	2	PPMAL13P4	PPMAL13P4	Plasmodiu	c 800	17	3. 5	1565	14	FLANJ8	FLANJ8	Influenza A
c 728	18	3. 7	293431	2	PPMAL13P4	PPMAL13P4	Plasmodiu	c 801	17	3. 5	1565	14	FLANPAG	FLANPAG	Influenza A
c 729	18	3. 7	295015	2	AC006842	AC006842	Caenorhab	c 802	17	3. 5	1565	14	FLANPAP	FLANPAP	Influenza A
c 730	18	3. 7	299300	2	AC006881	AC006881	Caenorhab	c 803	17	3. 5	1565	14	FLASH82NP	FLASH82NP	Influenza A



c 950	17	3.5	14947	2	AC014403	AC014403 Drosophil
c 951	17	3.5	16137	3	AF040651	AF040651 Caenorhab
c 952	17	3.5	16157	1	AE001670	AE001670 Chlamydia
953	17	3.5	16435	1	AE001125	AE001125 Borrelia
954	17	3.5	16754	4	AF217811	AF217811 Tupala be
c 955	17	3.5	17286	2	AC109930	AC109930 Rattus no
c 956	17	3.5	19507	2	AC110133	AC110133 Rattus no
c 957	17	3.5	19510	3	CE132H5	281524 Caenorhabdi
c 958	17	3.5	21668	2	AC107478	AC107478 Rattus no
c 959	17	3.5	21698	3	AF026204	AF026204 Caenorhab
c 960	17	3.5	22004	2	AC017362	AC017362 Drosophil
c 961	17	3.5	22300	3	CE13D2	250739 Caenorhabdi
c 962	17	3.5	22973	3	AF025458	AF025458 Caenorhab
963	17	3.5	23055	2	AC102486	AC102486 Mus muscu
964	17	3.5	23135	3	AC024766	AC024766 Caenorhab
c 965	17	3.5	23797	8	AP004258	AP004258 Oryza sat
c 966	17	3.5	24130	2	AC018303	AC018303 Drosophil
c 967	17	3.5	24177	1	AE000785	AE000785 Borrelia
c 968	17	3.5	24629	3	CE070D5	270685 Caenorhabdi
c 969	17	3.5	25065	9	AC074098	AC074098 Homo sapi
c 970	17	3.5	25347	3	CEC18D4	281474 Caenorhabdi
971	17	3.5	25426	3	CE139A3A	AC006747 Caenorhab
972	17	3.5	25520	3	AF099918	AF099918 Caenorhab
973	17	3.5	25646	1	AE008891	AE008891 Salmonell
974	17	3.5	26618	3	DMFRXIII	250152 D.melanogas
c 975	17	3.5	26853	2	AC108942	AC108942 Mus muscu
c 976	17	3.5	27368	3	CE08D7	212017 Caenorhabdi
c 977	17	3.5	28601	1	AE000784	AE000784 Borrelia
c 978	17	3.5	29034	9	HS2423947	AJ243947 Homo sapi
c 979	17	3.5	29095	3	U29097	U29097 Caenorhabdi
c 980	17	3.5	29344	3	CEY116A8B	AL021469 Caenorhab
c 981	17	3.5	30451	3	CEG16D6	281472 Caenorhabdi
982	17	3.5	30560	9	AF361252	AF361252 Homo sapi
983	17	3.5	30848	3	CE90393	237983 Caenorhabdi
c 984	17	3.5	31202	2	AC013022	AC013022 Drosophil
985	17	3.5	31281	3	CEC01F6	268213 Caenorhabdi
986	17	3.5	31587	9	AC091438	AC091438 Homo sapi
c 987	17	3.5	31876	3	AF078783	AF078783 Caenorhab
c 988	17	3.5	32211	8	D89861	D89861 Cyanidiosch
c 989	17	3.5	32421	2	CEH25F02	293633 Caenorhabdi
c 990	17	3.5	32661	1	LPN7311	AJ007311 Legionell
c 991	17	3.5	32987	1	AB036666	AB036666 Wolbachia
c 992	17	3.5	33149	9	AL590142	AL590142 Human DNA
993	17	3.5	33539	3	U00067	U00067 Caenorhabdi
994	17	3.5	33556	3	U00036	U00036 Caenorhabdi
c 995	17	3.5	33571	9	AC016703	AC016703 Homo sapi
c 996	17	3.5	33858	8	SCU44030	U44030 Saccharomyc
c 997	17	3.5	34002	9	AL139805	AL139805 Human DNA
c 998	17	3.5	34836	9	AC006522	AC006522 Homo sapi
999	17	3.5	34919	3	AF100663	AF100663 Caenorhab
c1000	17	3.5	35241	3	CELY39A3B	AC006748 Caenorhab
ALIGNMENTS						
RESULT 1						
AR004267	AF004267	Sequence 1 from patent US 5747024.	489 bp	DNA	linear	PAT 04-DEC-1998
LOCUS	AR004267					
DEFINITION	Sequence 1 from patent US 5747024.					
ACCESSION	AR004267					
VERSION	AR004267.1	GI:3965146				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 489)					
AUTHORS	Grabstein, K.H. and Widmer, M.B.					
TITLE	vaccine adjuvant comprising interleukin-15					
JOURNAL	Patent: US 5747024-A 1 05-MAY-1998;					
FEATURES	Location/Qualifiers					
source	1..489					
/organism="unknown"						
Query Match 100.0%; Score 489; DB 6; Length 489;						
Best Local Similarity 100.0%; Pred. No. 8e-244;						
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	1	ATGAGAAATTCGAAACCCACATTTTCCAGAGTATTTCCATCCAGTGGCTACCTGTGTTTACTT	60			
Db	1	ATGAGAAATTCGAAACCCACATTTTCCAGAGTATTTCCATCCAGTGGCTACCTGTGTTTACTT	60			
QY	61	CTAAAGAGTCATTTTCTAACTGAAGCTGGCAATTCATGCTTTCATTTTGGGCTGTTTCACT	120			
Db	61	CTAAAGAGTCATTTTCTAACTGAAGCTGGCAATTCATGCTTTCATTTTGGGCTGTTTCACT	120			
QY	121	GCAGGGCTCCCTAAACAGAGCCAACTGGTGAATGTAATAGTGAATTTGAAAAAATTT	180			
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QY	181	GAAGATCTTATCTCAATCTATGATATTTGATGCTACTTTTATATACAGAAAGTGTGTTTCAAC	240			
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QY	241	CCCAGTTGCAAGGTAACAGCAATGAAAGTCTTCTTCTTGGAGTTGCAAGTATTTTCCACAT	300			
Db	241	CCCAGTTGCAAGGTAACAGCAATGAAAGTCTTCTTCTTGGAGTTGCAAGTATTTTCCACAT	300			
QY	301	GAGTCGGAGATACAGATATTCATGATACAGTAAAGAAATCTTATCATCTAGCAAAACAAC	360			
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QY	361	ATCTTGTCTTCTTAATGGGAATATAACAGATCTCGGATGCAAGAAATGTGAGGAACATAGAG	420			
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QY	421	GAAGAAATATTAAGAAATTTTTCGAGAGTTTGTACATATTTGTCCTCAATATGTTTCACTCAAC	480			
Db	421	GAAGAAATATTAAGAAATTTTTCGAGAGTTTGTACATATTTGTCCTCAATATGTTTCACTCAAC	480			
QY	481	ACTTCTTGA 489				
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RESULT 2						
AR024348	AR024348	Sequence 1 from patent US 5795966.	489 bp	DNA	linear	PAT 05-DEC-1998
LOCUS	AR024348					
DEFINITION	Sequence 1 from patent US 5795966.					
ACCESSION	AR024348					
VERSION	AR024348.1	GI:3977642				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 489)					
AUTHORS	Grabstein, K.H., Pettit, D.K. and Paxton, R.J.					
TITLE	Antagonists of interleukin-15					
JOURNAL	Patent: US 5795966-A 1 18-AUG-1998;					
FEATURES	Location/Qualifiers					
source	1..489					
/organism="unknown"						
BASE COUNT 162 a 81 c 92 g 154 t						
ORIGIN						
Query Match 100.0%; Score 489; DB 6; Length 489;						
Best Local Similarity 100.0%; Pred. No. 8e-244;						
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
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QY	61	CTAAAGAGTCATTTTCTAACTGAAGCTGGCAATTCATGCTTTCATTTTGGGCTGTTTCACT	120			
Db	61	CTAAAGAGTCATTTTCTAACTGAAGCTGGCAATTCATGCTTTCATTTTGGGCTGTTTCACT	120			
QY	121	GCAGGGCTCCCTAAACAGAGCCAACTGGTGAATGTAATAGTGAATTTGAAAAAATTT	180			
Db	121	GCAGGGCTCCCTAAACAGAGCCAACTGGTGAATGTAATAGTGAATTTGAAAAAATTT	180			
QY	181	GAAGATCTTATCTCAATCTATGATATTTGATGCTACTTTTATATACAGAAAGTGTGTTTCAAC	240			
Db	181	GAAGATCTTATCTCAATCTATGATATTTGATGCTACTTTTATATACAGAAAGTGTGTTTCAAC	240			
QY	241	CCCAGTTGCAAGGTAACAGCAATGAAAGTCTTCTTCTTGGAGTTGCAAGTATTTTCCACAT	300			
Db	241	CCCAGTTGCAAGGTAACAGCAATGAAAGTCTTCTTCTTGGAGTTGCAAGTATTTTCCACAT	300			
QY	301	GAGTCGGAGATACAGATATTCATGATACAGTAAAGAAATCTTATCATCTAGCAAAACAAC	360			
Db	301	GAGTCGGAGATACAGATATTCATGATACAGTAAAGAAATCTTATCATCTAGCAAAACAAC	360			
QY	361	ATCTTGTCTTCTTAATGGGAATATAACAGATCTCGGATGCAAGAAATGTGAGGAACATAGAG	420			
Db	361	ATCTTGTCTTCTTAATGGGAATATAACAGATCTCGGATGCAAGAAATGTGAGGAACATAGAG	420			
QY	421	GAAGAAATATTAAGAAATTTTTCGAGAGTTTGTACATATTTGTCCTCAATATGTTTCACTCAAC	480			
Db	421	GAAGAAATATTAAGAAATTTTTCGAGAGTTTGTACATATTTGTCCTCAATATGTTTCACTCAAC	480			
QY	481	ACTTCTTGA 489				
Db	481	ACTTCTTGA 489				
RESULT 2						
AR024348	AR024348	Sequence 1 from patent US 5795966.	489 bp	DNA	linear	PAT 05-DEC-1998
LOCUS	AR024348					
DEFINITION	Sequence 1 from patent US 5795966.					
ACCESSION	AR024348					
VERSION	AR024348.1	GI:3977642				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 489)					
AUTHORS	Grabstein, K.H., Pettit, D.K. and Paxton, R.J.					
TITLE	Antagonists of interleukin-15					
JOURNAL	Patent: US 5795966-A 1 18-AUG-1998;					
FEATURES	Location/Qualifiers					
source	1..489					
/organism="unknown"						
BASE COUNT 162 a 81 c 92 g 154 t						
ORIGIN						
Query Match 100.0%; Score 489; DB 6; Length 489;						
Best Local Similarity 100.0%; Pred. No. 8e-244;						
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	1	ATGAGAAATTCGAAACCCACATTTTCCAGAGTATTTCCATCCAGTGGCTACCTGTGTTTACTT	60			
Db	1	ATGAGAAATTCGAAACCCACATTTTCCAGAGTATTTCCATCCAGTGGCTACCTGTGTTTACTT	60			

Qy	61	CTAAGAGTCATTTCTAACTGAAGCTGGCATTTCATGCTTTCATTTTGGGCTGTTTCAGT	120
Db	61	CTAAGAGTCATTTCTAACTGAAGCTGGCATTTCATGCTTTCATTTTGGGCTGTTTCAGT	120
Qy	121	GCAGGGCTCCCTAAACAGAGCCCACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTT	180
Db	121	GCAGGGCTCCCTAAACAGAGCCCACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTT	180
Qy	181	GAAGATCTTATTTCAATCTATGCATATTTGATGCTACTTTATATACAGAAAGTGATGTTTCAC	240
Db	181	GAAGATCTTATTTCAATCTATGCATATTTGATGCTACTTTATATACAGAAAGTGATGTTTCAC	240
Qy	241	CCAGTTCGCAAGGTAACAGCAATGAAGTGTCTTCTCTGGAGTTGCAAGTTATTTTCACAT	300
Db	241	CCAGTTCGCAAGGTAACAGCAATGAAGTGTCTTCTCTGGAGTTGCAAGTTATTTTCACAT	300
Qy	301	GAGTCCGGAGATACAGATATTTCAATGATACAGTACAGAAATCTTATCATCCTAGCAAAACAC	360
Db	301	GAGTCCGGAGATACAGATATTTCAATGATACAGTACAGAAATCTTATCATCCTAGCAAAACAC	360
Qy	361	ATCTTGTCCTTAATGGGAATATAACGAATCTGGATGCAAAAGAAATGTGAGGAAGTACAG	420
Db	361	ATCTTGTCCTTAATGGGAATATAACGAATCTGGATGCAAAAGAAATGTGAGGAAGTACAG	420
Qy	421	GAAGAAATATTAAGAAATTTTTCAGAGTTTCTGATACATATTTGTCCAAATGTTTCATCAAC	480
Db	421	GAAGAAATATTAAGAAATTTTTCAGAGTTTCTGATACATATTTGTCCAAATGTTTCATCAAC	480
Qy	481	ACTTCTTTGA 489	
Db	481	ACTTCTTTGA 489	

RESULT 3

AR070282

LOCUS

Sequence 4 from patent US 5892001.

AR070282

ACCESSION

AR070282.1 GI:7221170

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

Unknown.

Unknown.

Unclassified.

1 (bases 1 to 489)

Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.

Epithelium-derived T-cell factor antibodies

Patent: US 5892001-A 4 06-APR-1999;

Location/Qualifiers

1. .489

/organism="unknown"

162 a 81 c 92 g 154 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 100.0%;

Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Score 489; DB 6; Length 489;

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Db	1	ATGAGAATTTTCGAAACCCACATTTGAGAAGTATTTCCATCCAGTGCTACCTGTGTTTACTT	60
Qy	61	CTAAGAGTCATTTCTAACTGAAGCTGGCATTTCATGCTTTCATTTTGGGCTGTTTCAGT	120
Db	61	CTAAGAGTCATTTCTAACTGAAGCTGGCATTTCATGCTTTCATTTTGGGCTGTTTCAGT	120
Qy	121	GCAGGGCTCCCTAAACAGAGCCCACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTT	180
Db	121	GCAGGGCTCCCTAAACAGAGCCCACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTT	180
Qy	181	GAAGATCTTATTTCAATCTATGCATATTTGATGCTACTTTATATACAGAAAGTGATGTTTCAC	240

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Db 421 GAAAAAATATTAAAGATTTTTCGAGAGTTTTGTACATATTGTCCAAATGTTTCATCAAC 480  
Qy 481 ACTTCTTGA 489  
Db 481 ACTTCTTGA 489  
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LOCUS ARI22045  
DEFINITION Sequence 1 from patent US 6165466.  
ACCESSION ARI22045  
VERSION ARI22045.1 GI:14106362  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 489)  
AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.  
TITLE Antagonists of interleukin-15  
JOURNAL Patent: US 6165466-A 1 26-DEC-2000;  
FEATURES Location/Qualifiers  
source 1..489  
BASE COUNT 162 a 81 c 92 g 154 t  
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Best Local Similarity 100.0%; Pred. No. 8e-244;  
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Qy 181 GAAGATCTTATTCATCTATGCAATTAACAGCAATGAAGTCTTCTCTGGAGTTGCAAGTTATTTTCACAT 300  
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Qy 241 CCCAGTTGCAAGGTAACAGCAATTAACAGCAATGAAGTCTTCTCTGGAGTTGCAAGTTATTTTCACAT 360  
Db 241 CCCAGTTGCAAGGTAACAGCAATTAACAGCAATGAAGTCTTCTCTGGAGTTGCAAGTTATTTTCACAT 360  
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Qy 361 ATCTTGTCTTCTTAATGGGAATATAACAGAACTCTGGATGCAAGAATGTGAGGAACCTAGAG 480  
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Qy 481 ACTTCTTGA 489  
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RESULT 6  
LOCUS ARI22867  
DEFINITION Sequence 1 from patent US 6168783.  
ACCESSION ARI22867  
VERSION ARI22867.1 GI:14107833  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 489)  
AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.  
TITLE Antagonists of interleukin-15  
JOURNAL Patent: US 6168783-A 1 02-JAN-2001;  
FEATURES Location/Qualifiers  
source 1..489  
BASE COUNT 162 a 81 c 92 g 154 t  
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Query Match 100.0%; Score 489; DB 6; Length 489;  
Best Local Similarity 100.0%; Pred. No. 8e-244;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Qy 481 ACTTCTTGA 489  
Db 481 ACTTCTTGA 489  
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LOCUS ARI25104  
DEFINITION Sequence 1 from patent US 6177079.  
ACCESSION ARI25104  
VERSION ARI25104.1 GI:14111166  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 489)  
AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.  
TITLE Antagonists of interleukin-15  
JOURNAL Patent: US 6177079-A 1 23-JAN-2001;  
FEATURES Location/Qualifiers  
source 1..489

BASE COUNT 162 a 81 c 92 g 154 t  
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Query Match 100.0%; Score 489; DB 6; Length 489;  
Best Local Similarity 100.0%; Pred. No. 8e-244;  
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QY 1 ATGAGAATTTTGGAAACACACATTTTCCAGAGTATTTCCATCCAGTCTACCTGCTGTTTACTT 60  
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QY 181 GAAGATCTTATTTCAATCTATGCAATTAATGATGCTTCTTCTTCTTGGAGTTGCAAGTTATTTCCACAT 240  
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QY 241 CCCAGTTGCAAGTAAACAGCAATTAACAGAACTCGGATGTAATAAGTGAATTTGAAAAAATT 300  
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QY 481 ACTTCTTGA 489  
Db 481 ACTTCTTGA 489

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LOCUS AX006785 489 bp DNA linear PAT 06-SEP-2000  
DEFINITION Sequence 3 from Patent WO0002582.  
ACCESSION AX006785  
VERSION AX006785.1 GI:9994821  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 489)  
AUTHORS Londei,M., Quarantino,S. and Maiuri,L.  
TITLE Treatment of celiac disease with interleukin-15 antagonists  
JOURNAL Patent: WO 0002582-A 3 20-JAN-2000;  
LONDEI MARCO (GB); QUARANTINO SONIA (GB); MATHILDA AND TERENCE  
KENNEDY I (GB); MAIURI LUIGI (IT)  
FEATURES Location/Qualifiers  
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BASE COUNT 162 a 81 c 92 g 154 t

## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 8e-244;  
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QY 121 GCAGGGCTCCCTAAACAGAGCCAACTGGTGAATGTAATAAGTGAATTTGAAAAAATT 180  
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QY 181 GAAGATCTTATTTCAATCTATGCAATTAATGATGCTTCTTCTTCTTGGAGTTGCAAGTTATTTCCACAT 240  
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QY 241 CCCAGTTGCAAGTAAACAGCAATTAACAGAACTCGGATGTAATAAGTGAATTTGAAAAAATT 300  
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QY 421 GAAAAAATATTAAAGAAATTTTGGCAGAGTTTGTGACATATTTGCCAAATGTTTCATCAAC 480  
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QY 481 ACTTCTTGA 489  
Db 481 ACTTCTTGA 489

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DEFINITION Sequence 1 from patent US 5552303.  
ACCESSION I25782  
VERSION I25782.1 GI:1605652  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 489)  
AUTHORS Grabstein,K., Anderson,D., Eisenman,J., Fung,V. and Rauch,C.  
TITLE DNA encoding epithelium-derived T-cell factor  
JOURNAL Patent: US 5552303-A 1 03-SEP-1996;  
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BASE COUNT 162 a 81 c 92 g 154 t  
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Db 1 ATGAGAATTTTGGAAACACACATTTTCCAGAGTATTTCCATCCAGTCTACCTGCTGTTTACTT 60

QY	61	CTAAGAGTCATTTTCTTAAGTGAAGCTGGCATTGATGCTTCATTTTGGGCTGTTTCAGT	120
Db	61	CTAAGAGTCATTTTCTTAAGTGAAGCTGGCATTGATGCTTCATTTTGGGCTGTTTCAGT	120
QY	121	GCAGGGCTCCCTAAACAGAGCCAACTGGGTGAATGTAATGAAGTGAATTTGAAAAAAATT	180
Db	121	GCAGGGCTCCCTAAACAGAGCCAACTGGGTGAATGTAATGAAGTGAATTTGAAAAAAATT	180
QY	181	GAAGATCTTTATTCATCTATGCATATTTGATGCTACTTTATATACAGAAAGTGTTCAC	240
Db	181	GAAGATCTTTATTCATCTATGCATATTTGATGCTACTTTATATACAGAAAGTGTTCAC	240
QY	241	CCAGTTGCAAGTAAACAGCAATGAAGTCTTCTCTTGGAGTTGCAAGTTATTTTCACAT	300
Db	241	CCAGTTGCAAGTAAACAGCAATGAAGTCTTCTCTTGGAGTTGCAAGTTATTTTCACAT	300
QY	301	GAGTCGGAGATACAGATATTTTCATGATACAGTAGAGAAATCTTATCATCTAGCAAAACAC	360
Db	301	GAGTCGGAGATACAGATATTTTCATGATACAGTAGAGAAATCTTATCATCTAGCAAAACAC	360
QY	361	ATCTTGTCTTCTTAATGGAATATAACAGAAATCTGGATGCAAGAAATGTGAGAACTAGAG	420
Db	361	ATCTTGTCTTCTTAATGGAATATAACAGAAATCTGGATGCAAGAAATGTGAGAACTAGAG	420
QY	421	GAAGATCTTTATTCATCTATGCATATTTGATGCTACTTTATATACAGAAAGTGTTCAC	480
Db	421	GAAGATCTTTATTCATCTATGCATATTTGATGCTACTTTATATACAGAAAGTGTTCAC	480
QY	481	ACTTCTTTGA 489	
Db	481	ACTTCTTTGA 489	
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DEFINITION	Sequence 4 from patent US 5707616.		
ACCESSION	I79220		
VERSION	I79220.1 GI:3207510		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 489)		
AUTHORS	Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.		
TITLE	Method for treating or preventing gastrointestinal disease with epithelium-derived T-cell factor		
JOURNAL	Patent: US 5707616-A 4 13-JAN-1998;		
FEATURES	Location/Qualifiers		
source	1..489		
BASE COUNT	162 a 81 c 92 g 154 t		
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Best Local Similarity	100.0%;	Pred. No. 8e-244;	
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QY	61	CTAAGAGTCATTTTCTTAAGTGAAGCTGGCATTGATGCTTCATTTTGGGCTGTTTCAGT	120
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QY	121	GCAGGGCTCCCTAAACAGAGCCAACTGGGTGAATGTAATGAAGTGAATTTGAAAAAAATT	180
Db	121	GCAGGGCTCCCTAAACAGAGCCAACTGGGTGAATGTAATGAAGTGAATTTGAAAAAAATT	180
QY	181	GAAGATCTTTATTCATCTATGCATATTTGATGCTACTTTATATACAGAAAGTGTTCAC	240
Db	181	GAAGATCTTTATTCATCTATGCATATTTGATGCTACTTTATATACAGAAAGTGTTCAC	240
QY	241	CCAGTTGCAAGTAAACAGCAATGAAGTCTTCTCTTGGAGTTGCAAGTTATTTTCACAT	300
Db	241	CCAGTTGCAAGTAAACAGCAATGAAGTCTTCTCTTGGAGTTGCAAGTTATTTTCACAT	300
QY	301	GAGTCGGAGATACAGATATTTTCATGATACAGTAGAGAAATCTTATCATCTAGCAAAACAC	360
Db	301	GAGTCGGAGATACAGATATTTTCATGATACAGTAGAGAAATCTTATCATCTAGCAAAACAC	360
QY	361	ATCTTGTCTTCTTAATGGAATATAACAGAAATCTGGATGCAAGAAATGTGAGAACTAGAG	420
Db	361	ATCTTGTCTTCTTAATGGAATATAACAGAAATCTGGATGCAAGAAATGTGAGAACTAGAG	420
QY	421	GAAGATCTTTATTCATCTATGCATATTTGATGCTACTTTATATACAGAAAGTGTTCAC	480
Db	421	GAAGATCTTTATTCATCTATGCATATTTGATGCTACTTTATATACAGAAAGTGTTCAC	480
QY	481	ACTTCTTTGA 489	
Db	481	ACTTCTTTGA 489	
RESULT	10		
LOCUS	I28850	489 bp	DNA linear PAT 06-FEB-1997
DEFINITION	Sequence 4 from patent US 5574138.		
ACCESSION	I28850		
VERSION	I28850.1 GI:1819631		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 489)		
AUTHORS	Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.		
TITLE	Epithelium-derived T-cell factor		
JOURNAL	Patent: US 5574138-A 4 12-NOV-1996;		
FEATURES	Location/Qualifiers		
source	1..489		
BASE COUNT	162 a 81 c 92 g 154 t		
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Best Local Similarity	100.0%;	Pred. No. 8e-244;	
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Db	1	ATGAGAAATTTTGGAAACACATTTTGAAGATATTTCCATCCAGTGTACCTGCTGTTTACTT	60
QY	61	CTAAGAGTCATTTTCTTAAGTGAAGCTGGCATTGATGCTTCATTTTGGGCTGTTTCAGT	120
Db	61	CTAAGAGTCATTTTCTTAAGTGAAGCTGGCATTGATGCTTCATTTTGGGCTGTTTCAGT	120
QY	121	GCAGGGCTCCCTAAACAGAGCCAACTGGGTGAATGTAATGAAGTGAATTTGAAAAAAATT	180
Db	121	GCAGGGCTCCCTAAACAGAGCCAACTGGGTGAATGTAATGAAGTGAATTTGAAAAAAATT	180
QY	181	GAAGATCTTTATTCATCTATGCATATTTGATGCTACTTTATATACAGAAAGTGTTCAC	240
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Db 361 ATCTGTGCTTCTTAATGGGAATATACAGAATCTGGATGCAAGAATGTGAGGAACCTAGAG 420
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Qy 481 ACTTCTTTGA 489
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Db 481 ACTTCTTTGA 489
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RESULT 12
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DEFINITION Cercopithecus aethiops simian interleukin 15 mRNA, complete cds.
ACCESSION U03099
VERSION U03099.1 GI:493521
SOURCE African green monkey.
ORGANISM Cercopithecus aethiops
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Cercopithecus.
REFERENCE 1 (bases 1 to 1275)
Grabstein,K.H., Eisenman,J., Shanebeck,K., Rauch,C., Srinivasan,S.,
Fung,V., Beers,C., Richardson,J., Schoenborn,M.A., Ahldeh,M.,
Johnson,L., Alderson,M.R., Watson,J.D., Anderson,D.M. and Giri,J.G.
Cloning of a T cell growth factor that interacts with the beta
chain of the interleukin-2 receptor
Science 264, 965-968 (1994)
94233380
REFERENCE 2 (bases 1 to 1275)
Anderson,D.M.
Direct Submission
Submitted (02-NOV-1993) Dink M. Anderson, Immunex Research and
Development Corp., 51 University St., Seattle, WA 98101, USA
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BASE COUNT 366 a 264 c 278 g 367 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 6.9e-244;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13
AB000555
LOCUS Macaca fascicularis mRNA for interleukin-15 precursor, complete cds.
DEFINITION AB000555
ACCESSION AB000555
VERSION AB000555.1 GI:1799529
KEYWORDS Interleukin-15 precursor; IL-15.
SOURCE Macaca fascicularis peripheral blood mononuclear cells cDNA to mRNA.
ORGANISM Macaca fascicularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
REFERENCE 1 (bases 1 to 492)
Tatsumi,M.
Direct Submission
Submitted (20-JAN-1997) Masashi Tatsumi, National Institute of
Health, Department of Veterinary Science, Toyama-23-1,
Shinjuku-ku, Tokyo 162, Japan (E-mail:tatsuenih.go.jp,
Tel:81-3-5285-1111, Fax:81-3-5285-1179)
REFERENCE 2 (bases 1 to 492)
Tatsumi,M.
Molecular cloning and expression of cynomolgus monkey
interleukin-15
Unpublished (1997)
FEATURES
source
1..492
Location/Qualifiers
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/db_xref="taxon:9541"
/cell_type="peripheral blood mononuclear cells"
sig_peptide 1..144
CDS 1..489
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/protein_id="BAA19149.1"
/db_xref="GI:1799530"
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KTEANWNVISDLKTIQSMHIDATLYTESDVHPSCVKVTAMKCFLELQVISHES
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Query Match 86.5%; Score 423; DB 9; Length 492; Best Local Similarity 100.0%; Pred. No. 2.1e-209; Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;										Query Match 86.5%; Score 423; DB 9; Length 559; Best Local Similarity 100.0%; Pred. No. 2e-209; Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;																													
Qy	67	AGTCATTTCTAACTGAAGCTGGCATTGCTTCATTTTGGGCTGTTTCAGTGCAGGG	126	Db	67	AGTCATTTCTAACTGAAGCTGGCATTGCTTCATTTTGGGCTGTTTCAGTGCAGGG	126	Qy	127	CTCCCTAAAAACAGAAGCAACTGGGTGAATGAATAAGTGATTGGAAGAAATTTGAAGAT	186	Db	127	CTCCCTAAAAACAGAAGCAACTGGGTGAATGAATAAGTGATTGGAAGAAATTTGAAGAT	186	Qy	187	CTTATTCATCTATGATATTTGATGCTACTTTATATACAGAAAGTGATGTTACACCCAGT	246	Db	187	CTTATTCATCTATGATATTTGATGCTACTTTATATACAGAAAGTGATGTTACACCCAGT	246	Qy	247	TGCAAGGTAAACAGCAATGAAGTCTTTCTCTGGAGTTGCAAGTTATTTTCACATGAGTCC	306	Db	247	TGCAAGGTAAACAGCAATGAAGTCTTTCTCTGGAGTTGCAAGTTATTTTCACATGAGTCC	306								
Qy	307	GGAGATACAGATATTCATGATACAGTAGAGAAATCTTATCATCCTAGCAACAAACATCTTG	366	Db	307	GGAGATACAGATATTCATGATACAGTAGAGAAATCTTATCATCCTAGCAACAAACATCTTG	366	Qy	367	TCCTCTAATGGGAATATAACAGAACTCTGGATGCAAGAAATGTGAGGAAGTCTGAGGAACTAGAGAAAA	426	Db	367	TCCTCTAATGGGAATATAACAGAACTCTGGATGCAAGAAATGTGAGGAAGTCTGAGGAACTAGAGAAAA	426	Qy	427	AATATTAAAGAAATTTTGCAGAGTTTGTGACATATTTGCCAAATGTTCCAAATGTTTCATCAACACTTCT	486	Db	427	AATATTAAAGAAATTTTGCAGAGTTTGTGACATATTTGCCAAATGTTTCATCAACACTTCT	486	Qy	487	TGA 489		Db	487	TGA 489									
RESULT 14										RESULT 15																													
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LOCUS										LOCUS																													
DEFINITION										DEFINITION																													
Macaca mulatta interleukin-15 (IL-15) mRNA, complete cds.										Sequence 13 from patent US 5892001.																													
ACCESSION										ACCESSION																													
U19843										AR070289																													
VERSION										VERSION																													
U19843.1 GI:644803										AR070289.1 GI:7221177																													
KEYWORDS										KEYWORDS																													
SOURCE										SOURCE																													
rhesus monkey.										Unknown.																													
ORGANISM										ORGANISM																													
Macaca mulatta										Macaca mulatta																													
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;										Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;																													
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;										Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;																													
Cercopitheciinae; Macaca.										Cercopitheciinae; Macaca.																													
1 (bases 1 to 559)										1 (bases 1 to 559)																													
Villinger, F., Brar, S.S., Mayne, A., Chikkala, N. and Ansari, A.A.										Villinger, F., Brar, S.S., Mayne, A., Chikkala, N. and Ansari, A.A.																													
Comparative sequence analysis of cytokine genes from human and										Comparative sequence analysis of cytokine genes from human and																													
nonhuman primates										nonhuman primates																													
J. Immunol. 155 (8), 3946-3954 (1995)										J. Immunol. 155 (8), 3946-3954 (1995)																													
JOURNAL										JOURNAL																													
MEDLINE										MEDLINE																													
96003435										96003435																													
2 (bases 1 to 559)										2 (bases 1 to 559)																													
REFERENCE										REFERENCE																													
AUTHORS										AUTHORS																													
Villinger, F.J.										Villinger, F.J.																													
TITLE										TITLE																													
Submitted (13-JAN-1995) Francois J. Villinger, Emory University,										Submitted (13-JAN-1995) Francois J. Villinger, Emory University,																													
Pathology, 1327 Clifton Rd, Atlanta, GA 30322, USA										Pathology, 1327 Clifton Rd, Atlanta, GA 30322, USA																													
FEATURES										FEATURES																													
source										source																													
1. .559										1. .559																													
/organism="Macaca mulatta"										/organism="Macaca mulatta"																													
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/cell_type="peripheral blood mononuclear cells"										/cell_type="peripheral blood mononuclear cells"																													

JOURNAL FEATURES	Patent: US 5892001-A 13 06-APR-1999; Location/Qualifiers 1..345
source	/organism="unknown"
BASE COUNT	124 a 50 c 64 g
ORIGIN	107 t

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Query Match          70.6%; Score 345; DB 6; Length 345;
Best Local Similarity 100.0%; Pred. No. 1e-168;
Matches 345; Conservative 0; Mismatches 0; Indels
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Qy	145	AAC	GGGTGAATGTAATAAGTGAATTTGAAAAAAATTTGAAGATCTTTATTCAATCTATGCAT	204
Db	1	AAC	GGGTGAATGTAATAAGTGAATTTGAAAAAAATTTGAAGATCTTTATTCAATCTATGCAT	60
Qy	205	ATT	GATGCTACTTTATATACAGAAAGTGATGTTACCCCGAGTTGCAAGGTAACAGCAATG	264
Db	61	ATT	GATGCTACTTTATATACAGAAAGTGATGTTACCCCGAGTTGCAAGGTAACAGCAATG	120
Qy	265	AAG	GCTTTCTCTGGAGTTGCAAGTTATTTACATGATAGTCCGGAGATACAGATATTTCAT	324
Db	121	AAG	GCTTTCTCTGGAGTTGCAAGTTATTTACATGATAGTCCGGAGATACAGATATTTCAT	180
Qy	325	GAT	ACAGTAGAAAAATCTTTATCATCCTAGCAAAACAACATCTTGCTCTCTAAATGGGAATATA	384
Db	181	GAT	ACAGTAGAAAAATCTTTATCATCCTAGCAAAACAACATCTTGCTCTCTAAATGGGAATATA	240
Qy	385	AC	AAGTCTGGATGCAAGAAATGTGAGGAAGTACAGGAAAAAAATATATAAGAAATTTTGG	444
Db	241	AC	AAGTCTGGATGCAAGAAATGTGAGGAAGTACAGGAAAAAAATATATAAGAAATTTTGG	300
Qy	445	CAG	AGTTTGTACATATGTGCCAAATGTTATCAACACTTCTTGA	489
Db	301	CAG	AGTTTGTACATATGTGCCAAATGTTATCAACACTTCTTGA	345

RESULT	16
AR085748	
LOCUS	
DEFINITION	AR085748
ACCESSION	Sequence 13 from patent US 5985262.
VERSION	AR085748
KEYWORDS	AR085748.1 GI:10012514
SOURCE	.
ORGANISM	Unknown. Ununknown. Unclassified.
REFERENCE	1 (bases 1 to 345)
AUTHORS	Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE	Method of treatment with epithelium derived T-cell factor
JOURNAL	Patent: US 598262-A I3 16-Nov-1999;
FEATURES	Location/Qualifiers . .345 <del>/organism= "unknown"</del> 124 a     50 c     64 g     107 t
source	
BASE COUNT	
ORIGIN	

	Query Match	70.6%	Score 345;	DB 6;	Length 345;
	Best Local Similarity	100.0%;	Pred. No. 1e-168;		
	Matches 345;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	145	AACCTGGGTGAATGTAATAAGCTGATTTCAAAAAAATTCGAAGATCTTATTCATCTATGCGAT	204		
Db	1	AACCTGGGTGAATGTAATAAGCTGATTTCAAAAAAATTCGAAGATCTTATTCATCTATGCGAT	60		
QY	205	ATTGATGCTACTTTATATACAGAAAGTGATGTTCCACCCCGAGTTCCAAAGGTAAACAGCAATG	264		
Db	61	ATTGATGCTACTTTATATACAGAAAGTGATGTTCCACCCCGAGTTCCAAAGGTAAACAGCAATG	120		
QY	265	AAGTGCTTTCTCTGGAGTTGCCAGTTATTTCACATCAGTGCCGAGATACAGATATTTCAT	324		
Db	121	AAGTGCTTTCTCTGGAGTTGCCAGTTATTTCACATCAGTGCCGAGATACAGATATTTCAT	180		

QY	325	GATACAGTAGAAATCTTATCATCTAGCAACAACATCTTGTCTCTTAATGGGAATATA	384
Db	181	GATACAGTAGAAATCTTATCATCTAGCAACAACATCTTGTCTCTTAATGGGAATATA	240
QY	385	ACAGAATCTGGATGCAAGAAGTGTGAGGAACCTAGAGGAAAAAATATTAAACAATTTTGG	444
Db	241	ACAGAATCTGGATGCAAGAAGTGTGAGGAACCTAGAGGAAAAAATATTAAACAATTTTGG	300
QY	445	CAGAGTTTTGTACATATTGTCCAAATGTTCAACACACTTCTTGA	489
Db	301	CAGAGTTTTGTACATATTGTCCAAATGTTCAACACACTTCTTGA	345
RESULT	17		
LOCUS	I28857	345 bp	linear
DEFINITION	Sequence 13 from patent US 5574138.		
ACCESSION	I28857		
VERSION	I28857.1		
KEYWORDS	. GI:1819641		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 345)		
TITLE	Grabstein, K.H., Anderson, D.M., Eisenman, J.R., Fung, V. and Rauch, C.		
JOURNAL	Epithelium-derived T-cell factor		
FEATURES	Patent: US 5574138-A 13 12-NOV-1996;		
	Location/Qualifiers		
source	1. .345		
	/organism="unknown"		
BASE COUNT	124 a	50 c	64 g
ORIGIN			107 t

Query Match	70.6%	Score 345;	DB 6;	Length 345;	
Best Local Similarity	100.0%;	Pred. No. 1e-168;			
Matches 345;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	145	AAC7GGGTGAATGAAATGAAGTGATTTGAAAAAAATTTGAAGATCTTATTTCAATCTATGCAT	204		
Db					
	1	AAC7GGGTGAATGAAATGAAGTGATTTGAAAAAAATTTGAAGATCTTATTTCAATCTATGCAT	60		
QY	205	ATTGATGCTACTTTATATACAGAAAGTGATGTTTCACCCCGAGTTGCAAGGTAACAGCAATG	264		
Db					
	61	ATTGATGCTACTTTATATACAGAAAGTGATGTTTCACCCCGAGTTGCAAGGTAACAGCAATG	120		
QY	265	AAGTGCTTTCTCTGGGAGTTGCAAGTTATTTACATGAGTCCGGAGATACAGATATTTTCAT	324		
Db					
	121	AAGTGCTTTCTCTGGGAGTTGCAAGTTATTTACATGAGTCCGGAGATACAGATATTTTCAT	180		
QY	325	GATACAGTAGAAAATCTTATCATCTTAGCAACAACATCTTGCTTCTATGGAATATA	384		
Db					
	181	GATACAGTAGAAAATCTTATCATCTTAGCAACAACATCTTGCTTCTATGGAATATA	240		
QY	385	ACAGAAATCTGGATGCAAGAATGTGAGGAATCTAGAGAAAAAATATTTAAAGAAATTTTTCG	444		
Db					
	241	ACAGAAATCTGGATGCAAGAATGTGAGGAATCTAGAGAAAAAATATTTAAAGAAATTTTTCG	300		
QY	445	CAGAGTTTTCATCATATTTGCCAAATGTTTCATCAACACTTCTTTGA	489		
Db					
	301	CAGAGTTTTCATCATATTTGCCAAATGTTTCATCAACACTTCTTTGA	345		

RESULT	18
I79227	
LOCUS	
DEFINITION	I79227
ACCESSION	Sequence 13 from patent US 570616.
I79227	
VERSION	I79227.1 GI:3207517
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
DNA	linear
345 bp	PAT 10-JUN-1998



KEYWORDS SOURCE Unknown. ORGANISM Unknown. UNCLASSIFIED. REFERENCE 1 (bases 1 to 489) AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J. TITLE Antagonists of Interleukin-15 JOURNAL JOURNAL Patent: US 5795966-A 2 18-AUG-1998; FEATURES Location/Qualifiers source 1..489 /organism="unknown" BASE COUNT 159 a 79 c 95 g 156 t ORIGIN

Query Match 21.9%; Score 107; DB 6; Length 489; Best Local Similarity 99.4%; Pred. No. 1.2e-44; Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCAATTTGGGCTGTTTCAGTGCAGGG 126  
Db 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCAATTTGGGCTGTTTCAGTGCAGGG 126  
QY 127 CTCCTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186  
Db 127 CTCCTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186  
QY 187 CTTATTCAATCTATCATATTGCTACTTTATATAC 224  
Db 187 CTTATTCAATCTATCATATTGCTACTTTATATAC 224

RESULT 22 AR070281 LOCUS AR070281 489 bp DNA linear PAT 18-FEB-2000 DEFINITION Sequence 1 from patent US 5892001. ACCESSION AR070281 VERSION AR070281.1 GI:7221169 KEYWORDS SOURCE Unknown. ORGANISM Unknown. UNCLASSIFIED. REFERENCE 1 (bases 1 to 489) AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C. TITLE Epithelium-derived T-cell factor antibodies JOURNAL JOURNAL Patent: US 5892001-A 1 06-APR-1999; FEATURES Location/Qualifiers source 1..489 /organism="unknown" BASE COUNT 159 a 79 c 95 g 156 t ORIGIN

Query Match 21.9%; Score 107; DB 6; Length 489; Best Local Similarity 99.4%; Pred. No. 1.2e-44; Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCAATTTGGGCTGTTTCAGTGCAGGG 126  
Db 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCAATTTGGGCTGTTTCAGTGCAGGG 126  
QY 127 CTCCTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186  
Db 127 CTCCTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186  
QY 187 CTTATTCAATCTATCATATTGCTACTTTATATAC 224  
Db 187 CTTATTCAATCTATCATATTGCTACTTTATATAC 224

RESULT 23 AR085740 LOCUS AR085740 489 bp DNA linear PAT 07-SEP-2000

DEFINITION Sequence 1 from patent US 5985262. ACCESSION AR085740 VERSION AR085740.1 GI:10012506 KEYWORDS SOURCE Unknown. ORGANISM Unknown. UNCLASSIFIED. REFERENCE 1 (bases 1 to 489) AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C. TITLE Method of treatment with epithelium derived T-cell factor JOURNAL JOURNAL Patent: US 5985262-A 1 16-NOV-1999; FEATURES Location/Qualifiers source 1..489 /organism="unknown" BASE COUNT 159 a 79 c 95 g 156 t ORIGIN

Query Match 21.9%; Score 107; DB 6; Length 489; Best Local Similarity 99.4%; Pred. No. 1.2e-44; Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCAATTTGGGCTGTTTCAGTGCAGGG 126  
Db 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCAATTTGGGCTGTTTCAGTGCAGGG 126  
QY 127 CTCCTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186  
Db 127 CTCCTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186  
QY 187 CTTATTCAATCTATCATATTGCTACTTTATATAC 224  
Db 187 CTTATTCAATCTATCATATTGCTACTTTATATAC 224

RESULT 24 AR094649 LOCUS AR094649 489 bp DNA linear PAT 08-SEP-2000 DEFINITION Sequence 5 from patent US 6001973. ACCESSION AR094649 VERSION AR094649.1 GI:10021763 KEYWORDS SOURCE Unknown. ORGANISM Unknown. UNCLASSIFIED. REFERENCE 1 (bases 1 to 489) AUTHORS Strom,T.B. and Maslinski,W. TITLE Antagonists of Interleukin-15 JOURNAL JOURNAL Patent: US 6001973-A 5 14-DEC-1999; FEATURES Location/Qualifiers source 1..489 /organism="unknown" BASE COUNT 159 a 80 c 95 g 155 t ORIGIN

Query Match 21.9%; Score 107; DB 6; Length 489; Best Local Similarity 99.4%; Pred. No. 1.2e-44; Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCAATTTGGGCTGTTTCAGTGCAGGG 126  
Db 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCAATTTGGGCTGTTTCAGTGCAGGG 126  
QY 127 CTCCTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186  
Db 127 CTCCTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186  
QY 187 CTTATTCAATCTATCATATTGCTACTTTATATAC 224  
Db 187 CTTATTCAATCTATCATATTGCTACTTTATATAC 224

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RESULT 25
AR094650
LOCUS AR094650 489 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 7 from patent US 6001973.
ACCESSION AR094650
VERSION AR094650.1 GI:10021765
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 489)
AUTHORS Strom,T.B. and Maslinski,W.
TITLE Antagonists of Interleukin-15
JOURNAL Patent: US 6001973-A 7 14-DEC-1999;
FEATURES
Location/Qualifiers
source
BASE COUNT 158 a 80 c 96 g 155 t
ORIGIN

Query Match 21.9%; Score 107; DB 6; Length 489;
Best Local Similarity 99.4%; Pred. No. 1.2e-44;
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126
Db 67 AGTCATTTTCTAACTGAAGCTGGCATTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126
QY 127 CTCCTTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTGAAGAT 186
Db 127 CTCCTTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTGAAGAT 186
QY 187 CTTATTCAATCTATGCATATTCGCTACTTTATATAC 224
Db 187 CTTATTCAATCTATGCATATTCGCTACTTTATATAC 224

RESULT 26
AR122046
LOCUS AR122046 489 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 2 from patent US 6165466.
ACCESSION AR122046
VERSION AR122046.1 GI:14106363
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 489)
AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.
TITLE Antagonists of Interleukin-15
JOURNAL Patent: US 6165466-A 2 26-DEC-2000;
FEATURES
Location/Qualifiers
source
BASE COUNT 159 a 79 c 95 g 156 t
ORIGIN

Query Match 21.9%; Score 107; DB 6; Length 489;
Best Local Similarity 99.4%; Pred. No. 1.2e-44;
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126
Db 67 AGTCATTTTCTAACTGAAGCTGGCATTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126
QY 127 CTCCTTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTGAAGAT 186
Db 127 CTCCTTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTGAAGAT 186
QY 187 CTTATTCAATCTATGCATATTCGCTACTTTATATAC 224
Db 187 CTTATTCAATCTATGCATATTCGCTACTTTATATAC 224

RESULT 27
AR122868
LOCUS AR122868 489 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 2 from patent US 6168783.
ACCESSION AR122868
VERSION AR122868.1 GI:14107834
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 489)
AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.
TITLE Antagonists of Interleukin-15
JOURNAL Patent: US 6168783-A 2 02-JAN-2001;
FEATURES
Location/Qualifiers
source
BASE COUNT 159 a 79 c 95 g 156 t
ORIGIN

Query Match 21.9%; Score 107; DB 6; Length 489;
Best Local Similarity 99.4%; Pred. No. 1.2e-44;
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126
Db 67 AGTCATTTTCTAACTGAAGCTGGCATTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126
QY 127 CTCCTTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTGAAGAT 186
Db 127 CTCCTTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTGAAGAT 186
QY 187 CTTATTCAATCTATGCATATTCGCTACTTTATATAC 224
Db 187 CTTATTCAATCTATGCATATTCGCTACTTTATATAC 224
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Db 187 CTTATTCAATCTATGCATATTCGCTACTTTATATAC 224

RESULT 27
AR122868
LOCUS AR122868 489 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 2 from patent US 6168783.
ACCESSION AR122868
VERSION AR122868.1 GI:14107834
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 489)
AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.
TITLE Antagonists of Interleukin-15
JOURNAL Patent: US 6168783-A 2 02-JAN-2001;
FEATURES
Location/Qualifiers
source
BASE COUNT 159 a 79 c 95 g 156 t
ORIGIN

Query Match 21.9%; Score 107; DB 6; Length 489;
Best Local Similarity 99.4%; Pred. No. 1.2e-44;
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126
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QY 127 CTCCTTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTGAAGAT 186
Db 127 CTCCTTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTGAAGAT 186
QY 187 CTTATTCAATCTATGCATATTCGCTACTTTATATAC 224
Db 187 CTTATTCAATCTATGCATATTCGCTACTTTATATAC 224

RESULT 28
AR125105
LOCUS AR125105 489 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 2 from patent US 6177079.
ACCESSION AR125105
VERSION AR125105.1 GI:14111167
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 489)
AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.
TITLE Antagonists of Interleukin-15
JOURNAL Patent: US 6177079-A 2 23-JAN-2001;
FEATURES
Location/Qualifiers
source
BASE COUNT 159 a 79 c 95 g 156 t
ORIGIN

Query Match 21.9%; Score 107; DB 6; Length 489;
Best Local Similarity 99.4%; Pred. No. 1.2e-44;
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126
Db 67 AGTCATTTTCTAACTGAAGCTGGCATTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126
QY 127 CTCCTTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTGAAGAT 186
Db 127 CTCCTTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTGAAGAT 186
QY 187 CTTATTCAATCTATGCATATTCGCTACTTTATATAC 224
Db 187 CTTATTCAATCTATGCATATTCGCTACTTTATATAC 224
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QY 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224  
Db 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224

## RESULT 29

AX006786  
LOCUS AX006786 489 bp DNA linear PAT 06-SEP-2000  
DEFINITION Sequence 4 from Patent WO0002582.  
ACCESSION AX006786  
VERSION AX006786.1 GI:9994822

## KEYWORDS

SOURCE human.

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 489)

Londei, M., Quaratino, S. and Maiuri, L.

Treatment of celiac disease with interleukin-15 antagonists

Patent: WO 0002582-A 4 20-JAN-2000;

LONDEI MARCO (GB); QUARATINO SONIA (GB); MATHILDA AND TERENCE

KENNEDY I (GB); MAIURI LUIGI (IT)

Location/Qualifiers

1..489

/organism="Homo sapiens"

/db\_xref="taxon:9606"

159 a 79 c 95 g 156 t

## BASE COUNT

## ORIGIN

Query Match 21.9%; Score 107; DB 6; Length 489;  
Best Local Similarity 99.4%; Pred. No. 1.2e-44;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126

Db 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126

QY 127 CTCCTTAAACAGAGCAACTGGTGAATGTAATAGTGAATTTGAAAAAATTGAAGAT 186

Db 127 CTCCTTAAACAGAGCAACTGGTGAATGTAATAGTGAATTTGAAAAAATTGAAGAT 186

QY 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224

Db 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224

## RESULT 30

AX320242  
LOCUS AX320242 489 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 1 from Patent WO0187330.  
ACCESSION AX320242  
VERSION AX320242.1 GI:17901650

## KEYWORDS

SOURCE human.

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (sites)

Strom, T.B. and Maslinski, W.

Compositions and methods for achieving immune suppression

Patent: WO 0187330-A 1 22-NOV-2001;

Beth Israel Deaconess Medical Center, Inc. (US)

Location/Qualifiers

1..489

/organism="Homo sapiens"

/db\_xref="taxon:9606"

1..489

/note="unnamed protein product"

/codon\_start=1

/protein\_id="CAD19389.1"

/db\_xref="GI:17901651"

/translation="MRISKPHLSISIQCYLCILLNSHFLTEAGIHVFLGCFSGALP  
KTEANWNVISDLKKIEDLIQSMHIDATLYTESDVHPSCVTAMKCFLELOVISLES  
GDASIHDVTVENLIILANSSNGNVTESGCKECEELEEKNIKEFLDSFVHIQMFIN  
TS"

BASE COUNT 158 a 79 c 96 g 156 t  
ORIGIN

Query Match 21.9%; Score 107; DB 6; Length 489;

Best Local Similarity 99.4%; Pred. No. 1.2e-44;

Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126

Db 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126

QY 127 CTCCTTAAACAGAGCAACTGGTGAATGTAATAGTGAATTTGAAAAAATTGAAGAT 186

Db 127 CTCCTTAAACAGAGCAACTGGTGAATGTAATAGTGAATTTGAAAAAATTGAAGAT 186

QY 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224

Db 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224

## RESULT 31

AX320244  
LOCUS AX320244 489 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 3 from Patent WO0187330.  
ACCESSION AX320244  
VERSION AX320244.1 GI:17901652

## KEYWORDS

SOURCE human.

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (sites)

Strom, T.B. and Maslinski, W.

Compositions and methods for achieving immune suppression

Patent: WO 0187330-A 3 22-NOV-2001;

Beth Israel Deaconess Medical Center, Inc. (US)

Location/Qualifiers

1..489

/organism="Homo sapiens"

/db\_xref="taxon:9606"

1..489

/note="unnamed protein product"

/codon\_start=1

/protein\_id="CAD19390.1"

/db\_xref="GI:17901653"

/translation="MRISKPHLSISIQCYLCILLNSHFLTEAGIHVFLGCFSGALP  
KTEANWNVISDLKKIEDLIQSMHIDATLYTESDVHPSCVTAMKCFLELOVISLES  
GDASIHDVTVENLIILANSSNGNVTESGCKECEELEEKNIKEFLDSFVHIQMFIN  
TS"

BASE COUNT 159 a 79 c 95 g 156 t  
ORIGIN

Query Match 21.9%; Score 107; DB 6; Length 489;

Best Local Similarity 99.4%; Pred. No. 1.2e-44;

Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126

Db 67 AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126

QY 127 CTCCTTAAACAGAGCAACTGGTGAATGTAATAGTGAATTTGAAAAAATTGAAGAT 186

Db 127 CTCCTTAAACAGAGCAACTGGTGAATGTAATAGTGAATTTGAAAAAATTGAAGAT 186

QY 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224

Db 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224

RESULT	32	33
LOCUS	BD008811	BD008812
DEFINITION	Antagonists of interleukin-15.	Antagonists of interleukin-15.
ACCESSION	BD008811	BD008812
VERSION	BD008811.1 GI:18637184	BD008812.1 GI:18637185
KEYWORDS	JP 2001502521-A/4.	JP 2001502521-A/5.
SOURCE	unidentified.	unidentified.
ORGANISM	unclassified.	unclassified.
REFERENCE	1 (bases 1 to 489)	1 (bases 1 to 489)
AUTHORS	Strom, T. and Maslinski, W.	Strom, T. and Maslinski, W.
TITLE	Antagonists of interleukin-15	Antagonists of interleukin-15
JOURNAL	Patent: JP 2001502521-A 4 27-FEB-2001;	Patent: JP 2001502521-A 5 27-FEB-2001;
COMMENT	BETH ISRAEL DEACONESS MEDICAL CENTER	BETH ISRAEL DEACONESS MEDICAL CENTER
OS	Unidentified	Unidentified
PN	JP 2001502521-A/4	JP 2001502521-A/5
PD	27-FEB-2001	27-FEB-2001
PF	25-APR-1997 JP 1997539046	25-APR-1997 JP 1997539046
PI	26-APR-1996 US 60/016634	
PC	TERRY STROM, WLODZIMIERZ MASLINSKI	
CC	C12N15/24, C07K14/54, A61K38/20, C12N15/62, G01N33/68 CC	
Strandedness:	Single;	
CC Topology:	Linear;	
FH key	Location/Qualifiers	
FT source	1..489	
FEATURES	source	source
BASE COUNT	159 a 80 c 95 g 155 t	
ORIGIN		
Query Match	21.9%; Score 107; DB 6; Length 489;	
Best Local Similarity	99.4%; Pred. No. 1.2e-44;	
Matches	157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	67 AGTCATTTTCTAACTGAAGCTGGCATTGCTCTTCAATTTGGGCTGTTTCAGTGCAGGG 126	
Db	67 AGTCATTTTCTAACTGAAGCTGGCATTGCTCTTCAATTTGGGCTGTTTCAGTGCAGGG 126	
QY	127 CTCCTAAAACAGAGCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTTGAAGAT 186	
Db	127 CTCCTAAAACAGAGCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTTGAAGAT 186	
QY	187 CTTATTCATCTATGCATATTTGATGCTACTTTATATAC 224	
Db	187 CTTATTCATCTATGCATATTTGATGCTACTTTATATAC 224	
RESULT	34	
LOCUS	I25783	
DEFINITION	Sequence 4 from patent US 5552303.	
ACCESSION	I25783	
VERSION	I25783.1 GI:1605653	
KEYWORDS	Unknown.	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 489)	
AUTHORS	Grabstein, K., Anderson, D., Eisenman, J., Fung, V. and Rauch, C.	
TITLE	DNA encoding epithelium-derived T-cell factor	
JOURNAL	Patent: US 5552303-A 4 03-SEP-1996;	
FEATURES	source	
BASE COUNT	159 a 79 c 95 g 156 t	
ORIGIN		
Query Match	21.9%; Score 107; DB 6; Length 489;	
Best Local Similarity	99.4%; Pred. No. 1.2e-44;	
Matches	157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	67 AGTCATTTTCTAACTGAAGCTGGCATTGCTCTTCAATTTGGGCTGTTTCAGTGCAGGG 126	
Db	67 AGTCATTTTCTAACTGAAGCTGGCATTGCTCTTCAATTTGGGCTGTTTCAGTGCAGGG 126	
QY	127 CTCCTAAAACAGAGCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTTGAAGAT 186	
Db	127 CTCCTAAAACAGAGCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTTGAAGAT 186	
QY	187 CTTATTCATCTATGCATATTTGATGCTACTTTATATAC 224	
Db	187 CTTATTCATCTATGCATATTTGATGCTACTTTATATAC 224	
RESULT	35	
LOCUS	I28849	
DEFINITION	Antagonists of interleukin-15.	
ACCESSION	BD008812	
VERSION	BD008812.1 GI:18637185	
KEYWORDS	JP 2001502521-A/5.	
SOURCE	unidentified.	
ORGANISM	unclassified.	
REFERENCE	1 (bases 1 to 489)	
AUTHORS	Strom, T. and Maslinski, W.	
TITLE	Antagonists of interleukin-15	
JOURNAL	Patent: JP 2001502521-A 5 27-FEB-2001;	
COMMENT	BETH ISRAEL DEACONESS MEDICAL CENTER	
OS	Unidentified	
PN	JP 2001502521-A/5	
PD	27-FEB-2001	
PF	25-APR-1997 JP 1997539046	

LOCUS I28849 489 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 1 from patent US 5574138.  
ACCESSION I28849  
VERSION I28849.1 GI:1819629  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 489)  
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.  
TITLE Epithelium-derived T-cell factor  
JOURNAL Patent: US 5574138-A 1 12-NOV-1996;  
FEATURES Location/Qualifiers  
source 1. 489  
BASE COUNT 159 a 79 c 95 g 156 t  
ORIGIN  
Query Match 21.9%; Score 107; DB 6; Length 489;  
Best Local Similarity 99.4%; Pred. No. 1.2e-44;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 67 AGTCATTTCTAACTGAAGCTGGCATTTCATCTTTCATTTTGGGCTGTTTCAGTGCAGGG 126  
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Db 67 AGTCATTTCTAACTGAAGCTGGCATTTCATCTTTCATTTTGGGCTGTTTCAGTGCAGGG 126  
|||||  
Qy 127 CTCCTTAAACAGAGCCCACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186  
|||||  
Db 127 CTCCTTAAACAGAGCCCACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186  
|||||  
Qy 187 CTTATTCATCTATGCATATTCATGCTACTTTATATAC 224  
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Db 187 CTTATTCATCTATGCATATTCATGCTACTTTATATAC 224  
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RESULT 36  
LOCUS I62692 489 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 1 from patent US 5660824.  
ACCESSION I62692  
VERSION I62692.1 GI:2480400  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 489)  
AUTHORS Grabstein,K.H., Quinn,L.S. and Troutt,A.B.  
TITLE Muscle trophic factor  
JOURNAL Patent: US 5660824-A 1 26-AUG-1997;  
FEATURES Location/Qualifiers  
source 1. 489  
BASE COUNT 159 a 79 c 95 g 156 t  
ORIGIN  
Query Match 21.9%; Score 107; DB 6; Length 489;  
Best Local Similarity 99.4%; Pred. No. 1.2e-44;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 67 AGTCATTTCTAACTGAAGCTGGCATTTCATCTTTCATTTTGGGCTGTTTCAGTGCAGGG 126  
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Db 67 AGTCATTTCTAACTGAAGCTGGCATTTCATCTTTCATTTTGGGCTGTTTCAGTGCAGGG 126  
|||||  
Qy 127 CTCCTTAAACAGAGCCCACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186  
|||||  
Db 127 CTCCTTAAACAGAGCCCACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186  
|||||  
Qy 187 CTTATTCATCTATGCATATTCATGCTACTTTATATAC 224  
|||||  
Db 187 CTTATTCATCTATGCATATTCATGCTACTTTATATAC 224  
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RESULT 37  
LOCUS I79219 489 bp DNA linear PAT 10-JUN-1998  
DEFINITION Sequence 1 from patent US 5707616.  
ACCESSION I79219  
VERSION I79219.1 GI:3207509  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 489)  
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.  
TITLE Method for treating or preventing gastrointestinal disease with  
epithelium-derived T-cell factor  
JOURNAL Patent: US 5707616-A 1 13-JAN-1998;  
FEATURES Location/Qualifiers  
source 1. 489  
BASE COUNT 159 a 79 c 95 g 156 t  
ORIGIN  
Query Match 21.9%; Score 107; DB 6; Length 489;  
Best Local Similarity 99.4%; Pred. No. 1.2e-44;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 67 AGTCATTTTCTAACTGAAGCTGGCATTTCATCTTTCATTTTGGGCTGTTTCAGTGCAGGG 126  
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Db 67 AGTCATTTTCTAACTGAAGCTGGCATTTCATCTTTCATTTTGGGCTGTTTCAGTGCAGGG 126  
|||||  
Qy 127 CTCCTTAAACAGAGCCCACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186  
|||||  
Db 127 CTCCTTAAACAGAGCCCACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186  
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Qy 187 CTTATTCATCTATGCATATTCATGCTACTTTATATAC 224  
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Db 187 CTTATTCATCTATGCATATTCATGCTACTTTATATAC 224  
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RESULT 38  
LOCUS ARI03280 1202 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 11 from patent US 6087172.  
ACCESSION ARI03280  
VERSION ARI03280.1 GI:12814868  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1202)  
AUTHORS Veerapaneni,D., Hamanaka,S. and Nozawa,I.  
TITLE Ribozymes targeted to human IL-15 mRNA  
JOURNAL Patent: US 6087172-A 11 11-JUL-2000;  
FEATURES Location/Qualifiers  
source 1. 1202  
BASE COUNT 355 a 219 c 249 g 379 t  
ORIGIN  
Query Match 21.9%; Score 107; DB 6; Length 1202;  
Best Local Similarity 99.4%; Pred. No. 1e-44;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 67 AGTCATTTTCTAACTGAAGCTGGCATTTCATCTTTCATTTTGGGCTGTTTCAGTGCAGGG 126  
|||||  
Db 383 AGTCATTTTCTAACTGAAGCTGGCATTTCATCTTTCATTTTGGGCTGTTTCAGTGCAGGG 442  
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Qy 127 CTCCTTAAACAGAGCCCACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186  
|||||  
Db 443 CTCCTTAAACAGAGCCCACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 502  
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Qy 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224  
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Db 503 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 540

RESULT 39  
LOCUS AX024715 1202 bp DNA linear PAT 15-SEP-2000  
DEFINITION Sequence 1 from Patent WO0028019.  
ACCESSION AX024715  
VERSION AX024715.1 GI:10184794  
KEYWORDS human.  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1202)  
AUTHORS Doudevani,A. and Chalmovitz,C.  
TITLE Antisense oligomer  
JOURNAL Patent: WO 0028019-A 1 18-MAY-2000;  
MOR RESEARCH APPLIC LTD (IL) ; DOUDEVANI AMOS (IL) ; UNIV BEN  
GURION (IL) ; CHALMOVITZ CIDIO (IL)  
FEATURES Location/Qualifiers  
source  
1. .1202  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"

BASE COUNT 355 a 219 c 249 g 379 t  
ORIGIN

Query Match 21.9%; Score 107; DB 6; Length 1202;  
Best Local Similarity 99.4%; Pred. No.1e-44;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 67 AGTCATTTCTAACCTGAAGCTGGCATTTCATCTTCATTTGGGCTGTTTCAGTCGAGG 126  
Db 383 AGTCATTTCTAACCTGAAGCTGGCATTTCATCTTCATTTGGGCTGTTTCAGTCGAGG 442  
Qy 127 CTCCTCTAAACAGAGCCCACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTTGAAGAT 186  
Db 443 CTTCTCTAAACAGAGCCCACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTTGAAGAT 502  
Qy 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224  
|||||  
Db 503 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 540

RESULT 40  
AX301227  
LOCUS AX301227 1202 bp DNA linear PAT 30-NOV-2001  
DEFINITION Sequence 1 from Patent WO0185920.  
ACCESSION AX301227  
VERSION AX301227.1 GI:17382318  
KEYWORDS human.  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (sites)  
AUTHORS Banachereau,J.F., Mohamadzadeh,M. and Palucka,A.K.  
TITLE Compositions and methods for producing antigen-presenting cells  
JOURNAL Patent: WO 0185920-A 1 15-NOV-2001;  
Baylor Research Institute (US)  
FEATURES Location/Qualifiers  
source  
1. .1202  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"

CDS  
317..805  
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/db\_xref="GI:17382319"  
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KTEANWVNVISDLKKIEDLIQSMHIDATLTSTEDVHPSCVKVTAMKCFLLLEQVLSLES  
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TS"  
BASE COUNT 355 a 219 c 249 g 379 t  
ORIGIN

Query Match 21.9%; Score 107; DB 6; Length 1202;  
Best Local Similarity 99.4%; Pred. No.1e-44;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 67 AGTCATTTCTAACCTGAAGCTGGCATTTCATCTTCATTTGGGCTGTTTCAGTCGAGG 126  
Db 383 AGTCATTTCTAACCTGAAGCTGGCATTTCATCTTCATTTGGGCTGTTTCAGTCGAGG 442  
Qy 127 CTCCTCTAAACAGAGCCCACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTTGAAGAT 186  
Db 443 CTTCTCTAAACAGAGCCCACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTTGAAGAT 502  
Qy 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224  
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Db 503 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 540

RESULT 41  
HSU14407  
LOCUS HSU14407 1202 bp mRNA linear PRI 21-SEP-1994  
DEFINITION Human interleukin 15 (IL15) mRNA, complete cds.  
ACCESSION U14407  
VERSION U14407.1 GI:540098  
KEYWORDS human.  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1202)  
AUTHORS Grabsstein,K.K., Eisenman,J., Sheanebeck,K., Rauch,C.,  
Srinivasan,S., Fung,V., Beers,C., Richardson,J., Schoenborn,M.A.,  
Ahdieh,M., Johnson,L., Alderson,M.R., Watson,J.D., Anderson,D.M.  
and Giri,J.G.  
TITLE Cloning of a T cell growth factor that interacts with the beta  
chain of the interleukin-2 receptor  
JOURNAL Science 264 (5161), 965-968 (1994)  
MEDLINE 9423380  
REFERENCE Anderson,D.M.  
AUTHORS Direct Submission  
TITLE Submitted (06-SEP-1994) Dirk M. Anderson, Immunex Research and  
JOURNAL Development Corp., 51, University St., Seattle, WA 98101, USA  
FEATURES Location/Qualifiers  
source  
1. .1202  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/cell\_line="IMTLH"  
/cell\_type="stromal"  
/tissue\_type="Bone marrow"  
1. .1202  
/gene="IL15"  
314..460  
/gene="IL15"  
/evidence="experimental"  
317..805  
/gene="IL15"  
/note="cytokine; T cell growth factor; secreted protein"  
/codon\_start=1  
/product="Interleukin 15"  
/protein\_id="AAA21551.1"  
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KTEANWVNVISDLKKIEDLIQSMHIDATLTSTEDVHPSCVKVTAMKCFLLLEQVLSLES  
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461..802  
mat\_peptide

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/product="unnamed"
671..678
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/note="encodes N-glycosylation site"
695..703
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794..802
/gene="IL15"
/note="encodes N-glycosylation site"

BASE COUNT      355 a   219 c   249 g   379 t
ORIGIN

Query Match      21.9%; Score 107; DB 9; Length 1202;
Best Local Similarity 99.4%; Pred. No. 1e-44;
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  67 AGTCATTTCTAAGCTGGCATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGG 126
      |||||||
Db  383 AGTCATTTCTAAGCTGGCATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGG 442

Qy  127 CTCCTAAACAGAGCCAACTGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGAT 186
      |||||||
Db  443 CTCCTAAACAGAGCCAACTGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGAT 502

Qy  187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224
      |||||||
Db  503 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 540

RESULT 42
HSIL15MR1
LOCUS      HSIL15MR1                      643 bp      mRNA      linear      PRI 27-SEP-1996
DEFINITION H. sapiens mRNA for interleukin-15 (cell line NCIH69).
ACCESSION  X94222
VERSION    X94222.1 GI:1495459
KEYWORDS   interleukin-15.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 643)
AUTHORS   Meazza,R., Verdiani,S., Biassoni,R., Coppolecchia,M., Gaggero,A.,
            Orengo,A.M., Colombo,M.P., Azzarone,B. and Ferrini,S.
            Identification of a novel interleukin-15 (IL-15) transcript isoform
            generated by alternative splicing in human small cell lung cancer
            cell lines
JOURNAL    Oncogene 12 (10), 2187-2192 (1996)
MEDLINE    96218668
REFERENCE  2 (bases 1 to 643)
AUTHORS   Ferrini,S.
            Direct Submission
TITLE      Submitted (12-DEC-1995) S. Ferrini, Istituto Nazionale Ricerca
            Cancro, Pharmacology, Largo R. Benzi 10, Genova, 16132, Italy
FEATURES   Location/Qualifiers
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                /protein_id="CAA63913.1"
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Query Match      21.9%; Score 107; DB 9; Length 1202;
Best Local Similarity 99.4%; Pred. No. 1e-44;
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  67 AGTCATTTCTAAGCTGGCATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGG 126
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Db  383 AGTCATTTCTAAGCTGGCATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGG 442

Qy  127 CTCCTAAACAGAGCCAACTGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGAT 186
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Db  443 CTCCTAAACAGAGCCAACTGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGAT 502

Qy  187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224
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Db  503 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 540

RESULT 42
HSIL15MR1
LOCUS      HSIL15MR1                      643 bp      mRNA      linear      PRI 27-SEP-1996
DEFINITION H. sapiens mRNA for interleukin-15 (cell line NCIH69).
ACCESSION  X94222
VERSION    X94222.1 GI:1495459
KEYWORDS   interleukin-15.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 643)
AUTHORS   Meazza,R., Verdiani,S., Biassoni,R., Coppolecchia,M., Gaggero,A.,
            Orengo,A.M., Colombo,M.P., Azzarone,B. and Ferrini,S.
            Identification of a novel interleukin-15 (IL-15) transcript isoform
            generated by alternative splicing in human small cell lung cancer
            cell lines
JOURNAL    Oncogene 12 (10), 2187-2192 (1996)
MEDLINE    96218668
REFERENCE  2 (bases 1 to 643)
AUTHORS   Ferrini,S.
            Direct Submission
TITLE      Submitted (12-DEC-1995) S. Ferrini, Istituto Nazionale Ricerca
            Cancro, Pharmacology, Largo R. Benzi 10, Genova, 16132, Italy
FEATURES   Location/Qualifiers
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                /tissue_type="SCLC"
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Best Local Similarity 100.0%; Pred. No. 2e-38;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  130 CCTAAACAGAGCCAACTGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGATCTT 189
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Db  271 CCTAAACAGAGCCAACTGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGATCTT 330

Qy  190 ATTCAATCTATGCATATTGATGCTACTTTATATAC 224
      |||||||
Db  331 ATTCAATCTATGCATATTGATGCTACTTTATATAC 365

RESULT 43
HSIL15MR2
LOCUS      HSIL15MR2                      643 bp      mRNA      linear      PRI 27-SEP-1996
DEFINITION H. sapiens mRNA for interleukin-15 (cell line NCIH82).
ACCESSION  X94223
VERSION    X94223.1 GI:1495461
KEYWORDS   interleukin-15.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 643)
AUTHORS   Meazza,R., Verdiani,S., Biassoni,R., Coppolecchia,M., Gaggero,A.,
            Orengo,A.M., Colombo,M.P., Azzarone,B. and Ferrini,S.
            Identification of a novel interleukin-15 (IL-15) transcript isoform
            generated by alternative splicing in human small cell lung cancer
            cell lines
JOURNAL    Oncogene 12 (10), 2187-2192 (1996)
MEDLINE    96218668
REFERENCE  2 (bases 1 to 643)
AUTHORS   Ferrini,S.
            Direct Submission
TITLE      Submitted (12-DEC-1995) S. Ferrini, Istituto Nazionale Ricerca
            Cancro, Pharmacology, Largo R. Benzi 10, Genova, 16132, Italy
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Query Match      19.4%; Score 95; DB 9; Length 643;
Best Local Similarity 100.0%; Pred. No. 2e-38;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  130 CCTAAACAGAGCCAACTGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGATCTT 189
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TLYTESDVHPSCKVTAMKFLLEQLVLSLESGDASIHDTVENLIILANNSLSSNGNVT
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BASE COUNT      201 a   111 c   123 g   208 t
ORIGIN

Query Match      19.4%; Score 95; DB 9; Length 643;
Best Local Similarity 100.0%; Pred. No. 2e-38;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  130 CCTAAACAGAGCCAACTGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGATCTT 189
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TLYTESDVHPSCKVTAMKFLLEQLVLSLESGDASIHDTVENLIILANNSLSSNGNVT
ESGKCEELEEKNIKEFLQSFVHVQMFINTS"

BASE COUNT      200 a   111 c   124 g   208 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2e-38;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  130 CCTAAACAGAGCCAACTGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGATCTT 189
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QY 190 ATTCATCTCATGATATTGATGCTACTTTATATAC 224
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Db 331 ATTCATCTCATGATATTGATGCTACTTTATATAC 365

RESULT 44
AR087004 1248 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1 from patent US 5985663.
ACCESSION AR087004
VERSION AR087004.1 GI:10013770
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1248)
AUTHORS Bennett,C.Frank and Cowser,L.M.
TITLE Antisense Inhibition of Interleukin-15 expression
JOURNAL Patent: US 5985663-A 1 16-NOV-1999;
FEATURES Location/Qualifiers
source 1..1248
/organism="unknown"
BASE COUNT 397 a 209 c 223 g 419 t
ORIGIN

Query Match 19.4%; Score 95; DB 6; Length 1248;
Best Local Similarity 100.0%; Pred. No. 1.8e-38;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 CCTAAACAGAACCACTGGTGAATGTAATAGTATTGAAAAAATTGAAGATCTT 189
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Db 567 CCTAAACAGAACCACTGGTGAATGTAATAGTATTGAAAAAATTGAAGATCTT 626
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QY 190 ATTCATCTCATGATATTGATGCTACTTTATATAC 224
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Db 627 ATTCATCTCATGATATTGATGCTACTTTATATAC 661
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RESULT 45
AF031167 1248 bp mRNA linear PRI 23-JAN-1998
LOCUS Homo sapiens interleukin 15 precursor (IL-15) mRNA, complete cds.
DEFINITION AF031167
ACCESSION AF031167
VERSION AF031167.1 GI:2739159
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1248)
AUTHORS Tagaya,Y., Kurys,G., Thies,T.A., Losi,J.M., Azimi,N., Hanover,J.A.,
Bamford,R.N. and Waldmann,T.A.
TITLE Generation of secretable and nonsecretable interleukin 15 isoforms
through alternate usage of signal peptides
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (26), 14444-14449 (1997)
MEDLINE 98070771
REFERENCE 2 (bases 1 to 1248)
AUTHORS Tagaya,Y., Kurys,G., Thies,T.A., Losi,J.M., Azimi N., Bamford,R.N.
and Waldmann,T.A.
TITLE Direct Submission
JOURNAL Submitted (22-OCT-1997) Metabolism Branch, National Cancer
Institute, Bldg. 10 /Rm. 4B 47, 9000 Rockville Pike, Bethesda, MD
20892, USA
FEATURES Location/Qualifiers
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939201, ref. Jerpseth, J., et al., Strategies 5(1), 1992"
1..1248
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ESGCKECEBELEKKNIKEFLQSFVHIVQMFINTS"
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/feature="short signal peptide"
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BASE COUNT 397 a 209 c 223 g 419 t
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Best Local Similarity 100.0%; Pred. No. 1.8e-38;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 CCTAAACAGAACCACTGGTGAATGTAATAGTATTGAAAAAATTGAAGATCTT 189
|||||
Db 567 CCTAAACAGAACCACTGGTGAATGTAATAGTATTGAAAAAATTGAAGATCTT 626
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QY 190 ATTCATCTCATGATATTGATGCTACTTTATATAC 224
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Db 627 ATTCATCTCATGATATTGATGCTACTTTATATAC 661
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RESULT 46
HSIL15 486 bp mRNA linear PRI 30-MAY-1997
LOCUS H. sapiens mRNA for interleukin-15.
DEFINITION Y09908
ACCESSION Y09908.1 GI:2143255
VERSION Y09908.1 GI:2143255
KEYWORDS Igkv signal peptide; IL-15 gene; Interleukin-15.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 486)
AUTHORS Meazza,R. and Ferrini,S.
TITLE Expression of two IL-15 mRNA isoforms in human tumors does not
correlate with secretion: role of different signal peptides
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 486)
JOURNAL Direct Submission
AUTHORS Submitted (08-APR-1997) S. Ferrini, IST, Immunopharmacology, Largo
R. Benzi 10, Genova, 16132, ITALY
REMARK revised by author
FEATURES Location/Qualifiers
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BASE COUNT 154 a 81 c 100 g 151 t  
ORIGIN

Query Match 17.2%; Score 84; DB 9; Length 486;  
Best Local Similarity 100.0%; Pred. No. 1.2e-32;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 201 GCATATTGATGCTACTTTATATAC 224  
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RESULT 47  
AR070288  
LOCUS AR070288 345 bp DNA linear PAT 18-FEB-2000  
DEFINITION Sequence 12 from patent US 5892001.  
ACCESSION AR070288  
VERSION AR070288.1 GI:7221176

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 345)

AUTHORS Grabstein,K.H.; Anderson,D.M.; Eisenman,J.R.; Fung,V. and Rauch,C.  
TITLE Epithelium-derived T-cell factor antibodies  
JOURNAL Patent: US 5892001-A 12 06-APR-1999;  
FEATURES Location/Qualifiers  
source 1..345

BASE COUNT 121 a 49 c 68 g 107 t  
ORIGIN

Query Match 16.4%; Score 80; DB 6; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1.5e-30;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGATCTTATTCAATCTATGCAT 204  
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Db 1 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGATCTTATTCAATCTATGCAT 60  
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QY 205 ATTGATGCTACTTTATATAC 224  
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Db 61 ATTGATGCTACTTTATATAC 80  
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RESULT 48  
AR085747  
LOCUS AR085747 345 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 12 from patent US 5985262.  
ACCESSION AR085747  
VERSION AR085747.1 GI:10012513

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 345)

AUTHORS Grabstein,K.H.; Anderson,D.M.; Eisenman,J.R.; Fung,V. and Rauch,C.  
TITLE Method of treatment with epithelium derived T-cell factor  
JOURNAL Patent: US 5985262-A 12 16-NOV-1999;  
FEATURES Location/Qualifiers  
source 1..345

BASE COUNT 121 a 49 c 68 g 107 t  
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.5e-30;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGATCTTATTCAATCTATGCAT 204  
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QY 205 ATTGATGCTACTTTATATAC 224  
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Db 61 ATTGATGCTACTTTATATAC 80  
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RESULT 49  
I28856  
LOCUS I28856 345 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 12 from patent US 5574138.  
ACCESSION I28856  
VERSION I28856.1 GI:1819640

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 345)

AUTHORS Grabstein,K.H.; Anderson,D.M.; Eisenman,J.R.; Fung,V. and Rauch,C.  
TITLE Epithelium-derived T-cell factor  
JOURNAL Patent: US 5574138-A 12 12-NOV-1996;  
FEATURES Location/Qualifiers  
source 1..345

BASE COUNT 121 a 49 c 68 g 107 t  
ORIGIN

Query Match 16.4%; Score 80; DB 6; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1.5e-30;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGATCTTATTCAATCTATGCAT 204  
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QY 205 ATTGATGCTACTTTATATAC 224  
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Db 61 ATTGATGCTACTTTATATAC 80  
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RESULT 50  
I79226  
LOCUS I79226 345 bp DNA linear PAT 10-JUN-1998  
DEFINITION Sequence 12 from patent US 5707616.  
ACCESSION I79226  
VERSION I79226.1 GI:3207516

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 345)

AUTHORS Grabstein,K.H.; Anderson,D.M.; Eisenman,J.R.; Fung,V. and Rauch,C.  
TITLE Method for treating or preventing gastrointestinal disease with  
epithelium-derived T-cell factor  
JOURNAL Patent: US 5707616-A 12 13-JAN-1998;  
FEATURES Location/Qualifiers  
source 1..345

BASE COUNT 121 a 49 c 68 g 107 t  
ORIGIN

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Db	1	AACTGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGATCTTATTCAATCTATGCAT	60							
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Job time: 5130 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

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Perfect score: 489

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Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	489	100.0	489	1 US-08-393-305-1	Sequence 1, Appli
3	489	100.0	489	1 US-08-535-733-1	Sequence 1, Appli
4	489	100.0	489	1 US-08-726-817-1	Sequence 1, Appli
5	489	100.0	489	1 US-08-504-042-4	Sequence 4, Appli
6	489	100.0	489	1 US-08-392-317B-2	Sequence 2, Appli
7	489	100.0	489	2 US-08-725-969-1	Sequence 1, Appli
8	489	100.0	489	2 US-08-794-524-1	Sequence 1, Appli
9	489	100.0	489	3 US-09-134-132-2	Sequence 2, Appli
10	489	100.0	489	4 US-09-134-134A-2	Sequence 2, Appli
11	489	100.0	489	4 US-09-134-456-2	Sequence 2, Appli
12	489	100.0	489	4 US-09-196-427-2	Sequence 2, Appli
13	489	100.0	489	4 US-09-189-193-1	Sequence 1, Appli
14	489	100.0	489	5 PCT-US94-03793-1	Sequence 4, Appli
15	489	100.0	489	5 PCT-US96-06423-4	Sequence 1, Appli
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20	345	70.6	345	1 US-08-726-817-12	Sequence 12, Appli
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22	345	70.6	345	2 US-08-794-524-12	Sequence 12, Appli
23	345	70.6	345	4 US-09-189-193-12	Sequence 12, Appli
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27	107	21.9	489	1 US-08-726-817-4	Sequence 4, Appli

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102	16	3.3	1408	3	US-08-545-196B-11	Sequence 11, Appl	c 175	15	3.1	2056	4	US-09-334-601-12	Sequence 12, Appl
103	16	3.3	1408	3	US-08-545-196B-13	Sequence 13, Appl	c 176	15	3.1	2100	4	US-08-332-576-1	Sequence 1, Appl
c 104	16	3.3	1518	3	US-08-695-987-1	Sequence 1, Appl	177	15	3.1	2100	5	PCT-US95-13672-1	Sequence 1, Appl
105	16	3.3	1590	4	US-08-747-221B-23	Sequence 23, Appl	178	15	3.1	2381	1	US-08-021-608D-9	Sequence 9, Appl
106	16	3.3	1590	4	US-09-005-051-23	Sequence 23, Appl	179	15	3.1	2381	1	US-08-726-160-9	Sequence 9, Appl
c 107	16	3.3	1650	3	US-08-747-221B-21	Sequence 21, Appl	180	15	3.1	2381	5	PCT-US94-01782-9	Sequence 9, Appl
c 108	16	3.3	1650	3	US-08-747-221B-22	Sequence 22, Appl	181	15	3.1	2384	1	US-08-021-608D-1	Sequence 1, Appl
c 109	16	3.3	1650	4	US-09-005-051-21	Sequence 21, Appl	182	15	3.1	2384	1	US-08-726-160-1	Sequence 1, Appl
c 110	16	3.3	1650	4	US-09-005-051-22	Sequence 22, Appl	183	15	3.1	2384	5	PCT-US94-01782-1	Sequence 1, Appl
c 111	16	3.3	1716	5	PCT-US96-05320A-541	Sequence 541, App	184	15	3.1	2417	1	US-07-953-695A-1	Sequence 1, Appl
c 112	16	3.3	1792	3	US-08-747-221B-18	Sequence 18, Appl	185	15	3.1	2417	1	US-08-267-259-1	Sequence 1, Appl
c 113	16	3.3	1792	3	US-08-747-221B-20	Sequence 20, Appl	c 186	15	3.1	2469	3	US-09-087-727-1	Sequence 1, Appl
c 114	16	3.3	1792	4	US-09-005-051-18	Sequence 18, Appl	187	15	3.1	2659	3	US-08-749-522-2	Sequence 2, Appl
c 115	16	3.3	1792	4	US-09-005-051-20	Sequence 20, Appl	188	15	3.1	2755	3	US-08-749-522-2	Sequence 2, Appl
c 116	16	3.3	1810	3	US-08-657-868B-3	Sequence 3, Appl	189	15	3.1	2839	4	US-09-160-496-3	Sequence 3, Appl
c 117	16	3.3	1867	1	US-07-955-905A-1	Sequence 1, Appl	c 190	15	3.1	3088	4	US-08-418-444A-1	Sequence 1, Appl
c 118	16	3.3	2136	1	US-08-321-587-1	Sequence 1, Appl	c 191	15	3.1	3160	4	US-08-936-165A-255	Sequence 255, App
c 119	16	3.3	2763	1	US-08-176-413-1	Sequence 1, Appl	c 192	15	3.1	3226	2	US-08-070-301-10	Sequence 10, Appl
c 120	16	3.3	2763	2	US-08-612-542B-1	Sequence 1, Appl	c 193	15	3.1	3240	4	US-09-262-773-7	Sequence 7, Appl
c 121	16	3.3	2763	2	US-08-772-113-1	Sequence 1, Appl	c 194	15	3.1	3244	4	US-09-262-773-3	Sequence 3, Appl
c 122	16	3.3	2763	4	US-09-199-137-1	Sequence 1, Appl	c 195	15	3.1	3264	4	US-09-262-773-5	Sequence 5, Appl
c 123	16	3.3	2763	5	PCT-US94-14919-1	Sequence 1, Appl	c 196	15	3.1	3268	4	US-09-262-773-1	Sequence 1, Appl
c 124	16	3.3	2763	5	PCT-US94-14920-1	Sequence 1, Appl	c 197	15	3.1	3319	2	US-08-960-022-19	Sequence 19, Appl
c 125	16	3.3	2854	2	US-08-724-394A-17	Sequence 17, Appl	c 198	15	3.1	3549	4	US-09-008-097-5	Sequence 5, Appl
c 126	16	3.3	3250	3	US-08-617-860B-1	Sequence 1, Appl	c 199	15	3.1	3879	4	US-08-916-352-1	Sequence 1, Appl
c 127	16	3.3	3271	3	US-08-545-196B-22	Sequence 22, Appl	c 200	15	3.1	4203	2	US-08-288-630-3	Sequence 3, Appl
c 128	16	3.3	3279	5	PCT-US93-03077-2	Sequence 2, Appl	c 201	15	3.1	4560	4	US-09-256-703-1	Sequence 1, Appl
c 129	16	3.3	3293	1	US-08-030-096-1	Sequence 1, Appl	c 202	15	3.1	4743	3	US-09-339-964-1	Sequence 1, Appl
c 130	16	3.3	3293	1	US-08-004-139B-2	Sequence 2, Appl	c 203	15	3.1	4970	1	US-08-764-100-14	Sequence 14, Appl
c 131	16	3.3	4707	2	US-08-811-492-2	Sequence 2, Appl	c 204	15	3.1	4970	1	US-08-764-100-20	Sequence 20, Appl
c 132	16	3.3	4707	5	PCT-US96-10545A-2	Sequence 2, Appl	c 205	15	3.1	5092	4	US-09-412-545-1	Sequence 1, Appl
c 133	16	3.3	5475	2	US-08-680-327-1	Sequence 1, Appl	c 206	15	3.1	5110	2	US-08-404-531B-4	Sequence 4, Appl
c 134	16	3.3	5475	4	US-09-228-246-3	Sequence 3, Appl	c 207	15	3.1	5110	2	US-08-404-531B-5	Sequence 5, Appl
c 135	16	3.3	10968	4	US-08-680-327-2	Sequence 2, Appl	c 208	15	3.1	5110	3	US-08-476-900A-4	Sequence 4, Appl
c 136	16	3.3	10968	4	US-09-228-246-1	Sequence 1, Appl	c 209	15	3.1	5110	3	US-08-476-900A-5	Sequence 5, Appl
c 137	16	3.3	246240	2	US-08-724-394A-20	Sequence 20, Appl	c 210	15	3.1	5110	3	US-08-488-546A-4	Sequence 4, Appl
c 138	16	3.3	246240	2	US-08-724-394A-21	Sequence 21, Appl	c 211	15	3.1	5632	4	US-09-560-594-3	Sequence 3, Appl
c 139	16	3.3	246240	2	US-08-724-394A-22	Sequence 22, Appl	c 212	15	3.1	5632	4	US-08-488-546A-5	Sequence 5, Appl
c 140	15	3.1	15	3	US-08-649-654-2	Sequence 2, Appl	c 213	15	3.1	5635	1	US-09-136-742A-3	Sequence 3, Appl
c 141	15	3.1	29	4	US-09-364-539-154	Sequence 154, App	c 214	15	3.1	5635	5	PCT-US93-11667-3	Sequence 3, Appl
c 142	15	3.1	114	1	US-08-184-941-11	Sequence 11, Appl	c 215	15	3.1	5635	5	PCT-US93-11667-3	Sequence 3, Appl
c 143	15	3.1	431	2	US-08-691-814B-84	Sequence 84, Appl	c 216	15	3.1	5872	3	US-08-411-768B-1	Sequence 1, Appl
c 144	15	3.1	489	1	US-08-334-254-7	Sequence 7, Appl	c 217	15	3.1	5872	3	US-08-411-768B-6	Sequence 6, Appl
c 145	15	3.1	489	5	PCT-US95-14792-7	Sequence 7, Appl	c 218	15	3.1	6126	2	US-08-951-912-3	Sequence 3, Appl
c 146	15	3.1	489	5	PCT-US95-14792-7	Sequence 7, Appl	c 219	15	3.1	6126	2	US-09-174-077-3	Sequence 3, Appl
c 147	15	3.1	602	4	US-09-328-111-220	Sequence 220, App	c 220	15	3.1	6129	1	US-07-637-621-1	Sequence 1, Appl
c 148	15	3.1	747	4	US-09-385-982-540	Sequence 540, App	c 221	15	3.1	6129	1	US-08-136-742A-1	Sequence 1, Appl
c 149	15	3.1	747	4	US-09-140-084-25	Sequence 25, App	c 222	15	3.1	6129	1	US-08-135-809A-1	Sequence 1, Appl
c 150	15	3.1	821	1	US-08-396-452-3	Sequence 3, Appl	c 223	15	3.1	6129	2	US-08-951-912-1	Sequence 1, Appl
c 151	15	3.1	821	4	US-09-169-119-3	Sequence 3, Appl	c 224	15	3.1	6129	2	US-08-951-912-5	Sequence 5, Appl
c 152	15	3.1	912	1	US-08-764-100-15	Sequence 15, Appl	c 225	15	3.1	6129	2	US-08-691-605-1	Sequence 1, Appl
c 153	15	3.1	912	1	US-08-764-100-22	Sequence 22, Appl	c 226	15	3.1	6129	3	US-09-248-026-1	Sequence 1, Appl
c 154	15	3.1	960	3	US-08-875-233-9	Sequence 9, Appl	c 227	15	3.1	6129	4	US-08-681-838A-1	Sequence 1, Appl
c 155	15	3.1	1093	1	US-08-525-505A-3	Sequence 3, Appl	c 228	15	3.1	6129	4	US-09-174-077-1	Sequence 1, Appl
c 156	15	3.1	1129	4	US-09-221-357-40	Sequence 40, Appl	c 229	15	3.1	6129	5	PCT-US93-11667-1	Sequence 1, Appl
c 157	15	3.1	1272	2	US-08-869-057-1	Sequence 3, Appl	c 230	15	3.1	6130	1	US-08-466-886-16	Sequence 16, Appl
c 158	15	3.1	1296	2	US-08-401-068-3	Sequence 3, Appl	c 231	15	3.1	6130	2	US-08-604-488-1	Sequence 1, Appl
c 159	15	3.1	1296	2	US-08-846-338-3	Sequence 3, Appl	c 232	15	3.1	6130	2	US-08-604-488-1	Sequence 1, Appl
c 160	15	3.1	1372	6	5189147-2	Patent No. 5189147	c 233	15	3.1	6130	2	US-08-469-461-1	Sequence 1, Appl
c 161	15	3.1	1650	2	US-08-500-635A-11	Sequence 11, Appl	c 234	15	3.1	6130	3	US-07-890-609-1	Sequence 1, Appl
c 162	15	3.1	1650	4	US-09-167-151-11	Sequence 11, Appl	c 235	15	3.1	6130	3	US-08-030-081-1	Sequence 1, Appl
c 163	15	3.1	1656	4	US-09-080-983-10	Sequence 10, Appl	c 236	15	3.1	6130	3	US-08-469-617-16	Sequence 16, Appl
c 164	15	3.1	1749	1	US-07-649-591B-2	Sequence 2, Appl	c 237	15	3.1	6146	6	5240846-4	Patent No. 5240846
c 165	15	3.1	1749	1	US-08-277-540-2	Sequence 2, Appl	c 238	15	3.1	6638	2	US-08-070-301-2	Sequence 2, Appl
c 166	15	3.1	1749	1	US-08-430-787A-2	Sequence 2, Appl	c 239	15	3.1	8225	4	US-08-793-618-1	Sequence 1, Appl
c 167	15	3.1	1794	3	US-09-012-515A-13	Sequence 13, Appl	c 240	15	3.1	8835	3	US-08-884-324-10	Sequence 10, Appl
c 168	15	3.1	1794	3	US-08-360-144A-13	Sequence 13, Appl	c 241	15	3.1	8855	2	US-08-542-003-1	Sequence 1, Appl
c 169	15	3.1	1794	3	PCT-US95-06722-13	Sequence 13, Appl	c 242	15	3.1	8855	2	US-08-322-760A-1	Sequence 1, Appl
c 170	15	3.1	1803	1	US-08-021-608D-7	Sequence 7, Appl	c 243	15	3.1	9972	3	US-08-836-022A-3	Sequence 3, Appl
c 171	15	3.1	1803	1	US-08-726-160-7	Sequence 7, Appl	c 244	15	3.1	9972	4	US-09-427-048A-3	Sequence 3, Appl
c 172	15	3.1	1803	5	PCT-US94-01782-7	Sequence 7, Appl	c 245	15	3.1	15500	4	US-09-080-983-1	Sequence 1, Appl
c 173	15	3.1	1812	4	US-09-008-097-3	Sequence 3, Appl	c 246	15	3.1	18596	4	US-09-318-448-11	Sequence 11, Appl

c 247	15	3.1	20137	4	US-09-262-773-206	Sequence 206, App	320	14	2.9	770	3	US-08-938-675A-1	Sequence 1, Appli
c 248	15	3.1	20138	4	US-09-262-773-9	Sequence 9, Appli	321	14	2.9	777	2	US-08-618-911-3	Sequence 3, Appli
c 249	15	3.1	22846	2	US-08-469-461-3	Sequence 3, Appli	322	14	2.9	777	2	US-08-618-911-5	Sequence 5, Appli
c 250	15	3.1	22846	3	US-07-890-609-3	Sequence 3, Appli	323	14	2.9	790	1	US-08-393-985-22	Sequence 22, Appl
c 251	15	3.1	23071	4	US-09-262-773-210	Sequence 210, App	324	14	2.9	808	1	US-07-768-437-2	Sequence 2, Appli
c 252	15	3.1	28994	3	US-08-884-324-14	Sequence 14, Appl	325	14	2.9	810	2	US-08-611-880-3	Sequence 3, Appli
c 253	15	3.1	152331	3	US-09-128-155-16	Sequence 16, Appl	326	14	2.9	824	1	US-08-158-353-1	Sequence 1, Appli
c 254	15	3.1	246240	2	US-08-724-394A-20	Sequence 20, Appl	327	14	2.9	827	1	US-08-117-373-6	Sequence 6, Appli
c 255	15	3.1	246240	2	US-08-724-394A-21	Sequence 21, Appl	328	14	2.9	837	1	US-08-331-082-1	Sequence 1, Appli
c 256	15	3.1	246240	2	US-08-724-394A-22	Sequence 22, Appl	329	14	2.9	837	4	US-09-570-367C-20	Sequence 20, Appl
c 257	14	2.9	20	3	US-08-962-503-8	Sequence 8, Appli	330	14	2.9	837	4	US-09-570-367C-22	Sequence 22, Appl
c 258	14	2.9	21	3	US-09-111-752-12	Sequence 12, Appl	331	14	2.9	852	4	US-09-277-565-24	Sequence 24, Appl
c 259	14	2.9	26	5	PCT-US92-08094-18	Sequence 18, Appl	332	14	2.9	854	4	US-09-064-693A-24	Sequence 24, Appl
c 260	14	2.9	28	3	US-08-737-841-22	Sequence 22, Appl	333	14	2.9	870	2	US-08-493-137-2	Sequence 2, Appli
c 261	14	2.9	40	4	US-09-306-290-41	Sequence 41, Appl	334	14	2.9	880	1	PCT-US95-07844-2	Sequence 2, Appli
c 262	14	2.9	109	2	US-08-482-920-12	Sequence 12, Appl	335	14	2.9	880	3	US-08-616-368A-7	Sequence 7, Appli
c 263	14	2.9	125	4	US-09-158-863C-54	Sequence 54, Appl	336	14	2.9	886	1	US-09-054-298-7	Sequence 7, Appli
c 264	14	2.9	161	3	US-09-065-474-96	Sequence 96, Appl	337	14	2.9	886	1	US-08-184-237-3	Sequence 3, Appli
c 265	14	2.9	161	3	US-09-065-474-97	Sequence 97, Appl	338	14	2.9	886	1	US-07-923-692C-3	Sequence 3, Appli
c 266	14	2.9	176	1	US-07-916-901-8	Sequence 8, Appli	339	14	2.9	895	3	US-08-483-502-3	Sequence 3, Appli
c 267	14	2.9	183	3	US-08-513-974B-306	Sequence 306, App	340	14	2.9	897	4	US-09-367-781-1	Sequence 1, Appli
c 268	14	2.9	183	3	US-08-513-974B-307	Sequence 307, App	341	14	2.9	954	4	US-08-555-722-1	Sequence 1, Appli
c 269	14	2.9	211	1	US-08-248-474-95	Sequence 95, Appl	342	14	2.9	1025	1	US-09-384-301-1	Sequence 1, Appli
c 270	14	2.9	213	3	US-08-756-849-95	Sequence 95, Appl	343	14	2.9	1037	1	US-08-365-103B-9	Sequence 9, Appli
c 271	14	2.9	256	4	US-08-905-223-66	Sequence 66, Appl	344	14	2.9	1048	3	US-08-626-994A-4	Sequence 4, Appli
c 272	14	2.9	277	4	US-09-328-111-224	Sequence 224, App	345	14	2.9	1056	3	US-09-065-474-138	Sequence 138, App
c 273	14	2.9	321	1	US-08-328-152A-21	Sequence 21, Appl	346	14	2.9	1056	3	US-08-065-474-140	Sequence 140, App
c 274	14	2.9	321	1	US-08-328-152A-25	Sequence 25, Appl	347	14	2.9	1059	4	US-08-476-102A-8	Sequence 8, Appli
c 275	14	2.9	331	1	US-08-171-385-1	Sequence 1, Appli	348	14	2.9	1078	4	US-09-492-543-28	Sequence 28, Appl
c 276	14	2.9	331	3	US-08-361-441B-1	Sequence 1, Appli	349	14	2.9	1189	1	US-08-307-591-2	Sequence 2, Appli
c 277	14	2.9	358	4	US-08-221-298-89	Sequence 89, Appl	350	14	2.9	1192	1	US-08-840-683-1	Sequence 1, Appli
c 278	14	2.9	367	1	US-08-745-977-2	Sequence 2, Appli	351	14	2.9	1212	3	US-09-031-485-17	Sequence 17, Appl
c 279	14	2.9	367	3	US-09-040-699A-2	Sequence 2, Appli	352	14	2.9	1227	1	US-08-847-429A-17	Sequence 17, Appl
c 280	14	2.9	372	1	US-08-474-633A-102	Sequence 102, App	353	14	2.9	1227	3	US-09-065-474-18	Sequence 18, Appl
c 281	14	2.9	393	1	US-08-328-152A-20	Sequence 2, Appli	354	14	2.9	1228	1	US-09-031-485-16	Sequence 16, Appl
c 282	14	2.9	399	1	US-08-328-152A-21	Sequence 21, Appl	355	14	2.9	1228	1	US-08-847-429A-16	Sequence 16, Appl
c 283	14	2.9	433	1	US-08-117-080-13	Sequence 13, Appl	356	14	2.9	1257	5	PCT-US94-00238-1	Sequence 5, Appli
c 284	14	2.9	433	2	US-08-471-329-13	Sequence 13, Appl	357	14	2.9	1274	1	US-08-900-491-5	Sequence 5, Appli
c 285	14	2.9	433	2	US-09-151-142-13	Sequence 13, Appl	358	14	2.9	1274	1	US-08-443-865-5	Sequence 5, Appli
c 286	14	2.9	446	1	US-08-104-072B-1	Sequence 1, Appli	359	14	2.9	1294	1	US-08-227-357-138	Sequence 138, App
c 287	14	2.9	446	1	US-08-358-160-68	Sequence 68, Appl	360	14	2.9	1335	1	US-08-107-684B-1	Sequence 1, Appli
c 288	14	2.9	498	1	US-08-365-103B-13	Sequence 13, Appl	361	14	2.9	1337	3	US-08-743-637B-32	Sequence 32, Appl
c 289	14	2.9	498	1	US-08-650-528-8	Sequence 8, Appli	362	14	2.9	1337	3	US-08-526-840B-32	Sequence 32, Appl
c 290	14	2.9	499	3	US-09-060-584-8	Sequence 8, Appli	363	14	2.9	1386	4	US-09-337-171-14	Sequence 14, Appl
c 291	14	2.9	499	3	US-09-413-140A-8	Sequence 8, Appli	364	14	2.9	1400	3	PCT-US93-07261-12	Sequence 12, Appl
c 292	14	2.9	501	1	US-08-365-103B-11	Sequence 11, Appl	365	14	2.9	1500	1	US-08-695-191-14	Sequence 14, Appl
c 293	14	2.9	567	1	US-08-262-424-2	Sequence 2, Appli	366	14	2.9	1500	5	PCT-US95-05966-1	Sequence 1, Appli
c 294	14	2.9	573	1	US-09-031-485-19	Sequence 19, Appl	367	14	2.9	1512	2	US-07-938-154-10	Sequence 10, Appl
c 295	14	2.9	573	1	US-09-031-485-21	Sequence 21, Appl	368	14	2.9	1555	3	PCT-US91-02311-10	Sequence 10, Appl
c 296	14	2.9	573	1	US-08-847-429A-19	Sequence 19, Appl	369	14	2.9	1578	3	US-08-504-878A-1	Sequence 1, Appli
c 297	14	2.9	573	1	US-08-847-429A-21	Sequence 21, Appl	370	14	2.9	1644	3	US-09-111-752-13	Sequence 13, Appl
c 298	14	2.9	573	3	US-09-065-474-19	Sequence 19, Appl	371	14	2.9				
c 299	14	2.9	573	3	US-09-065-474-21	Sequence 21, Appl	372	14	2.9				
c 300	14	2.9	595	4	US-09-276-531-63	Sequence 63, Appl	373	14	2.9				
c 301	14	2.9	595	1	US-08-328-152A-35	Sequence 35, Appl	374	14	2.9				
c 302	14	2.9	600	1	US-08-472-239-2	Sequence 2, Appli	375	14	2.9				
c 303	14	2.9	605	4	US-09-385-982-501	Sequence 501, App	376	14	2.9				
c 304	14	2.9	627	3	US-08-361-441B-4	Sequence 4, Appli	377	14	2.9				
c 305	14	2.9	630	4	US-08-235-836C-31	Sequence 31, Appl	378	14	2.9				
c 306	14	2.9	651	1	US-08-171-385-4	Sequence 4, Appli	379	14	2.9				
c 307	14	2.9	675	1	US-08-328-152A-30	Sequence 30, Appl	380	14	2.9				
c 308	14	2.9	686	2	US-08-522-421-7	Sequence 7, Appli	381	14	2.9				
c 309	14	2.9	693	4	US-09-328-111-795	Sequence 795, App	382	14	2.9				
c 310	14	2.9	703	4	US-09-247-155-79	Sequence 79, Appl	383	14	2.9				
c 311	14	2.9	704	4	US-08-896-164-49	Sequence 49, Appl	384	14	2.9				
c 312	14	2.9	707	4	US-08-998-416-745	Sequence 745, App	385	14	2.9				
c 313	14	2.9	708	3	US-08-955-937A-3	Sequence 3, Appli	386	14	2.9				
c 314	14	2.9	708	4	US-09-300-985-3	Sequence 3, Appli	387	14	2.9				
c 315	14	2.9	709	4	US-08-998-416-599	Sequence 599, App	388	14	2.9				
c 316	14	2.9	731	4	US-08-936-165A-170	Sequence 170, App	389	14	2.9				
c 317	14	2.9	732	4	US-08-916-576B-5	Sequence 5, Appli	390	14	2.9				
c 318	14	2.9	750	4	US-08-943-731-125	Sequence 125, App	391	14	2.9				
c 319	14	2.9	764	6	5215909-7	Patent No. 5215909	392	14	2.9				

c 393	14	2.9	1654	3	US-08-913-842-20	Sequence 20, Appl	c 466	14	2.9	2445	6	5215909-9	Patent No. 5215909
c 394	14	2.9	1660	1	US-08-626-994A-2	Sequence 2, Appl	c 467	14	2.9	2457	6	5344773-1	Patent No. 5344773
c 395	14	2.9	1660	1	US-08-957-742-2	Sequence 2, Appl	c 468	14	2.9	2483	4	US-08-894-324A-3	Sequence 3, Appl
c 396	14	2.9	1698	4	US-09-232-478-15	Sequence 15, Appl	c 469	14	2.9	2497	6	5185259-2	Patent No. 5185259
c 397	14	2.9	1717	1	US-08-229-515A-12	Sequence 12, Appl	c 470	14	2.9	2631	1	US-08-717-515-3	Sequence 3, Appl
c 398	14	2.9	1717	1	US-08-645-865-12	Sequence 12, Appl	c 471	14	2.9	2670	1	US-08-121-713D-61	Sequence 61, Appl
c 399	14	2.9	1762	1	US-08-105-483-284	Sequence 284, App	c 472	14	2.9	2670	1	US-08-835-268-61	Sequence 61, Appl
c 400	14	2.9	1762	1	US-08-709-209-284	Sequence 284, App	c 473	14	2.9	2670	1	US-09-060-692-61	Sequence 61, Appl
c 401	14	2.9	1762	1	US-08-458-101-284	Sequence 284, App	c 474	14	2.9	2670	3	US-08-833-391-61	Sequence 61, Appl
c 402	14	2.9	1784	2	US-08-808-931-19	Sequence 19, Appl	c 475	14	2.9	2670	4	US-09-060-610-61	Sequence 61, Appl
c 403	14	2.9	1784	3	US-08-808-323-19	Sequence 19, Appl	c 476	14	2.9	2670	5	PCT-US94-10151A-61	Sequence 61, Appl
c 404	14	2.9	1784	3	US-09-050-603A-19	Sequence 19, Appl	c 477	14	2.9	2729	1	US-08-412-431-2	Sequence 2, Appl
c 405	14	2.9	1784	3	US-09-102-420B-19	Sequence 19, Appl	c 478	14	2.9	2729	1	US-08-623-679-2	Sequence 2, Appl
c 406	14	2.9	1784	4	US-09-497-698-19	Sequence 19, Appl	c 479	14	2.9	2729	3	US-08-933-774-2	Sequence 2, Appl
c 407	14	2.9	1791	1	US-08-245-394-7	Sequence 7, Appl	c 480	14	2.9	2729	4	US-09-181-030-2	Sequence 2, Appl
c 408	14	2.9	1791	1	US-08-474-499-7	Sequence 7, Appl	c 481	14	2.9	2729	4	US-09-534-242-2	Sequence 2, Appl
c 409	14	2.9	1791	1	US-08-307-279A-7	Sequence 7, Appl	c 482	14	2.9	2729	4	US-09-454-854-2	Sequence 2, Appl
c 410	14	2.9	1791	5	PCT-US95-06211-7	Sequence 7, Appl	c 483	14	2.9	2769	4	US-09-118-408-1	Sequence 1, Appl
c 411	14	2.9	1800	6	5180581-1	Patent No. 5180581	c 484	14	2.9	2774	2	US-08-643-034A-1	Sequence 1, Appl
c 412	14	2.9	1811	2	US-08-808-931-9	Sequence 9, Appl	c 485	14	2.9	2774	2	US-08-648-650A-1	Sequence 1, Appl
c 413	14	2.9	1811	3	US-08-808-323-9	Sequence 9, Appl	c 486	14	2.9	2793	1	US-08-281-916-5	Sequence 5, Appl
c 414	14	2.9	1811	3	US-09-050-603A-9	Sequence 9, Appl	c 487	14	2.9	2793	2	US-08-460-725-7	Sequence 7, Appl
c 415	14	2.9	1811	3	US-09-102-420B-9	Sequence 9, Appl	c 488	14	2.9	2800	2	US-08-874-138-1	Sequence 1, Appl
c 416	14	2.9	1811	4	US-09-497-698-9	Sequence 9, Appl	c 489	14	2.9	2800	2	US-08-874-138-5	Sequence 5, Appl
c 417	14	2.9	1826	4	US-09-286-691-11	Sequence 11, Appl	c 490	14	2.9	2800	4	US-08-879-941-1	Sequence 1, Appl
c 418	14	2.9	1826	4	US-09-687-147-11	Sequence 11, Appl	c 491	14	2.9	2800	4	US-08-879-941-3	Sequence 3, Appl
c 419	14	2.9	1830	2	US-08-933-750C-79	Sequence 79, Appl	c 492	14	2.9	2800	4	US-09-747-116-1	Sequence 1, Appl
c 420	14	2.9	1830	3	US-09-234-613-79	Sequence 79, Appl	c 493	14	2.9	2800	4	US-09-747-116-3	Sequence 3, Appl
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c 422	14	2.9	1875	3	US-08-913-842-1	Sequence 1, Appl	c 495	14	2.9	2883	2	US-08-742-923A-7	Sequence 7, Appl
c 423	14	2.9	1879	3	US-08-961-083-219	Sequence 219, App	c 496	14	2.9	2937	6	5208144-7	Patent No. 5208144
c 424	14	2.9	1935	2	US-08-492-027A-9	Sequence 9, Appl	c 497	14	2.9	2992	2	US-08-841-349-10	Sequence 10, Appl
c 425	14	2.9	1964	1	US-08-328-322-9	Sequence 9, Appl	c 498	14	2.9	3000	1	US-07-841-997A-3	Sequence 3, Appl
c 426	14	2.9	1972	3	US-08-961-083-203	Sequence 203, App	c 499	14	2.9	3000	1	US-08-290-301-3	Sequence 3, Appl
c 427	14	2.9	1974	2	US-08-811-949-38	Sequence 38, Appl	c 500	14	2.9	3065	1	US-08-156-866-1	Sequence 1, Appl
c 428	14	2.9	1998	4	US-09-240-639-5	Sequence 5, Appl	c 501	14	2.9	3092	1	US-08-426-627-3	Sequence 3, Appl
c 429	14	2.9	2003	2	US-09-047-026A-5	Sequence 5, Appl	c 502	14	2.9	3095	6	5231168-1	Patent No. 5231168
c 430	14	2.9	2007	4	US-09-052-089A-7	Sequence 7, Appl	c 503	14	2.9	3104	1	US-07-415-307A-1	Sequence 1, Appl
c 431	14	2.9	2029	6	5187089-1	Patent No. 5187089	c 504	14	2.9	3104	1	US-08-371-320-1	Sequence 1, Appl
c 432	14	2.9	2029	6	5457090-1	Patent No. 5457090	c 505	14	2.9	3126	2	US-08-477-396A-3	Sequence 3, Appl
c 433	14	2.9	2029	6	5495001-6	Patent No. 5495001	c 506	14	2.9	3177	3	US-09-058-489-50	Sequence 50, Appl
c 434	14	2.9	2031	6	5495001-8	Patent No. 5495001	c 507	14	2.9	3253	1	US-08-426-627-5	Sequence 5, Appl
c 435	14	2.9	2032	6	5187089-3	Patent No. 5187089	c 508	14	2.9	3255	1	US-08-717-515-5	Sequence 5, Appl
c 436	14	2.9	2032	6	5457090-3	Patent No. 5457090	c 509	14	2.9	3381	3	US-08-937-195-1	Sequence 1, Appl
c 437	14	2.9	2058	4	US-09-091-725-16	Sequence 16, Appl	c 510	14	2.9	3381	3	US-08-937-195-2	Sequence 2, Appl
c 438	14	2.9	2075	1	US-08-238-163-3	Sequence 3, Appl	c 511	14	2.9	3381	4	US-08-915-152-1	Sequence 1, Appl
c 439	14	2.9	2097	1	US-08-393-985-1	Sequence 1, Appl	c 512	14	2.9	3381	4	US-08-915-152-2	Sequence 2, Appl
c 440	14	2.9	2101	2	US-08-811-949-42	Sequence 42, Appl	c 513	14	2.9	3381	5	PCT-US96-07627-1	Sequence 1, Appl
c 441	14	2.9	2119	4	US-09-227-357-48	Sequence 48, Appl	c 514	14	2.9	3381	5	PCT-US96-07627-2	Sequence 2, Appl
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c 443	14	2.9	2162	1	US-08-488-015B-3	Sequence 3, Appl	c 516	14	2.9	3454	4	US-09-082-059-1	Sequence 1, Appl
c 444	14	2.9	2162	1	US-08-488-015B-25	Sequence 25, Appl	c 517	14	2.9	3527	2	US-08-909-965C-7	Sequence 7, Appl
c 445	14	2.9	2162	3	US-09-013-881-9	Sequence 9, Appl	c 518	14	2.9	3600	3	US-08-894-731-1	Sequence 1, Appl
c 446	14	2.9	2178	2	US-08-492-027A-2	Sequence 2, Appl	c 519	14	2.9	3607	1	US-08-647-351B-1	Sequence 1, Appl
c 447	14	2.9	2181	6	5208144-36	Patent No. 5208144	c 520	14	2.9	3627	1	US-08-104-072B-6	Sequence 6, Appl
c 448	14	2.9	2190	2	US-08-492-027A-7	Sequence 7, Appl	c 521	14	2.9	3627	1	US-08-351-413-7	Sequence 7, Appl
c 449	14	2.9	2214	4	US-08-943-731-57	Sequence 57, Appl	c 522	14	2.9	3627	2	US-09-025-583-7	Sequence 7, Appl
c 450	14	2.9	2312	1	US-08-102-942A-1	Sequence 1, Appl	c 523	14	2.9	3706	1	US-08-207-904-16	Sequence 16, Appl
c 451	14	2.9	2312	4	US-09-037-179B-1	Sequence 1, Appl	c 524	14	2.9	3831	2	US-08-717-515-7	Sequence 7, Appl
c 452	14	2.9	2327	4	US-09-071-709-5	Sequence 5, Appl	c 525	14	2.9	3850	2	US-08-371-377-22	Sequence 22, Appl
c 453	14	2.9	2335	2	US-08-300-584-3	Sequence 3, Appl	c 526	14	2.9	4084	2	US-08-568-459A-1	Sequence 1, Appl
c 454	14	2.9	2335	4	US-08-476-123-3	Sequence 3, Appl	c 527	14	2.9	4084	2	US-08-487-826B-1	Sequence 2, Appl
c 455	14	2.9	2345	3	US-08-955-937A-1	Sequence 1, Appl	c 528	14	2.9	4084	6	5198347-5	Patent No. 5198347
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c 457	14	2.9	2359	1	US-08-188-582-4	Sequence 4, Appl	c 530	14	2.9	4342	2	US-08-436-054-1	Sequence 1, Appl
c 458	14	2.9	2359	1	US-08-646-715-4	Sequence 4, Appl	c 531	14	2.9	4342	5	PCT-US95-08812-1	Sequence 1, Appl
c 459	14	2.9	2381	2	US-08-318-826A-9	Sequence 9, Appl	c 532	14	2.9	4379	3	US-08-592-214A-17	Sequence 17, Appl
c 460	14	2.9	2400	6	5215909-13	Patent No. 5215909	c 533	14	2.9	4379	3	US-09-149-976-17	Sequence 17, Appl
c 461	14	2.9	2404	2	US-08-868-577-19	Sequence 19, Appl	c 534	14	2.9	4483	1	US-08-181-271A-5	Sequence 5, Appl
c 462	14	2.9	2412	1	US-08-437-027-18	Sequence 18, Appl	c 535	14	2.9	4483	1	US-08-449-315-5	Sequence 5, Appl
c 463	14	2.9	2416	2	US-08-318-826A-8	Sequence 8, Appl	c 536	14	2.9	4483	1	US-08-444-803-5	Sequence 5, Appl
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c 465	14	2.9	2416	4	US-09-334-489-2	Sequence 2, Appl	c 538	14	2.9	4483	1	US-08-456-265A-5	Sequence 5, Appl

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608	14	2.9	9581	2	US-08-790-519-1	Sequence 1, Appli	c 681	13	2.7	21	3	US-08-962-503-6	Sequence 6, Appli
609	14	2.9	9581	2	US-07-925-695-1	Sequence 1, Appli	c 682	13	2.7	21	4	US-09-192-657A-34	Sequence 34, Appli
610	14	2.9	9589	1	US-07-925-695-1	Sequence 1, Appli	c 683	13	2.7	21	4	US-09-192-657A-35	Sequence 35, Appli
611	14	2.9	9589	1	US-07-925-695-2	Sequence 2, Appli	c 684	13	2.7	21	4	US-09-192-657A-35	Sequence 35, Appli

c 685	13	2.7	24	2	US-08-839-306-3	Sequence 3, Appli	758	13	2.7	262	4	US-08-991-789A-256	Sequence 256, App
c 686	13	2.7	24	2	US-09-002-177-5	Sequence 5, Appli	759	13	2.7	262	4	US-09-062-451-256	Sequence 256, App
c 687	13	2.7	24	2	US-09-374-584-5	Sequence 5, Appli	c 760	13	2.7	265	4	US-09-172-108-10	Sequence 10, Appl
c 688	13	2.7	27	1	US-08-392-317B-3	Sequence 3, Appli	c 761	13	2.7	265	4	US-09-221-298-55	Sequence 55, Appl
c 689	13	2.7	27	1	US-08-392-317B-4	Sequence 4, Appli	c 762	13	2.7	267	4	US-08-818-112-31	Sequence 31, Appl
c 690	13	2.7	27	2	US-08-951-871-16	Sequence 16, Appl	763	13	2.7	267	4	US-08-818-111-31	Sequence 31, Appl
c 691	13	2.7	27	3	US-09-134-132-3	Sequence 3, Appli	764	13	2.7	267	4	US-09-056-556-31	Sequence 31, Appl
c 692	13	2.7	27	3	US-09-134-132-4	Sequence 4, Appli	765	13	2.7	269	3	US-08-851-843A-80	Sequence 80, Appl
c 693	13	2.7	27	3	US-09-134-134A-3	Sequence 3, Appli	766	13	2.7	269	4	US-08-974-549A-584	Sequence 584, App
c 694	13	2.7	27	4	US-09-134-134A-4	Sequence 4, Appli	767	13	2.7	269	4	US-08-854-050-80	Sequence 80, Appl
c 695	13	2.7	27	4	US-09-134-456-3	Sequence 3, Appli	768	13	2.7	269	4	US-09-430-323-80	Sequence 80, Appl
c 696	13	2.7	27	4	US-09-134-456-4	Sequence 4, Appli	c 769	13	2.7	271	1	US-08-254-404-18	Sequence 18, Appl
c 697	13	2.7	27	4	US-09-134-456-5	Sequence 5, Appli	c 770	13	2.7	271	2	US-08-327-451E-18	Sequence 18, Appl
c 698	13	2.7	27	4	US-09-196-427-3	Sequence 3, Appli	c 771	13	2.7	271	2	US-08-458-109-18	Sequence 18, Appl
c 699	13	2.7	27	4	US-09-196-427-4	Sequence 4, Appli	c 772	13	2.7	271	3	US-08-231-196-18	Sequence 18, Appl
c 700	13	2.7	28	4	US-09-263-904-5	Sequence 5, Appli	c 773	13	2.7	272	4	US-08-991-789A-280	Sequence 280, App
c 701	13	2.7	29	2	US-08-816-155B-21	Sequence 21, Appl	c 774	13	2.7	272	4	US-09-062-451-280	Sequence 280, App
c 702	13	2.7	29	3	US-09-079-587-21	Sequence 21, Appl	c 775	13	2.7	275	2	US-08-675-508-18	Sequence 18, Appl
c 703	13	2.7	30	1	US-08-437-067-3	Sequence 3, Appli	776	13	2.7	276	1	US-08-261-304-6	Sequence 6, Appli
c 704	13	2.7	30	1	US-08-079-511-2	Sequence 2, Appli	777	13	2.7	288	4	US-08-821-994-57	Sequence 57, Appl
c 705	13	2.7	30	4	US-08-733-202-3	Sequence 3, Appli	778	13	2.7	288	4	US-09-556-868-1	Sequence 1, Appli
c 706	13	2.7	31	4	US-08-001-063-16	Sequence 16, Appl	c 779	13	2.7	290	1	US-08-248-474-69	Sequence 69, Appl
c 707	13	2.7	31	6	5185441-7	Patent No. 5185441	c 780	13	2.7	290	3	US-08-756-849-69	Sequence 69, Appl
c 708	13	2.7	38	3	US-08-339-708A-23	Sequence 23, Appl	c 781	13	2.7	294	4	US-09-472-971-6	Sequence 6, Appli
c 709	13	2.7	39	2	US-08-398-590A-51	Sequence 51, Appl	c 782	13	2.7	298	2	US-08-557-309B-14	Sequence 14, Appl
c 710	13	2.7	39	4	US-08-894-997-53	Sequence 53, Appl	c 783	13	2.7	298	3	US-08-714-918-54	Sequence 54, Appl
c 711	13	2.7	42	3	US-08-962-503-1	Sequence 1, Appli	c 784	13	2.7	298	3	US-08-834-306-14	Sequence 14, Appl
c 712	13	2.7	48	1	US-07-609-716-71	Sequence 71, Appl	c 785	13	2.7	298	4	US-09-265-315-54	Sequence 54, Appl
c 713	13	2.7	48	3	US-08-475-411A-71	Sequence 71, Appl	c 786	13	2.7	298	4	US-09-265-315-54	Sequence 54, Appl
c 714	13	2.7	48	4	US-09-237-712-75	Sequence 75, Appl	c 787	13	2.7	298	4	US-08-993-674A-14	Sequence 14, Appl
c 715	13	2.7	48	4	US-08-478-029A-71	Sequence 71, Appl	c 788	13	2.7	298	4	US-09-266-417-54	Sequence 54, Appl
c 716	13	2.7	56	3	US-07-609-716-70	Sequence 70, Appl	c 789	13	2.7	300	4	US-08-991-789A-64	Sequence 64, Appl
c 717	13	2.7	56	3	US-08-475-411A-70	Sequence 70, Appl	790	13	2.7	300	4	US-09-062-451-64	Sequence 64, Appl
c 718	13	2.7	56	4	US-08-478-029A-70	Sequence 70, Appl	c 791	13	2.7	302	2	US-08-235-515A-26	Sequence 26, Appl
c 719	13	2.7	61	1	US-07-609-716-74	Sequence 74, Appl	792	13	2.7	305	4	US-08-821-994-81	Sequence 81, Appl
c 720	13	2.7	61	3	US-08-475-411A-74	Sequence 74, Appl	793	13	2.7	307	4	US-08-821-994-81	Sequence 81, Appl
c 721	13	2.7	61	4	US-08-478-029A-74	Sequence 74, Appl	794	13	2.7	309	3	US-08-339-708A-11	Sequence 11, Appl
c 722	13	2.7	62	1	US-07-609-716-75	Sequence 75, Appl	c 795	13	2.7	311	4	US-08-180-371-11	Sequence 11, Appl
c 723	13	2.7	62	3	US-08-475-411A-75	Sequence 75, Appl	796	13	2.7	313	4	US-09-040-984-64	Sequence 64, Appl
c 724	13	2.7	62	4	US-08-478-029A-75	Sequence 75, Appl	797	13	2.7	313	4	US-09-123-912-64	Sequence 10, Appl
c 725	13	2.7	69	2	US-08-410-654B-30	Sequence 30, Appl	798	13	2.7	314	1	US-08-525-507-10	Sequence 10, Appl
c 726	13	2.7	69	2	US-08-474-851-30	Sequence 30, Appl	799	13	2.7	315	1	US-08-328-152A-29	Sequence 29, Appl
c 727	13	2.7	69	2	US-08-481-560-30	Sequence 30, Appl	c 800	13	2.7	319	4	US-09-328-111-38	Sequence 38, Appl
c 728	13	2.7	80	1	US-08-471-985A-86	Sequence 86, Appl	801	13	2.7	322	4	US-09-199-637A-434	Sequence 434, App
c 729	13	2.7	80	5	PCF-US95-12401A-86	Sequence 86, Appl	802	13	2.7	322	4	US-08-821-994-55	Sequence 55, Appl
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c 731	13	2.7	117	1	US-08-299-498A-41	Sequence 41, Appl	804	13	2.7	333	1	US-08-328-152A-23	Sequence 23, Appl
c 732	13	2.7	117	5	PCF-US95-10813-41	Sequence 41, Appl	805	13	2.7	336	1	US-08-328-152A-27	Sequence 27, Appl
c 733	13	2.7	132	1	US-07-609-716-76	Sequence 76, Appl	c 806	13	2.7	358	1	US-08-254-404-19	Sequence 19, Appl
c 734	13	2.7	132	3	US-08-475-411A-76	Sequence 76, Appl	c 807	13	2.7	358	2	US-08-327-451E-19	Sequence 19, Appl
c 735	13	2.7	132	4	US-08-478-029A-76	Sequence 76, Appl	c 808	13	2.7	358	2	US-08-458-109-19	Sequence 19, Appl
c 736	13	2.7	137	4	US-08-821-994-85	Sequence 85, Appl	c 809	13	2.7	358	3	US-08-231-196-19	Sequence 19, Appl
c 737	13	2.7	140	3	US-09-035-220-1	Sequence 1, Appli	c 810	13	2.7	366	2	US-08-853-659A-11	Sequence 11, Appl
c 738	13	2.7	175	1	US-07-609-716-82	Sequence 82, Appl	c 811	13	2.7	366	2	US-08-875-972-26	Sequence 26, Appl
c 739	13	2.7	175	3	US-08-475-411A-82	Sequence 82, Appl	c 812	13	2.7	388	2	US-08-744-670-2	Sequence 2, Appli
c 740	13	2.7	175	4	US-08-478-029A-82	Sequence 82, Appl	c 813	13	2.7	388	2	US-09-149-933-2	Sequence 2, Appli
c 741	13	2.7	180	3	US-09-004-113-13	Sequence 13, Appl	814	13	2.7	396	4	US-09-040-984-77	Sequence 77, Appl
c 742	13	2.7	180	4	US-09-065-019-1	Sequence 1, Appli	815	13	2.7	396	4	US-09-123-912-77	Sequence 77, Appl
c 743	13	2.7	182	4	US-09-269-617-4	Sequence 4, Appli	c 816	13	2.7	398	4	US-09-065-019-2	Sequence 2, Appli
c 744	13	2.7	197	4	US-08-118-200-13	Sequence 13, Appl	c 817	13	2.7	399	3	US-08-713-569-6	Sequence 6, Appli
c 745	13	2.7	197	4	US-08-458-745-13	Sequence 13, Appl	c 818	13	2.7	399	3	US-08-713-569-6	Sequence 6, Appli
c 746	13	2.7	232	5	PCF-US93-06251-44	Sequence 44, Appl	819	13	2.7	402	1	US-08-328-152A-12	Sequence 12, Appl
c 747	13	2.7	234	2	US-08-840-683-3	Sequence 3, Appli	820	13	2.7	408	1	US-08-328-152A-22	Sequence 22, Appl
c 748	13	2.7	234	2	US-08-555-722-3	Sequence 3, Appli	c 821	13	2.7	417	3	US-08-714-918-106	Sequence 106, App
c 749	13	2.7	234	4	US-09-384-301-3	Sequence 3, Appli	c 822	13	2.7	417	3	US-09-265-315-106	Sequence 106, App
c 750	13	2.7	243	2	US-08-727-688-7	Sequence 7, Appli	c 823	13	2.7	417	4	US-09-265-315-106	Sequence 106, App
c 751	13	2.7	243	4	US-09-172-108-12	Sequence 12, Appl	c 824	13	2.7	417	4	US-09-266-417-106	Sequence 106, App
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c 753	13	2.7	251	2	US-08-600-993A-21	Sequence 21, Appl	c 826	13	2.7	423	1	US-08-470-179-45	Sequence 45, Appl
c 754	13	2.7	251	2	US-08-600-993A-59	Sequence 59, Appl	c 827	13	2.7	432	4	US-08-905-223-134	Sequence 134, App
c 755	13	2.7	257	2	US-08-727-688-6	Sequence 6, Appli	c 828	13	2.7	432	3	US-09-188-930-221	Sequence 221, App
c 756	13	2.7	258	4	US-08-976-259-129	Sequence 129, App	c 829	13	2.7	435	4	US-09-007-119-3	Sequence 3, Appli
c 757	13	2.7	261	2	US-08-245-511-55	Sequence 55, Appl	830	13	2.7	446	2	US-08-796-414B-5	Sequence 5, Appli

C 831	13	2.7	447	3	US-09-358-580-5	Sequence 5, Appli	C 904	13	2.7	658	4	US-09-671-545A-2	Sequence 2, Appli
C 832	13	2.7	450	1	US-08-090-523-28	Sequence 28, Appl	C 905	13	2.7	660	1	US-07-730-853-5	Sequence 5, Appli
C 833	13	2.7	450	1	US-08-398-627-28	Sequence 28, Appl	C 906	13	2.7	660	1	US-08-280-041-5	Sequence 5, Appli
C 834	13	2.7	450	1	US-08-406-857-28	Sequence 2, Appli	C 907	13	2.7	660	2	US-08-726-306A-28	Sequence 28, Appl
C 835	13	2.7	450	1	US-08-596-024-4	Sequence 4, Appli	C 908	13	2.7	661	4	US-09-328-111-54	Sequence 54, Appl
C 836	13	2.7	450	4	US-09-020-818-4	Sequence 4, Appli	C 909	13	2.7	666	4	US-08-896-164-7	Sequence 7, Appli
C 837	13	2.7	450	4	US-08-907-740-4	Sequence 4, Appli	C 910	13	2.7	673	4	US-08-998-416-59	Sequence 59, Appl
C 838	13	2.7	450	5	PCT-US94-07072-2	Sequence 2, Appli	C 911	13	2.7	675	4	US-08-821-994-52	Sequence 52, Appl
C 839	13	2.7	452	4	US-09-123-912-107	Sequence 107, App	C 912	13	2.7	676	4	US-08-998-416-799	Sequence 799, App
C 840	13	2.7	455	6	5278286-1	Patent No. 5278286	C 913	13	2.7	678	2	US-08-951-871-3	Sequence 3, Appli
C 841	13	2.7	459	2	US-08-852-807-19	Sequence 19, Appl	C 914	13	2.7	679	4	US-08-821-994-54	Sequence 54, Appl
C 842	13	2.7	461	3	US-09-058-389A-20	Sequence 20, Appl	C 915	13	2.7	679	4	US-08-998-416-865	Sequence 865, App
C 843	13	2.7	464	4	US-08-098-327E-33	Sequence 33, Appl	C 916	13	2.7	686	4	PCT-US95-15781-4	Sequence 4, Appli
C 844	13	2.7	464	4	US-08-462-625-33	Sequence 33, Appl	C 917	13	2.7	687	5	US-08-840-683-2	Sequence 2, Appli
C 845	13	2.7	472	4	US-09-269-617-2	Sequence 2, Appli	C 918	13	2.7	688	2	US-08-555-722-2	Sequence 2, Appli
C 846	13	2.7	472	4	US-08-943-731-123	Sequence 123, App	C 919	13	2.7	688	4	US-09-384-301-2	Sequence 2, Appli
C 847	13	2.7	473	4	US-08-905-223-112	Sequence 112, App	C 920	13	2.7	690	4	US-09-459-956-2	Sequence 2, Appli
C 848	13	2.7	474	3	US-08-851-843A-81	Sequence 81, Appl	C 921	13	2.7	694	1	US-08-358-171-25	Sequence 25, Appl
C 849	13	2.7	474	4	US-08-974-549A-586	Sequence 586, App	C 922	13	2.7	694	3	US-09-090-947-25	Sequence 25, Appl
C 850	13	2.7	474	4	US-08-854-050-81	Sequence 81, Appl	C 923	13	2.7	694	4	US-09-328-111-616	Sequence 616, App
C 851	13	2.7	474	4	US-09-430-323-81	Sequence 81, Appl	C 924	13	2.7	696	1	US-08-181-271A-11	Sequence 11, Appl
C 852	13	2.7	489	4	US-09-199-637A-430	Sequence 430, App	C 925	13	2.7	696	1	US-08-449-315-11	Sequence 11, Appl
C 853	13	2.7	511	1	US-08-412-614-97	Sequence 97, Appl	C 926	13	2.7	696	1	US-08-449-043-11	Sequence 11, Appl
C 854	13	2.7	511	1	US-08-412-614-98	Sequence 98, Appl	C 927	13	2.7	696	1	US-08-456-265A-11	Sequence 11, Appl
C 855	13	2.7	511	2	US-08-635-761-97	Sequence 97, Appl	C 928	13	2.7	696	1	US-08-455-244-11	Sequence 11, Appl
C 856	13	2.7	511	2	US-08-635-761-98	Sequence 98, Appl	C 929	13	2.7	696	1	US-08-455-244-11	Sequence 11, Appl
C 857	13	2.7	511	4	US-09-312-520-97	Sequence 97, Appl	C 930	13	2.7	696	1	US-08-454-876-11	Sequence 11, Appl
C 858	13	2.7	511	4	US-09-312-520-98	Sequence 98, Appl	C 931	13	2.7	696	2	US-08-457-364-11	Sequence 11, Appl
C 859	13	2.7	515	2	US-08-975-316-42	Sequence 42, Appl	C 932	13	2.7	696	2	US-08-456-262-11	Sequence 11, Appl
C 860	13	2.7	518	1	US-08-485-284A-2	Sequence 2, Appli	C 933	13	2.7	696	2	US-08-456-240-11	Sequence 11, Appl
C 861	13	2.7	520	4	US-09-439-313-388	Sequence 388, App	C 934	13	2.7	696	2	US-08-455-736-11	Sequence 11, Appl
C 862	13	2.7	522	4	US-08-936-165A-12	Sequence 12, Appl	C 935	13	2.7	696	2	US-08-455-736-11	Sequence 11, Appl
C 863	13	2.7	523	1	US-07-865-662F-2	Sequence 2, Appli	C 936	13	2.7	696	2	US-08-971-217-11	Sequence 11, Appl
C 864	13	2.7	523	4	US-08-374-219B-2	Sequence 2, Appli	C 937	13	2.7	697	4	US-09-350-600-11	Sequence 11, Appl
C 865	13	2.7	526	4	US-09-328-111-261	Sequence 261, App	C 938	13	2.7	697	4	US-09-357-251-27	Sequence 27, Appl
C 866	13	2.7	538	1	US-08-525-507-13	Sequence 13, Appl	C 939	13	2.7	702	4	US-09-228-986-61	Sequence 61, Appl
C 867	13	2.7	542	4	US-09-305-639-5	Sequence 5, Appli	C 940	13	2.7	707	4	US-08-896-164-1	Sequence 1, Appli
C 868	13	2.7	547	4	US-09-337-171-15	Sequence 15, Appl	C 941	13	2.7	715	4	US-08-998-416-788	Sequence 788, App
C 869	13	2.7	551	4	US-09-328-111-814	Sequence 814, App	C 942	13	2.7	718	4	US-08-998-416-961	Sequence 961, App
C 870	13	2.7	553	2	US-08-721-488-7	Sequence 7, Appli	C 943	13	2.7	720	2	US-08-722-343-4	Sequence 4, Appli
C 871	13	2.7	554	3	US-08-840-146-16	Sequence 16, Appl	C 944	13	2.7	720	3	US-09-204-328-4	Sequence 4, Appli
C 872	13	2.7	554	3	US-09-360-220-16	Sequence 16, Appl	C 945	13	2.7	720	4	US-08-998-416-789	Sequence 789, App
C 873	13	2.7	571	4	US-08-858-207A-262	Sequence 262, App	C 946	13	2.7	723	1	US-08-338-009B-1	Sequence 1, Appli
C 874	13	2.7	581	4	US-07-671-545A-1	Sequence 1, Appli	C 947	13	2.7	723	1	US-08-597-583-1	Sequence 1, Appli
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C 876	13	2.7	586	4	US-09-001-141-3	Sequence 3, Appli	C 949	13	2.7	723	5	PCT-US95-14717-1	Sequence 1, Appli
C 877	13	2.7	586	4	US-09-328-111-588	Sequence 588, App	C 950	13	2.7	726	4	US-09-039-982A-37	Sequence 37, Appl
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C 880	13	2.7	601	2	US-08-184-009-168	Sequence 168, App	C 953	13	2.7	735	3	US-08-750-145A-23	Sequence 23, Appl
C 881	13	2.7	601	2	US-08-458-356-168	Sequence 168, App	C 954	13	2.7	735	3	US-08-975-698A-27	Sequence 27, Appl
C 882	13	2.7	601	4	US-08-460-736-168	Sequence 168, App	C 955	13	2.7	735	4	US-09-417-090-27	Sequence 27, Appl
C 883	13	2.7	609	4	US-08-460-736-168	Sequence 168, App	C 956	13	2.7	735	4	US-09-727-578-27	Sequence 27, Appl
C 884	13	2.7	612	3	US-08-906-769-146	Sequence 146, App	C 957	13	2.7	738	1	US-08-188-582-23	Sequence 23, Appl
C 885	13	2.7	612	3	US-08-906-769-146	Sequence 146, App	C 958	13	2.7	738	1	US-08-646-715-23	Sequence 23, Appl
C 886	13	2.7	612	3	US-08-639-075A-146	Sequence 146, App	C 959	13	2.7	738	1	US-08-998-416-262	Sequence 262, App
C 887	13	2.7	612	4	US-09-012-431-146	Sequence 146, App	C 960	13	2.7	742	4	US-08-998-416-1028	Sequence 1028, Ap
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C 889	13	2.7	612	4	US-08-906-613-146	Sequence 146, App	C 962	13	2.7	750	3	US-09-167-717-3	Sequence 3, Appli
C 890	13	2.7	619	4	US-08-936-165A-179	Sequence 179, App	C 963	13	2.7	753	1	US-08-328-152A-16	Sequence 16, Appl
C 891	13	2.7	620	4	US-08-858-207A-73	Sequence 73, Appl	C 964	13	2.7	753	4	US-08-466-465-1	Sequence 1, Appli
C 892	13	2.7	622	4	US-09-385-982-184	Sequence 184, App	C 965	13	2.7	754	4	US-09-328-111-447	Sequence 447, App
C 893	13	2.7	628	1	US-08-686-878A-1	Sequence 1, Appli	C 966	13	2.7	764	2	US-08-858-207A-2	Sequence 2, Appli
C 894	13	2.7	628	4	US-09-328-111-55	Sequence 55, Appl	C 967	13	2.7	768	2	US-08-222-719-27	Sequence 27, Appl
C 895	13	2.7	635	4	US-09-328-111-56	Sequence 56, Appl	C 968	13	2.7	768	2	US-08-470-925-27	Sequence 27, Appl
C 896	13	2.7	639	4	US-08-031-295-1	Sequence 1, Appli	C 969	13	2.7	768	2	US-08-471-613-27	Sequence 27, Appl
C 897	13	2.7	639	4	US-07-903-580-1	Sequence 1, Appli	C 970	13	2.7	768	5	PCT-US93-10443-27	Sequence 27, Appl
C 898	13	2.7	642	1	US-08-483-115-67	Sequence 67, Appl	C 971	13	2.7	771	4	US-09-277-716-19	Sequence 19, Appl
C 899	13	2.7	642	1	US-08-465-388-67	Sequence 67, Appl	C 972	13	2.7	775	3	US-08-961-083-89	Sequence 89, Appl
C 900	13	2.7	642	3	US-08-946-026-33	Sequence 33, Appl	C 973	13	2.7	777	4	US-09-007-119-12	Sequence 12, Appl
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ALIGNMENTS

RESULT 1  
US-08-031-399-4  
; Sequence 4, Application US/08031399  
; Patent No. 5552303  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: Epithelium-derived T-cell Factor  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/031.399  
; FILING DATE: 19930308  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Launer, Charlene  
; REGISTRATION NUMBER: 33,035  
; REFERENCE/DOCKET NUMBER: 2811  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-587-0430  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..489

US-08-031-399-4  
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Best Local Similarity 100.0%; Pred. No. 7.le-220; Indels 0; Gaps 0;  
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RESULT 2  
US-08-393-305-1  
; Sequence 1, Application US/08393305  
; Patent No. 5574138  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/393,305  
; FILING DATE: 22-FEB-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:

; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 480052.409C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-622-4900  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..489  
; US-08-393-305-1

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Best Local Similarity 100.0%; Pred. No. 7.1e-220;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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RESULT 3  
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; Sequence 1, Application US/08535733  
; Patent No. 5660824  
; GENERAL INFORMATION:  
; APPLICANT: Quinn, LeBris  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Troutt, Anthony B.  
; TITLE OF INVENTION: Muscle-Trophic Factor  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington

; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: System 7, Word 5.1a  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/535,733  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Malaska, Stephen L.  
; REGISTRATION NUMBER: 32,655  
; REFERENCE/DOCKET NUMBER: 2833  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-587-0430  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..489  
; US-08-535-733-1

Query Match 100.0%; Score 489; DB 1; Length 489;  
Best Local Similarity 100.0%; Pred. No. 7.1e-220;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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RESULT 4  
US-08-726-817-1

; Sequence 1, Application US/08726817  
; Patent No. 5707616  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/726,817  
; FILING DATE: 04-OCT-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/393,305  
; FILING DATE: 22-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 480052.409C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-622-4900  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..489  
US-08-726-817-1

Query Match 100.0%; Score 489; DB 1; Length 489;  
Best Local Similarity 100.0%; Pred. No. 7.le-220;  
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RESULT 5  
US-08-504-042-4  
; Sequence 4, Application US/08504042  
; Patent No. 5747024  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: Epithelium-derived T-cell Factor  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/504,042  
; FILING DATE: 19-JUL-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/031,399  
; FILING DATE: 08-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Launer, Charlene  
; REGISTRATION NUMBER: 33,035  
; REFERENCE/DOCKET NUMBER: 2811  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-587-0430  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
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Query Match 100.0%; Score 489; DB 1; Length 489;  
Best Local Similarity 100.0%; Pred. No. 7.le-220;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 6

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US-08-392-317B-2
; Sequence 2, Application US/08392317B
; Patent No. 5795966
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Paxton, Raymond
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Antagonists of IL-15
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Word for Windows 95, 7.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/392,317B
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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; NAME/KEY: CDS
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US-08-392-317B-2
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Query Match 100.0%; Score 489; DB 1: Length 489;
Best Local Similarity 100.0%; Pred No. 7,le-220;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 ATGAGAAATTTGGAACACATTTGAGAAGTATTTCCATCCAGTCTACTTGTGTTTACTT 60
QY 61 CTAACAGTCATTTCTAACTGAAGCTGGCATTGCTCTTCAATTTGGGCTGTTTCAGT 120
DB 61 CTAACAGTCATTTCTAACTGAAGCTGGCATTGCTCTTCAATTTGGGCTGTTTCAGT 120
QY 121 GCAGGGCTTCTTAAACAGAGCAACTGGGTGAATGTAATAAGTGATTTGAAAAAAT 180
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QY 421 GAAAAAATATTAAAGAAATTTTGGCAGAGTTTGTGTACATATTGTCACAAATGTTTCATCAAC 480
DB 421 GAAAAAATATTAAAGAAATTTTGGCAGAGTTTGTGTACATATTGTCACAAATGTTTCATCAAC 480
QY 481 ACTTCTTTGA 489
DB 481 ACTTCTTTGA 489
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## RESULT 7

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US-08-725-969-1
; Sequence 1, Application US/08725969
; Patent No. 5892001
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Anderson, Dirk
; APPLICANT: Eisenman, June
; APPLICANT: Fung, Victor
; APPLICANT: Rauch, Charles
; TITLE OF INVENTION: EPITHELIIUM-DERIVED T-CELL FACTOR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/725,969
; FILING DATE: 04-OCT-1996
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/393,305
; FILING DATE: 22-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 480052.409C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..489
; US-08-725-969-1

Query Match 100.0%; Score 489; DB 2; Length 489;
Best Local Similarity 100.0%; Pred. No. 7.le-220;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACCCACATTTGAGAAGTATTTCCATCCAGTGCCTACTTGTGTTTACTT 60
Db 1 ATGAGAAATTCGAAACCCACATTTGAGAAGTATTTCCATCCAGTGCCTACTTGTGTTTACTT 60
QY 61 CTAACAGTCATTTTCTAACTGAAGTGGCATTTCATGCTCTTCTTCAATTTTGGGCTGTTTCAGT 120
Db 61 CTAACAGTCATTTTCTAACTGAAGTGGCATTTCATGCTCTTCTTCAATTTTGGGCTGTTTCAGT 120
QY 121 GCAGGGCTTCCTAAACAGAGCCAACTGGTGAATGTAATAAGTATTTGAAAAAAATTT 180
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Db 361 AGTTTGTCTTCTAATGGGAATGTAACAGATCTGGATGCAAAAGTGTGAGGAACCTGGAG 420
QY 421 GAAAAAATATTAAGAATTTTTCGAGAGTTTGTGCATATTTGCCAATATTTGCCAATATTTTCAATCAAC 480
Db 421 GAAAAAATATTAAGAATTTTTCGAGAGTTTGTGCATATTTGCCAATATTTTCAATCAAC 480
QY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489

RESULT 8
US-08-794-524-1
; Sequence 1, Application US/08794524
; Patent No. 5985262
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Anderson, Dirk
; APPLICANT: Eisenman, June
; APPLICANT: Fung, Victor
; APPLICANT: Rauch, Charles
```

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; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/794,524
; FILING DATE: 03-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/393,305
; FILING DATE: 22-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 480052.409C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..489
; US-08-794-524-1
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Query Match 100.0%; Score 489; DB 2; Length 489;
Best Local Similarity 100.0%; Pred. No. 7.le-220;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACCCACATTTGAGAAGTATTTCCATCCAGTGCCTACTTGTGTTTACTT 60
Db 1 ATGAGAAATTCGAAACCCACATTTGAGAAGTATTTCCATCCAGTGCCTACTTGTGTTTACTT 60
QY 61 CTAACAGTCATTTTCTAACTGAAGTGGCATTTCATGCTCTTCTTCAATTTTGGGCTGTTTCAGT 120
Db 61 CTAACAGTCATTTTCTAACTGAAGTGGCATTTCATGCTCTTCTTCAATTTTGGGCTGTTTCAGT 120
QY 121 GCAGGGCTTCCTAAACAGAGCCAACTGGTGAATGTAATAAGTATTTGAAAAAAATTT 180
Db 121 GCAGGGCTTCCTAAACAGAGCCAACTGGTGAATGTAATAAGTATTTGAAAAAAATTT 180
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QY 241 CCAGGTGCAAAAGTAAACAGCAATTTGAGAGTGTCTTCTCTGGAGTTACAAGTTATTTTCACTT 300
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QY 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAGAAAATCTGATCATCTCCCTAGCAACAAC 360
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QY 361 AGTTTGTCTTCTAATGGGAATGTAACAGATCTGGATGCAAAAGTGTGAGGAACCTGGAG 420
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Db 421 GAAAAAATATTAAAGAATTTTTCGAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480  
QY 481 ACTTCTTGA 489  
Db 481 ACTTCTTGA 489  
RESULT 9  
US-09-134-132-2  
; Sequence 2, Application US/09134132  
; Patent No. 6013480  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Paxton, Raymond  
; APPLICANT: Pettit, Dean  
; TITLE OF INVENTION: Antagonists of IL-15  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: Word for Windows 95, 7.0  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/134,132  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/392,317  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Malaska, Stephen L.  
; REGISTRATION NUMBER: 32,655  
; REFERENCE/DOCKET NUMBER: 2831  
; TELEPHONE: 206-587-0430  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..489  
US-09-134-132-2  
Query Match 100.0%; Score 489; DB 3; Length 489;  
Best Local Similarity 100.0%; Pred. No. 7.1e-220;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGAGAATTCGAAACACATTGTGAGAAGTATTTCATCCAGTGCCTACTTTGGCTGTTTCAGT 60  
Db 1 ATGAGAATTCGAAACACATTGTGAGAAGTATTTCATCCAGTGCCTACTTTGGCTGTTTCAGT 60  
QY 61 CTAACAGTCATTTCTTAAGTCGATGCGATTCATGCTTCAATTTGGCTGTTTCAGT 120  
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QY 121 GCAGGGCTTCCTAAAACAGAAGCAACTGGTGAATGTAATAGTCATTTGAAAAAAT 180  
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Db 181 GAAGATCTTATTCAATCTATGCAATATTGATGCTACTTTTATATACGGAAGTGTTCAC 240  
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QY 301 GAGTCCGGAGATGCAAGTATTTCATGATACAGTAGAAAAATCTGATCATCTAGCAAAACAC 360  
Db 301 GAGTCCGGAGATGCAAGTATTTCATGATACAGTAGAAAAATCTGATCATCTAGCAAAACAC 360  
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QY 421 GAAAAAATATTAAAGAATTTTTCGAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480  
Db 421 GAAAAAATATTAAAGAATTTTTCGAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480  
QY 481 ACTTCTTGA 489  
Db 481 ACTTCTTGA 489  
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US-09-134-134A-2  
; Sequence 2, Application US/09134134A  
; Patent No. 6165466  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Paxton, Raymond  
; APPLICANT: Pettit, Dean  
; TITLE OF INVENTION: Antagonists of IL-15  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: Word for Windows 95, 7.0  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/134,134A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/392,317  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Malaska, Stephen L.  
; REGISTRATION NUMBER: 32,655  
; REFERENCE/DOCKET NUMBER: 2831  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-587-0430  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..489  
US-09-134-134A-2  
Query Match 100.0%; Score 489; DB 4; Length 489;  
Best Local Similarity 100.0%; Pred. No. 7.1e-220;

Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAAATTCGAAACCCACATTTGAGAAGTATTTCCATCCAGTCTACTTGTGTTTACTT 60  
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Db 1 ATGAGAAATTCGAAACCCACATTTGAGAAGTATTTCCATCCAGTCTACTTGTGTTTACTT 60

Qy 61 CTAACAGCTCAATTTCTTAAGTGAAGCTGGCATTCATGCTCTTCAATTTTGGGCTGTTTCAGT 120  
|||||  
Db 61 CTAACAGCTCAATTTCTTAAGTGAAGCTGGCATTCATGCTCTTCAATTTTGGGCTGTTTCAGT 120

Qy 121 GCAGGCTTCCTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTT 180  
|||||  
Db 121 GCAGGCTTCCTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTT 180

Qy 181 GAAGATCTTATTAATCAATCTATGTCATATTCATGCTACTTTATATACGGAAGTGATTTCCAC 240  
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Db 181 GAAGATCTTATTAATCAATCTATGTCATATTCATGCTACTTTATATACGGAAGTGATTTCCAC 240

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Db 241 CCCAGTTGCAAGATTAACAGCAATGAAGTGCTTTCTCTTGGAGTTACAAGTTATTTCACTT 300

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Db 301 GAGTCCGAGATGCAAGTATTCATCATACAGTAGAATACTGATCATCTTAGCAAAACAAC 360

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Db 361 AGTTGTCTTCTTAATGGAATGTAACAGAACTCGGATGCAAAAGATGTGAGGAACCTGGAG 420

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Db 421 GAAAAAATATTAAGAATTTTTCAGAGTTTGTGACATATTTGTCACATATTTGTCACAACTGATCAAC 480

Qy 481 ACTTCTTGA 489  
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Db 481 ACTTCTTGA 489

RESULT 11  
US-09-134-456-2  
; Sequence 2, Application US/09134456  
; Patent No. 6168783  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Faxton, Raymond  
; APPLICANT: Pettit, Dean  
; TITLE OF INVENTION: Antagonists of IL-15  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: Word for Windows 95, 7.0  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/134,456  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/392,317  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Malaska, Stephen L.  
; REGISTRATION NUMBER: 32,655  
; REFERENCE/DOCKET NUMBER: 2831  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-587-0430  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; - NAME/KEY: CDS  
; LOCATION: 1..489  
; US-09-134-456-2

Query Match 100.0%; Score 489; DB 4; Length 489;  
Best Local Similarity 100.0%; Pred. No. 7.1e-220;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAAATTCGAAACCCACATTTGAGAAGTATTTCCATCCAGTCTACTTGTGTTTACTT 60  
Db 1 ATGAGAAATTCGAAACCCACATTTGAGAAGTATTTCCATCCAGTCTACTTGTGTTTACTT 60

Qy 61 CTAACAGCTCAATTTCTTAAGTGAAGCTGGCATTCATGCTCTTCAATTTTGGGCTGTTTCAGT 120  
Db 61 CTAACAGCTCAATTTCTTAAGTGAAGCTGGCATTCATGCTCTTCAATTTTGGGCTGTTTCAGT 120

Qy 121 GCAGGCTTCCTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTT 180  
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Qy 181 GAAGATCTTATTAATCAATCTATGTCATATTCATGCTACTTTATATACGGAAGTGATTTCCAC 240  
Db 181 GAAGATCTTATTAATCAATCTATGTCATATTCATGCTACTTTATATACGGAAGTGATTTCCAC 240

Qy 241 CCCAGTTGCAAGATTAACAGCAATGAAGTGCTTTCTCTTGGAGTTACAAGTTATTTCACTT 300  
Db 241 CCCAGTTGCAAGATTAACAGCAATGAAGTGCTTTCTCTTGGAGTTACAAGTTATTTCACTT 300

Qy 301 GAGTCCGAGATGCAAGTATTCATGATACAGTAGAATACTGATCATCTTAGCAAAACAAC 360  
Db 301 GAGTCCGAGATGCAAGTATTCATGATACAGTAGAATACTGATCATCTTAGCAAAACAAC 360

Qy 361 AGTTGTCTTCTTAATGGAATGTAACAGAACTCGGATGCAAAAGATGTGAGGAACCTGGAG 420  
Db 361 AGTTGTCTTCTTAATGGAATGTAACAGAACTCGGATGCAAAAGATGTGAGGAACCTGGAG 420

Qy 421 GAAAAAATATTAAGAATTTTTCAGAGTTTGTGACATATTTGTCACATATTTGTCACAACTGATCAAC 480  
Db 421 GAAAAAATATTAAGAATTTTTCAGAGTTTGTGACATATTTGTCACATATTTGTCACAACTGATCAAC 480

Qy 481 ACTTCTTGA 489  
Db 481 ACTTCTTGA 489

RESULT 12  
US-09-196-427-2  
; Sequence 2, Application US/09196427  
; Patent No. 6177079  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Paxton, Raymond  
; APPLICANT: Pettit, Dean  
; TITLE OF INVENTION: Antagonists of IL-15  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: Word for Windows 95, 7.0  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: US/09/196.427  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/392,317  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2831  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0430  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..489  
US-09-196-427-2

Query Match 100.0%; Score 489; DB 4; Length 489;  
Best Local Similarity 100.0%; Pred. No. 7.le-220;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGAGAAATTCGAAACCCACATTTGAGAAGTATTTCCATCCAGTGTACTTGTGTTACTT 60  
Db 1 ATGAGAAATTCGAAACCCACATTTGAGAAGTATTTCCATCCAGTGTACTTGTGTTACTT 60  
Qy 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTTCTTCAATTTGGGCTGTTTCAGT 120  
Db 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTTCTTCAATTTGGGCTGTTTCAGT 120  
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Db 361 AGTTTGCTTCTTAATGGGAATGTACAGAACTCGATGATCAAGAAATGTGAGAACTGGAG 420  
Qy 421 GAAAAAATATTAAGAAATTTTTCAGAGTGTTCGAGATTTTGTACATATTTGCCAAATCTTCATCAC 480  
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Db 481 ACTTCTTGA 489

RESULT 13  
US-09-189-193-1

; Sequence 1, Application US/09189193  
; Patent No. 6184359  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/189,193  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/393,305  
; FILING DATE: 22-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 480052.409C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-622-4900  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..489  
; US-09-189-193-1

Query Match 100.0%; Score 489; DB 4; Length 489;  
Best Local Similarity 100.0%; Pred. No. 7.le-220;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGAGAAATTCGAAACCCACATTTGAGAAGTATTTCCATCCAGTGTACTTGTGTTACTT 60  
Db 1 ATGAGAAATTCGAAACCCACATTTGAGAAGTATTTCCATCCAGTGTACTTGTGTTACTT 60  
Qy 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTTCTTCAATTTGGGCTGTTTCAGT 120  
Db 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTTCTTCAATTTGGGCTGTTTCAGT 120  
Qy 121 GCAGGGCTTCCTAAACAGAGCCCAACTGGGTGAATGTAATAGTGATTTGAAAAAATTT 180  
Db 121 GCAGGGCTTCCTAAACAGAGAGCCCAACTGGGTGAATGTAATAGTGATTTGAAAAAATTT 180  
Qy 181 GAAGATCTTATTCATCTATGCATATTTGATGCTACTTTATATACGGAAGTGTTCAC 240  
Db 181 GAAGATCTTATTCATCTATGCATATTTGATGCTACTTTATATACGGAAGTGTTCAC 240  
Qy 241 CCCAGTTCGAAAGTGAAGTATTCATGATACAGTAGAATACTGATCATCTAGCAAAACAC 300  
Db 241 CCCAGTTCGAAAGTGAAGTATTCATGATACAGTAGAATACTGATCATCTAGCAAAACAC 300  
Qy 301 GAGTCCGAGATGCAAGTATTCATGATACAGTAGAATACTGATCATCTAGCAAAACAC 360  
Db 301 GAGTCCGAGATGCAAGTATTCATGATACAGTAGAATACTGATCATCTAGCAAAACAC 360

Db 301 GAGTCCGGAGATGCAAGTATTTCATGATACAGTAGAGAAATCTGATCATCTCTAGCAAAACAC 360  
Qy 361 AGTTTGCTCTTAATGGAATGTAACAGAACTGGATGCAAGAAATGTGAGGAACCTGGAG 420  
Db 361 AGTTTGCTCTTAATGGAATGTAACAGAACTGGATGCAAGAAATGTGAGGAACCTGGAG 420  
Qy 421 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTTCATCAAC 480  
Db 421 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTTCATCAAC 480  
Qy 481 ACTTCTTGA 489  
Db 481 ACTTCTTGA 489

RESULT 14  
PCT-US94-03793-4  
; Sequence 4, Application PC/TUS9403793  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: Interleukin-15  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/03793  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Launer, Charlene  
; REGISTRATION NUMBER: 33,035  
; REFERENCE/DOCKET NUMBER: 2811  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-587-0430  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..489  
PCT-US94-03793-4

Query Match 100.0%; Score 489; DB 5; Length 489;  
Best Local Similarity 100.0%; Pred. No. 7.le-220;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAAATTCGAAACACATTTGAGAGATATTTCCATCCAGTCTACTGTGTTTACTTT 60  
Db 1 ATGAGAAATTCGAAACACATTTGAGAGATATTTCCATCCAGTCTACTGTGTTTACTTT 60  
Qy 61 CTAACAGTCATTTCTACTGAAGCTGGCATTCATGTCTTCATTTGGGCTGTTTCAGT 120  
Db 61 CTAACAGTCATTTCTACTGAAGCTGGCATTCATGTCTTCATTTGGGCTGTTTCAGT 120

Qy 121 GCAGGGCTTCTCTAAACAGAACCCCAACTGGGTGAATGTAAATAGTGATTTGAAAAAAATTT 180  
Db 121 GCAGGGCTTCTCTAAACAGAACCCCAACTGGGTGAATGTAAATAGTGATTTGAAAAAAATTT 180  
Qy 181 GAAATCTTATTCAATCTATGCATATTCATGCTACTTTATATACGGAAGTGATGTTTCAC 240  
Db 181 GAAATCTTATTCAATCTATGCATATTCATGCTACTTTATATACGGAAGTGATGTTTCAC 240  
Qy 241 CCCAGTTTCAAGTAACAGCAATGAAGTCTTCTCTTGGAGTTTACAAGTTTATTTCACCTT 300  
Db 241 CCCAGTTTCAAGTAACAGCAATGAAGTCTTCTCTTGGAGTTTACAAGTTTATTTCACCTT 300  
Qy 301 GAGTCCGGAGATGCAAGTATTTCATGATACAGTAGAAAACTGATCATCTCTAGCAAAACAC 360  
Db 301 GAGTCCGGAGATGCAAGTATTTCATGATACAGTAGAAAACTGATCATCTCTAGCAAAACAC 360  
Qy 361 AGTTTGCTCTTAATGGAATGTAACAGAACTGGATGCAAGAAATGTGAGGAACCTGGAG 420  
Db 361 AGTTTGCTCTTAATGGAATGTAACAGAACTGGATGCAAGAAATGTGAGGAACCTGGAG 420  
Qy 421 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTTCATCAAC 480  
Db 421 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTTCATCAAC 480  
Qy 481 ACTTCTTGA 489  
Db 481 ACTTCTTGA 489

RESULT 15  
PCT-US96-06423-1  
; Sequence 1, Application PC/TUS9606423  
; GENERAL INFORMATION:  
; APPLICANT: Immunex Corporation  
; TITLE OF INVENTION: Muscle Trophic Factor  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: System 7, Word 6.0  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/06423  
; FILING DATE: 07 May 1996  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Malaska, Stephen L.  
; REGISTRATION NUMBER: 32,655  
; REFERENCE/DOCKET NUMBER: 2833-WO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-587-0430  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..489  
PCT-US96-06423-1

Query Match 100.0%; Score 489; DB 5; Length 489;  
Best Local Similarity 100.0%; Pred. No. 7.le-220;

Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTTCGAAACACATTTGAGAGTATTTCCATCCAGTGCCTACTGTGTTTACTT 60  
 Db 1 ATGAGATTTTCGAAACACATTTGAGAGTATTTCCATCCAGTGCCTACTGTGTTTACTT 60

QY 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTTCTCAATTTGGCTGTTTCACT 120  
 Db 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTTCTCAATTTGGCTGTTTCACT 120

QY 121 GCAGGCTTCTTAAACAGAGCCAACTGGGTGAATGTAATAGTGAATTTGAAAAAATT 180  
 Db 121 GCAGGCTTCTTAAACAGAGCCAACTGGGTGAATGTAATAGTGAATTTGAAAAAATT 180

QY 181 GAAGATCTTATCAATCTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
 Db 181 GAAGATCTTATCAATCTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240

QY 241 CCCAGTTGCAAGTACAGCAATGAAGTCTTCTTCTTGGAGTTACAAGTTATTTTCACTT 300  
 Db 241 CCCAGTTGCAAGTACAGCAATGAAGTCTTCTTCTTGGAGTTACAAGTTATTTTCACTT 300

QY 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTACAGTACAGTACAGTACAGTACAGTAC 360  
 Db 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTACAGTACAGTACAGTACAGTACAGTAC 360

QY 361 AGTTGTCTTCTAAATGGGAATGTAACAGCAATGAGTCTTCTTCTTGGAGTTACAAGTTATTTTCACTT 420  
 Db 361 AGTTGTCTTCTAAATGGGAATGTAACAGCAATGAGTCTTCTTCTTGGAGTTACAAGTTATTTTCACTT 420

QY 421 GAAAAAATATTAAGAATTTTGGAGTATTTTGGAGTATTTTGGAGTATTTTGGAGTATTTTGGAG 480  
 Db 421 GAAAAAATATTAAGAATTTTGGAGTATTTTGGAGTATTTTGGAGTATTTTGGAGTATTTTGGAG 480

QY 481 ACTTCTTGA 489  
 Db 481 ACTTCTTGA 489

RESULT 16

US-08-962-503-11

; Sequence 11, Application US/08962503

; Patent No. 6087172

; GENERAL INFORMATION:

; APPLICANT: Veerapaneni, Dange

; APPLICANT: Hamaoka, Shoji

; APPLICANT: No. 6087172awa, Iwao

; TITLE OF INVENTION: RIBOZYMES TARGETED TO IL-15 MRNA

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 4225 Executive Square, Suite 1400

; CITY: La Jolla

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: FastSeq for Windows Version 2.0b

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/962,503

; FILING DATE: 31-OCT-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Halle, Ph.D., Lisa A

; REGISTRATION NUMBER: 38,347

; REFERENCE/DOCKET NUMBER: 09326/002001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619/678-5070

; TELEFAX: 619/678-5099

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1202 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

US-08-962-503-11

Query Match

Best Local Similarity 100.0%; Score 489; DB 3; Length 1202;

Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTTCGAAACACATTTGAGAGTATTTCCATCCAGTGCCTACTGTGTTTACTT 60  
 Db 317 ATGAGATTTTCGAAACACATTTGAGAGTATTTCCATCCAGTGCCTACTGTGTTTACTT 376

QY 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTTCTCAATTTGGCTGTTTCACT 120  
 Db 377 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTTCTCAATTTGGCTGTTTCACT 436

QY 121 GCAGGCTTCTTAAACAGAGCCAACTGGGTGAATGTAATAGTGAATTTGAAAAAATT 180  
 Db 437 GCAGGCTTCTTAAACAGAGCCAACTGGGTGAATGTAATAGTGAATTTGAAAAAATT 496

QY 181 GAAGATCTTATCAATCTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
 Db 497 GAAGATCTTATCAATCTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 556

QY 241 CCCAGTTGCAAGTACAGCAATGAAGTCTTCTTCTTGGAGTTACAAGTTATTTTCACTT 300  
 Db 557 CCCAGTTGCAAGTACAGCAATGAAGTCTTCTTCTTGGAGTTACAAGTTATTTTCACTT 616

QY 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTACAGTACAGTACAGTACAGTACAGTAC 360  
 Db 617 GAGTCCGGAGATGCAAGTATTCATGATACAGTACAGTACAGTACAGTACAGTACAGTAC 676

QY 361 AGTTGTCTTCTAAATGGGAATGTAACAGCAATGAGTCTTCTTCTTGGAGTTACAAGTTATTTTCACTT 420  
 Db 677 AGTTGTCTTCTAAATGGGAATGTAACAGCAATGAGTCTTCTTCTTGGAGTTACAAGTTATTTTCACTT 736

QY 421 GAAAAAATATTAAGAATTTTGGAGTATTTTGGAGTATTTTGGAGTATTTTGGAGTATTTTGGAG 480  
 Db 737 GAAAAAATATTAAGAATTTTGGAGTATTTTGGAGTATTTTGGAGTATTTTGGAGTATTTTGGAG 796

QY 481 ACTTCTTGA 489  
 Db 797 ACTTCTTGA 805

RESULT 17

US-08-842-947-5

; Sequence 5, Application US/08842947

; Patent No. 6001973

; GENERAL INFORMATION:

; APPLICANT: Strom, Terry B.

; APPLICANT: Maslinski, Wlodzimierz

; TITLE OF INVENTION: ANTAGONISTS OF INTERLEUKIN-15

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/842,947

; FILING DATE: 25-APR-1997

CLASSIFICATION: 432  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/016,634  
FILING DATE: 26-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 01948/039001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...486  
OTHER INFORMATION:  
US-08-842-947-5

Query Match 89.6%; Score 438; DB 3; Length 489;  
Best Local Similarity 99.8%; Pred. No. 5e-196;  
Matches 488; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGAATTCGAAACCCACATTTGAGAAGTATTTCCATCCAGTGTCTACTTGTGTTTACTT 60  
DB 1 ATGAGAATTCGAAACCCACATTTGAGAAGTATTTCCATCCAGTGTCTACTTGTGTTTACTT 60  
QY 61 CTAACAGTCATTTCTTAAGCTGCAATGCGATTCATGCTTCTTCAATTTTGGGCTGTTTCAGT 120  
DB 61 CTAACAGTCATTTCTTAAGCTGCAATGCGATTCATGCTTCTTCAATTTTGGGCTGTTTCAGT 120  
QY 121 GCAGGGCTTCCTAAACAGAGCCCAACTGGGTGAATGTAATAGTCAATTTGAAAAAAATTT 180  
DB 121 GCAGGGCTTCCTAAACAGAGCCCAACTGGGTGAATGTAATAGTCAATTTGAAAAAAATTT 180  
QY 181 GAAGATCTTATTCATCTATGATATTTGATGCTATTTATATACGGAAGTGTATTCAC 240  
DB 181 GAAGATCTTATTCATCTATGATATTTGATGCTATTTATATACGGAAGTGTATTCAC 240  
QY 241 CCAGTTCGCAAGTGAATGTAACAGATCTGGATGCAAGAAATGTCAGGAACGTGGAG 420  
DB 241 CCAGTTCGCAAGTGAATGTAACAGATCTGGATGCAAGAAATGTCAGGAACGTGGAG 420  
QY 421 GAAAAAATATTAAGAAATTTTTCAGAGATTTTGTACATATTTGTACATATTTGTCCAAATGTTTCATCAAC 480  
DB 421 GAAAAAATATTAAGAAATTTTTCAGAGATTTTGTACATATTTGTCCAAATGTTTCATCAAC 480  
QY 481 ACTTCTTGA 489  
DB 481 ACTTCTTGA 489

RESULT 18  
US-08-842-947-7  
Sequence 7, Application US/08842947  
Patent No. 6001973  
GENERAL INFORMATION:  
APPLICANT: Strom, Terry B.  
APPLICANT: Maslowski, Wlodzimierz  
TITLE OF INVENTION: ANTAGONISTS OF INTERLEUKIN-15

NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/842,947  
FILING DATE: 25-APR-1997  
CLASSIFICATION: 432  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/016,634  
FILING DATE: 26-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 01948/039001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...486  
OTHER INFORMATION:  
US-08-842-947-7

Query Match 80.4%; Score 393; DB 3; Length 489;  
Best Local Similarity 99.8%; Pred. No. 5.5e-175;  
Matches 443; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGAATTCGAAACCCACATTTGAGAAGTATTTCCATCCAGTGTCTACTTGTGTTTACTT 60  
DB 1 ATGAGAATTCGAAACCCACATTTGAGAAGTATTTCCATCCAGTGTCTACTTGTGTTTACTT 60  
QY 61 CTAACAGTCATTTCTTAAGCTGCAATGCGATTCATGCTTCTTCAATTTTGGGCTGTTTCAGT 120  
DB 61 CTAACAGTCATTTCTTAAGCTGCAATGCGATTCATGCTTCTTCAATTTTGGGCTGTTTCAGT 120  
QY 121 GCAGGGCTTCCTAAACAGAGCCCAACTGGGTGAATGTAATAGTCAATTTGAAAAAAATTT 180  
DB 121 GCAGGGCTTCCTAAACAGAGCCCAACTGGGTGAATGTAATAGTCAATTTGAAAAAAATTT 180  
QY 181 GAAGATCTTATTCATCTATGATATTTGATGCTATTTATATACGGAAGTGTATTCAC 240  
DB 181 GAAGATCTTATTCATCTATGATATTTGATGCTATTTATATACGGAAGTGTATTCAC 240  
QY 241 CCAGTTCGCAAGTGAATGTAACAGATCTGGATGCAAGAAATGTCAGGAACGTGGAG 420  
DB 241 CCAGTTCGCAAGTGAATGTAACAGATCTGGATGCAAGAAATGTCAGGAACGTGGAG 420  
QY 421 GAAAAAATATTAAGAAATTTTTCAGAGATTTTGTACATATTTGTCCAAATGTTTCATCAAC 480  
DB 421 GAAAAAATATTAAGAAATTTTTCAGAGATTTTGTACATATTTGTCCAAATGTTTCATCAAC 480  
QY 481 ACTTCTTGA 489  
DB 481 ACTTCTTGA 489

RESULT 18  
US-08-842-947-7  
Sequence 7, Application US/08842947  
Patent No. 6001973  
GENERAL INFORMATION:  
APPLICANT: Strom, Terry B.  
APPLICANT: Maslowski, Wlodzimierz  
TITLE OF INVENTION: ANTAGONISTS OF INTERLEUKIN-15

Db 421 GAAAAAATATTAAAGAAATTTTG 444  
|||||

RESULT 19  
US-08-393-305-12  
; Sequence 12, Application US/08393305  
; Patent No. 5574138  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: 22-FEB-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 480052.409C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-622-4900  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 345 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..345  
; US-08-393-305-12

Query Match 70.6%; Score 345; DB 1; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1.6e-152;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTTGAAGATCTTATTCAATCTATGCAT 204  
|||||  
Db 1 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTTGAAGATCTTATTCAATCTATGCAT 60  
QY 205 ATTGATGCTACTTTATATACGGAAAGTGTTCACCCCGAGTTGCAAGTAACAGCAATG 264  
|||||  
Db 61 ATTGATGCTACTTTATATACGGAAAGTGTTCACCCCGAGTTGCAAGTAACAGCAATG 120  
QY 265 AAGTGTCTTCTCTGTGGAGTTACAAAGTATTTCACCTTGAGTCCGAGATGCAAGTATTCAT 324  
|||||  
Db 121 AAGTGTCTTCTCTGTGGAGTTACAAAGTATTTCACCTTGAGTCCGAGATGCAAGTATTCAT 180  
QY 325 GATACAGTAGAAAACTGATCATCTAGCAACAACAGATTTGTCTTCTTAATGGGAATGTA 384  
|||||  
Db 181 GATACAGTAGAAAACTGATCATCTAGCAACAACAGATTTGTCTTCTTAATGGGAATGTA 240  
QY 385 ACAGAACTCTGGATGCAAGAAATGTGAGGAAGTGGAGGAAAAAATAATTAAGAAATTTTG 444  
|||||  
Db 241 ACAGAACTCTGGATGCAAGAAATGTGAGGAAGTGGAGGAAAAAATAATTAAGAAATTTTG 300  
|||||

QY 445 CAGAGTTTGTACATATGTCCAAATGTTTCATCAACACTTCTTGA 489  
|||||  
Db 301 CAGAGTTTGTACATATGTCCAAATGTTTCATCAACACTTCTTGA 345  
|||||

RESULT 20  
US-08-726-817-12  
; Sequence 12, Application US/08726817  
; Patent No. 5707616  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/726,817  
; FILING DATE: 04-OCT-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/393,305  
; FILING DATE: 22-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 480052.409C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-622-4900  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 345 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..345  
; US-08-726-817-12

Query Match 70.6%; Score 345; DB 1; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1.6e-152;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTTGAAGATCTTATTCAATCTATGCAT 204  
|||||  
Db 1 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTTGAAGATCTTATTCAATCTATGCAT 60  
QY 205 ATTGATGCTACTTTATATACGGAAAGTGTTCACCCCGAGTTGCAAGTAACAGCAATG 264  
|||||  
Db 61 ATTGATGCTACTTTATATACGGAAAGTGTTCACCCCGAGTTGCAAGTAACAGCAATG 120  
QY 265 AAGTGTCTTCTCTGTGGAGTTACAAAGTATTTCACCTTGAGTCCGAGATGCAAGTATTCAT 324  
|||||  
Db 121 AAGTGTCTTCTCTGTGGAGTTACAAAGTATTTCACCTTGAGTCCGAGATGCAAGTATTCAT 180  
QY 325 GATACAGTAGAAAACTGATCATCTAGCAACAACAGATTTGTCTTCTTAATGGGAATGTA 384  
|||||

Db 181 GATACAGTAGAAAATCTGATCATCTCTAGCAACAACACAGTTTGTCTCTTAATGGGAATGTA 240  
QY 385 ACAGAACTCTGGATGCAAAAGAAATGTGAGAACTGGAGGAAAAAATATTAAAGAAATTTTG 444  
Db 241 ACAGAACTCTGGATGCAAAAGAAATGTGAGAACTGGAGGAAAAAATATTAAAGAAATTTTG 300  
QY 445 ACAGATTTTGTACATATCTCCAAATGTTTCATCAACACTTCTTGA 489  
Db 301 CAGAGTTTGTACATATCTCCAAATGTTTCATCAACACTTCTTGA 345

RESULT 21  
US-08-725-969-12  
; Sequence 12, Application US/08725969  
; Patent No. 5892001  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/725,969  
; FILING DATE: 04-OCT-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/393,305  
; FILING DATE: 22-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mcmasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 480052.409C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-622-4900  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 345 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..345  
US-08-725-969-12

Query Match 70.6%; Score 345; DB 2; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1.6e-152;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTTGAAGATCTTATTCAATCTATGCAT 204  
Db 1 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTTGAAGATCTTATTCAATCTATGCAT 60  
QY 205 ATTGATGCTACTTTATATACGGAAGTGAATGTTTCACCCAGTTGCAAAAGTACACGAATG 264  
Db 61 ATTGATGCTACTTTATATACGGAAGTGAATGTTTCACCCAGTTGCAAAAGTACACGAATG 120  
QY 265 AAGTGTCTTCTCTTGGAGTTACAAGTTATTTCACTTGAGTCCGAGATGCAAGTATTCAT 324

Db 121 AAGTGTCTTCTCTTGGAGTTACAAGTTATTTCACTTTGAGTCCGAGATGCAAGTATTCAT 180  
QY 325 GATACAGTAGAAAATCTGATCATCTCTAGCAACAACACAGTTTGTCTCTTAATGGGAATGTA 384  
Db 181 GATACAGTAGAAAATCTGATCATCTCTAGCAACAACACAGTTTGTCTCTTAATGGGAATGTA 240  
QY 385 ACAGAACTCTGGATGCAAAAGAAATGTGAGAACTGGAGGAAAAAATATTAAAGAAATTTTG 444  
Db 241 ACAGAACTCTGGATGCAAAAGAAATGTGAGAACTGGAGGAAAAAATATTAAAGAAATTTTG 300  
QY 445 CAGAGTTTGTACATATCTCCAAATGTTTCATCAACACTTCTTGA 489  
Db 301 CAGAGTTTGTACATATCTCCAAATGTTTCATCAACACTTCTTGA 345

RESULT 22  
US-08-794-524-12  
; Sequence 12, Application US/08794524  
; Patent No. 5985262  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/794,524  
; FILING DATE: 03-FEB-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/393,305  
; FILING DATE: 22-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mcmasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 480052.409C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-622-4900  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 345 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..345  
US-08-794-524-12

Query Match 70.6%; Score 345; DB 2; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1.6e-152;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTTGAAGATCTTATTCAATCTATGCAT 204  
Db 1 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTTGAAGATCTTATTCAATCTATGCAT 60

QY 205 ATTGATCTACTTTATATACGGAAGTGATGTTTACACCCAGTTGCAAAAGTAACAGCAATG 264  
|||||  
Db 61 ATTGATCTACTTTATATACGGAAGTGATGTTTACACCCAGTTGCAAAAGTAACAGCAATG 120  
QY 265 AAGTGCCTTCTCTTGGAGTTACAAGTTATTTCACCTTGAGTCCGAGATGCAAGTATTTCAT 324  
|||||  
Db 121 AAGTGCCTTCTCTTGGAGTTACAAGTTATTTCACCTTGAGTCCGAGATGCAAGTATTTCAT 180  
QY 325 GATACAGTAGAAAATCTGATCATCTAGCAAAACAACAGTTTGTCTTCTTAATGGGAATGTA 384  
|||||  
Db 181 GATACAGTAGAAAATCTGATCATCTAGCAAAACAACAGTTTGTCTTCTTAATGGGAATGTA 240  
QY 385 ACAGAACTCTGGATGCAAAAGTAATGTGAGAACTGGAGGAAAAAATAATTAAGAATTTTTG 444  
|||||  
Db 241 ACAGAACTCTGGATGCAAAAGTAATGTGAGAACTGGAGGAAAAAATAATTAAGAATTTTTG 300  
QY 445 CAGAGTTTTGTACATATGTCCTCAAAATGTTTCATCAACACTTCTTGA 489  
|||||  
Db 301 CAGAGTTTTGTACATATGTCCTCAAAATGTTTCATCAACACTTCTTGA 345

RESULT 23  
US-09-189-193-12  
; Sequence 12, Application US/09189193  
; Patent No. 6184359  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/189,193  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/393,305  
; FILING DATE: 22-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McWaters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 480052.409C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-622-4900  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 345 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..345  
US-09-189-193-12

Query Match 70.6%; Score 345; DB 4; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1.6e-152;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 AACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGATCTTATTCAATCTATGCAT 204  
|||||  
Db 1 AACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGATCTTATTCAATCTATGCAT 60  
QY 205 ATTGATCTACTTTATATACGGAAGTGATGTTTACACCCAGTTGCAAAAGTAACAGCAATG 264  
|||||  
Db 61 ATTGATCTACTTTATATACGGAAGTGATGTTTACACCCAGTTGCAAAAGTAACAGCAATG 120  
QY 265 AAGTGCCTTCTCTTGGAGTTACAAGTTATTTCACCTTGAGTCCGAGATGCAAGTATTTCAT 324  
|||||  
Db 121 AAGTGCCTTCTCTTGGAGTTACAAGTTATTTCACCTTGAGTCCGAGATGCAAGTATTTCAT 180  
QY 325 GATACAGTAGAAAATCTGATCATCTAGCAAAACAACAGTTTGTCTTCTTAATGGGAATGTA 384  
|||||  
Db 181 GATACAGTAGAAAATCTGATCATCTAGCAAAACAACAGTTTGTCTTCTTAATGGGAATGTA 240  
QY 385 ACAGAACTCTGGATGCAAAAGTAATGTGAGAACTGGAGGAAAAAATAATTAAGAATTTTTG 444  
|||||  
Db 241 ACAGAACTCTGGATGCAAAAGTAATGTGAGAACTGGAGGAAAAAATAATTAAGAATTTTTG 300  
QY 445 CAGAGTTTTGTACATATGTCCTCAAAATGTTTCATCAACACTTCTTGA 489  
|||||  
Db 301 CAGAGTTTTGTACATATGTCCTCAAAATGTTTCATCAACACTTCTTGA 345

RESULT 24  
US-09-200-141-1  
; Sequence 1, Application US/09200141  
; Patent No. 5985663  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Lex M. Cowsett  
; TITLE OF INVENTION: ANTISENSE MODULATION OF Interleukin-15 EXPRESSION  
; FILE REFERENCE: RTS-0022  
; CURRENT APPLICATION NUMBER: US/09/200,141  
; CURRENT FILING DATE: 1998-11-25  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 1  
; LENGTH: 1248  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (519)..(926)  
US-09-200-141-1

Query Match 67.3%; Score 329; DB 2; Length 1248;  
Best Local Similarity 99.7%; Pred. No. 4.5e-145;  
Matches 379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 110 GCTGTTTCAGTGCAGGGCTTCTTAAACAGAACGCCAACTGGGTGAATGTAAAGTGATT 169  
|||||  
Db 547 gctgtttcagtgagggtcttctaaacagagccaaactgggtgaatgtaataagtgatt 606  
QY 170 TGAAGAAAAATTGAAGATCTTATTCAATCTATGATGATGCTACTTTATATACGAAA 229  
Db 607 tgaaaaaaattgaagatcttattcaatctatgcatattgatgctactttatatacggaaa 666  
QY 230 GTGATGTTTACACCCAGTTGCAAAAGTAACAGCAATGAAGTGCTTCTCTTGAGCTTACAAG 289  
|||||  
Db 667 gtgatgttccaccaggttcgaagtaacagcaatgaagtgccttctcttgaggttacaag 726  
QY 290 TTATTTTCACTTGAGTCCGGAGATGCAAGTATTTCATGATACAGTAGAAAAATCTGATCATCC 349  
Db 727 ttatttctacttgagtcgagatgcaagttattcatgatcatagagaaatctgatcatcc 786  
QY 350 TAGCAAAACAACAGTTTGTCTTCTTAATGGGAATGTACAGAACTGGATGCAAAAGATGTG 409  
Db 787 tagcaaacacagatttggtcttcttaattgggaatgtaacagaatctggatgcaagaatgtg 846  
QY 410 AGGAACCTGGAGGAAAAAATAATTAAGAATTTTTTGCAGAGATTTTGTACATATTGTCCAAA 469

Db 847 aggaactggagaaaaataattatttgcagagttttgtacatttgcctcaa 906  
|||||

QY 470 TGTTCATCAACACTTCTTGA 489  
|||||

Db 907 tgttcacacacttttga 926  
|||||

## RESULT 25

US-08-031-399-1  
; Sequence 1, Application US/08031399  
; Patent No. 5552303

## GENERAL INFORMATION:

APPLICANT: Grabstein, Kenneth

APPLICANT: Anderson, Dirk

APPLICANT: Eisenman, June

APPLICANT: Fung, Victor

APPLICANT: Rauch, Charles

TITLE OF INVENTION: Epithelium-derived T-cell Factor

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/031,399

FILING DATE: 19930308

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Launer, Charlene

REGISTRATION NUMBER: 33,035

REFERENCE/DOCKET NUMBER: 2811

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-587-0430

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 489 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 1..489

US-08-031-399-1

Query Match 21.9%; Score 107; DB 1; Length 489;

Best Local Similarity 99.4%; Pred. No. 3.1e-41;

Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTTCATCTCTTCAATTTTGGGCTGTTTCAGTGCAGG 126

Db 67 AGTCATTTTCTAACTGAAGCTGGCATTTCATCTCTTCAATTTTGGGCTGTTTCAGTGCAGG 126

QY 127 CTTCTAAAACAGAGCCAACTGGTGAATGTAATAGTATTGAAAAAATTGAAGAT 186

Db 127 CTTCTAAAACAGAGCCAACTGGTGAATGTAATAGTATTGAAAAAATTGAAGAT 186

QY 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224

Db 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224

## RESULT 27

US-08-726-817-4

; Sequence 4, Application US/08726817

; Patent No. 5707616

; GENERAL INFORMATION:

APPLICANT: Grabstein, Kenneth

APPLICANT: Anderson, Dirk

APPLICANT: Eisenman, June

APPLICANT: Fung, Victor

## RESULT 26

US-08-393-305-4

; Sequence 4, Application US/08393305

; Patent No. 5574138

; GENERAL INFORMATION:

APPLICANT: Grabstein, Kenneth

APPLICANT: Anderson, Dirk

APPLICANT: Eisenman, June

APPLICANT: Fung, Victor

APPLICANT: Rauch, Charles

TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/393,305

FILING DATE: 22-FEB-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Mcmasters, David D.

REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 480052.409C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-622-4900

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 489 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 1..489

US-08-393-305-4

Query Match 21.9%; Score 107; DB 1; Length 489;

Best Local Similarity 99.4%; Pred. No. 3.1e-41;

Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTTCATCTCTTCAATTTTGGGCTGTTTCAGTGCAGG 126

Db 67 AGTCATTTTCTAACTGAAGCTGGCATTTCATCTCTTCAATTTTGGGCTGTTTCAGTGCAGG 126

QY 127 CTTCTAAAACAGAGCCAACTGGTGAATGTAATAGTATTGAAAAAATTGAAGAT 186

Db 127 CTTCTAAAACAGAGCCAACTGGTGAATGTAATAGTATTGAAAAAATTGAAGAT 186

QY 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224

Db 187 CTTATTCAATCTATGCATATTGATGCTACTTTATATAC 224

; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/726,817  
; FILING DATE: 04-OCT-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/393,305  
; FILING DATE: 22-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 480052.409C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-622-4900  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; NAME/KEY: CDS  
; LOCATION: 1..489  
; US-08-726-817-4

Query Match 21.9%; Score 107; DB 1; Length 489;  
Best Local Similarity 99.4%; Pred. No. 3.1e-41;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 67 AGTCATTTTCTAACTGAAGCTGGCAATTCATGCTTCATTTTGGGCTGTTTCAGTCAGGG 126  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
67 AGTCATTTTCTAACTGAAGCTGGCAATTCATGCTTCATTTTGGGCTGTTTCAGTCAGGG 126  
  
QY 127 CTCCTAAACAGAGCCAACTGGGTGAATGTAATGAAGTGTTCGAAAAAATTGAAGAT 186  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
127 CTCCTAAACAGAGCCAACTGGGTGAATGTAATGAAGTGTTCGAAAAAATTGAAGAT 186  
  
QY 187 CTTATTCATCTATGCATATGATGCTACTTTATATAC 224  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
187 CTTATTCATCTATGCATATGATGCTACTTTATATAC 224

RESULT 28  
US-08-504-042-1  
; Sequence 1, Application US/08504042  
; Patent No. 5747024  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; TITLE OF INVENTION: Epithelium-derived T-cell Factor  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle

; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/504,042  
; FILING DATE: 19-JUL-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/031,399  
; FILING DATE: 08-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Launer, Charlene  
; REGISTRATION NUMBER: 33,035  
; REFERENCE/DOCKET NUMBER: 2811  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-587-0430  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..489  
; US-08-504-042-1

Query Match 21.9%; Score 107; DB 1; Length 489;  
Best Local Similarity 99.4%; Pred. No. 3.1e-41;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 67 AGTCATTTTCTAACTGAAGCTGGCAATTCATGCTTCATTTTGGGCTGTTTCAGTCAGGG 126  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
67 AGTCATTTTCTAACTGAAGCTGGCAATTCATGCTTCATTTTGGGCTGTTTCAGTCAGGG 126  
  
QY 127 CTCCTAAACAGAGCCAACTGGGTGAATGTAATGAAGTGTTCGAAAAAATTGAAGAT 186  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
127 CTCCTAAACAGAGCCAACTGGGTGAATGTAATGAAGTGTTCGAAAAAATTGAAGAT 186  
  
QY 187 CTTATTCATCTATGCATATGATGCTACTTTATATAC 224  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
187 CTTATTCATCTATGCATATGATGCTACTTTATATAC 224

RESULT 29  
US-08-392-317B-1  
; Sequence 1, Application US/08392317B  
; Patent No. 5795966  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Paxton, Raymond  
; APPLICANT: Pettit, Dean  
; TITLE OF INVENTION: Antagonists of IL-15  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: Word for Windows 95, 7.0  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/392.317B  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32.655  
REFERENCE/DOCKET NUMBER: 2831  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0430  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..342  
US-08-392-317B-1

Query Match 21.9%; Score 107; DB 1; Length 489;  
Best Local Similarity 99.4%; Pred. No. 3.le-41;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTGCTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126  
|||  
DB 67 AGTCATTTTCTAACTGAAGCTGGCATTGCTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126  
|||  
QY 127 CTTCCTAAACAGAGCCCACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTGAAGAT 186  
|||  
DB 127 CTCCCTAAACAGAGCCCACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTGAAGAT 186  
|||  
QY 187 CTATTCAATCATGATGATTTGATGCTACTTTATATAC 224  
|||  
DB 187 CTATTCAATCATGATGATTTGATGCTACTTTATATAC 224  
|||

RESULT 30  
US-08-725-969-4  
Sequence 4, Application US/08725969  
Patent No. 5892001  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Eisenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/725,969  
FILING DATE: 04-OCT-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION INFORMATION:

APPLICATION NUMBER: US 08/393,305  
FILING DATE: 22-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 480052.409C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..489  
US-08-725-969-4

Query Match 21.9%; Score 107; DB 2; Length 489;  
Best Local Similarity 99.4%; Pred. No. 3.le-41;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTGCTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126  
|||  
DB 67 AGTCATTTTCTAACTGAAGCTGGCATTGCTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126  
|||  
QY 127 CTTCCTAAACAGAGCCCACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTGAAGAT 186  
|||  
DB 127 CTCCCTAAACAGAGCCCACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTGAAGAT 186  
|||  
QY 187 CTATTCAATCATGATGATTTGATGCTACTTTATATAC 224  
|||  
DB 187 CTATTCAATCATGATGATTTGATGCTACTTTATATAC 224  
|||

RESULT 31  
US-08-794-524-4  
Sequence 4, Application US/08794524  
Patent No. 5985262  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Eisenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/794,524  
FILING DATE: 03-FEB-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION INFORMATION:  
APPLICATION NUMBER: US 08/393,305  
FILING DATE: 22-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 480052.409C2  
TELECOMMUNICATION INFORMATION:

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; TELEPHONE: 206-622-4900
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..489
US-08-794-524-4

Query Match          21.9%; Score 107; DB 2; Length 489;
Best Local Similarity 99.4%; Pred. No. 3.le-41;
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 57 AGTCATTTCCTAACTGAAGCTGGGATTCATGCTCTTCATTTGGGCTGTTTCAGTGCAGG 126
Db 67 AGTCATTTCCTAACTGAAGCTGGGATTCATGCTCTTCATTTGGGCTGTTTCAGTGCAGG 126
QY 127 CTCTCTAAACAGAGCCCACTGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGAT 186
Db 127 CTCTCTAAACAGAGCCCACTGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGAT 186
QY 187 CTTATTCAATCTATGCATATTCATGCTACTTTATATAC 224
Db 187 CTTATTCAATCTATGCATATTCATGCTACTTTATATAC 224

RESULT 32
US-09-134-132-1
; Sequence 1, Application US/09134132
; Patent No. 6013480
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Paxton, Raymond
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Antagonists of IL-15
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Word for Windows 95, 7.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,132
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/392,317
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO

; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..342
US-09-134-132-1

Query Match          21.9%; Score 107; DB 3; Length 489;
Best Local Similarity 99.4%; Pred. No. 3.le-41;
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTCCTAACTGAAGCTGGGATTCATGCTCTTCATTTGGGCTGTTTCAGTGCAGG 126
Db 67 AGTCATTTCCTAACTGAAGCTGGGATTCATGCTCTTCATTTGGGCTGTTTCAGTGCAGG 126
QY 127 CTCTCTAAACAGAGCCCACTGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGAT 186
Db 127 CTCTCTAAACAGAGCCCACTGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGAT 186
QY 187 CTTATTCAATCTATGCATATTCATGCTACTTTATATAC 224
Db 187 CTTATTCAATCTATGCATATTCATGCTACTTTATATAC 224

RESULT 33
US-09-134-134A-1
; Sequence 1, Application US/09134134A
; Patent No. 6165466
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Paxton, Raymond
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Antagonists of IL-15
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Word for Windows 95, 7.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,134A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/392,317
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..342
US-09-134-134A-1
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Query Match          21.9%; Score 107; DB 4; Length 489;
Best Local Similarity 99.4%; Pred. No. 3.1e-41;
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 67 AGTCATTTTCTAACTGAAGCTGGCATTTCATGCTTTCAATTTGGGCTGTTTCAGTGCAGG 126
    |||
Db 67 AGTCATTTTCTAACTGAAGCTGGCATTTCATGCTTTCAATTTGGGCTGTTTCAGTGCAGG 126
    |||

Qy 127 CTTCTAAACAGAGCCAACTGGTGAATGTAATAAGTATTTGAAAAAATTTGAAGAT 186
    |||
Db 127 CTTCTAAACAGAGCCAACTGGTGAATGTAATAAGTATTTGAAAAAATTTGAAGAT 186
    |||

Qy 127 CTTCTAAACAGAGCCAACTGGTGAATGTAATAAGTATTTGAAAAAATTTGAAGAT 186
    |||
Db 127 CTTCTAAACAGAGCCAACTGGTGAATGTAATAAGTATTTGAAAAAATTTGAAGAT 186
    |||

Qy 187 CTTATTCAATCTATGCATATTTGATGCTACTTTATATAC 224
    |||
Db 187 CTTATTCAATCTATGCATATTTGATGCTACTTTATATAC 224
    |||

RESULT 34
US-09-134-456-1
; Sequence 1, Application US/09134456
; Patent No. 6168783
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Paxton, Raymond
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Antagonists of IL-15
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Word for Windows 95, 7.0
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/134,456
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 08/392,317
; APPLICATION NUMBER: 08/392,317
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..342
US-09-134-456-1

Query Match          21.9%; Score 107; DB 4; Length 489;
Best Local Similarity 99.4%; Pred. No. 3.1e-41;
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 67 AGTCATTTTCTAACTGAAGCTGGCATTTCATGCTTTCAATTTGGGCTGTTTCAGTGCAGG 126
    |||
Qy 127 CTTCTAAACAGAGCCAACTGGTGAATGTAATAAGTATTTGAAAAAATTTGAAGAT 186
    |||
Db 127 CTTCTAAACAGAGCCAACTGGTGAATGTAATAAGTATTTGAAAAAATTTGAAGAT 186
    |||

Qy 187 CTTATTCAATCTATGCATATTTGATGCTACTTTATATAC 224
    |||
Db 187 CTTATTCAATCTATGCATATTTGATGCTACTTTATATAC 224
    |||

RESULT 35
US-09-196-427-1
; Sequence 1, Application US/09196427
; Patent No. 6177079
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Paxton, Raymond
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Antagonists of IL-15
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Word for Windows 95, 7.0
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/196,427
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 08/392,317
; APPLICATION NUMBER: 08/392,317
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..342
US-09-196-427-1

Query Match          21.9%; Score 107; DB 4; Length 489;
Best Local Similarity 99.4%; Pred. No. 3.1e-41;
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 67 AGTCATTTTCTAACTGAAGCTGGCATTTCATGCTTTCAATTTGGGCTGTTTCAGTGCAGG 126
    |||
Db 67 AGTCATTTTCTAACTGAAGCTGGCATTTCATGCTTTCAATTTGGGCTGTTTCAGTGCAGG 126
    |||

Qy 127 CTTCTAAACAGAGCCAACTGGTGAATGTAATAAGTATTTGAAAAAATTTGAAGAT 186
    |||
Db 127 CTTCTAAACAGAGCCAACTGGTGAATGTAATAAGTATTTGAAAAAATTTGAAGAT 186
    |||
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QY 187 CTTATTCAATCATGATATTGATGCTACTTTATATAC 224  
Db 187 CTTATTCAATCATGATATTGATGCTACTTTATATAC 224

RESULT 36  
US-09-189-193-4  
; Sequence 4, Application US/09189193  
; Patent No. 6184359  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/09/189,193  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/393,305  
; FILING DATE: 22-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 480052.409C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-622-4900  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..489

US-09-189-193-4

Query Match 21.9%; Score 107; DB 4; Length 489;  
Best Local Similarity 99.4%; Pred. No. 3.1e-41;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTTCATGCTTTCATTTTGGGCTGTTTCAGTCAGGG 126  
Db 67 AGTCATTTTCTAACTGAAGCTGGCATTTCATGCTTTCATTTTGGGCTGTTTCAGTCAGGG 126

QY 127 CTCCTAAACAGAGCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186  
Db 127 CTCCTAAACAGAGCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186

QY 187 CTTATTCAATCATGATATTGATGCTACTTTATATAC 224  
Db 187 CTTATTCAATCATGATATTGATGCTACTTTATATAC 224

RESULT 37

PCT-US94-03793-1  
; Sequence 1, Application PC/TUS9403793  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: Interleukin-15  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: PCT/US94/03793  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Launer, Charlene  
; REGISTRATION NUMBER: 33,035  
; REFERENCE/DOCKET NUMBER: 2811  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-587-0430  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..489

PCT-US94-03793-1

Query Match 21.9%; Score 107; DB 5; Length 489;  
Best Local Similarity 99.4%; Pred. No. 3.1e-41;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTTCTAACTGAAGCTGGCATTTCATGCTTTCATTTTGGGCTGTTTCAGTCAGGG 126  
Db 67 AGTCATTTTCTAACTGAAGCTGGCATTTCATGCTTTCATTTTGGGCTGTTTCAGTCAGGG 126

QY 127 CTCCTAAACAGAGCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186  
Db 127 CTCCTAAACAGAGCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186

QY 187 CTTATTCAATCATGATATTGATGCTACTTTATATAC 224  
Db 187 CTTATTCAATCATGATATTGATGCTACTTTATATAC 224

RESULT 38  
US-08-393-305-13  
; Sequence 13, Application US/08393305  
; Patent No. 5574138  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor

```
; APPLICANT: Rauch, Charles
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,305
; FILING DATE: 22-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 480052.409C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 345 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..345
;
US-08-393-305-13
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Query Match 16.4%; Score 80; DB 1; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.3e-28;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 145 AACTGGGTGAATGTAATAGTGATTGAAAAAATGAAGATCTTATTCAATCTATGCAT 204
Db 1 AACTGGGTGAATGTAATAGTGATTGAAAAAATGAAGATCTTATTCAATCTATGCAT 60
QY 205 ATTGATGCTACTTTATATAC 224
Db 61 ATTGATGCTACTTTATATAC 80
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RESULT 39
US-08-726-817-13
; Sequence 13, Application US/08726817
; Patent No. 5707616
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Anderson, Dirk
; APPLICANT: Eisenman, June
; APPLICANT: Fung, Victor
; APPLICANT: Rauch, Charles
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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```
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726.817
; FILING DATE: 04-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/393,305
; FILING DATE: 22-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 480052.409C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 345 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..345
;
US-08-726-817-13
```

```
Query Match 16.4%; Score 80; DB 1; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.3e-28;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 145 AACTGGGTGAATGTAATAGTGATTGAAAAAATGAAGATCTTATTCAATCTATGCAT 204
Db 1 AACTGGGTGAATGTAATAGTGATTGAAAAAATGAAGATCTTATTCAATCTATGCAT 60
QY 205 ATTGATGCTACTTTATATAC 224
Db 61 ATTGATGCTACTTTATATAC 80
```

```
RESULT 40
US-08-725-969-13
; Sequence 13, Application US/08725969
; Patent No. 5892001
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Anderson, Dirk
; APPLICANT: Eisenman, June
; APPLICANT: Fung, Victor
; APPLICANT: Rauch, Charles
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/725,969
; FILING DATE: 04-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/393,305
; FILING DATE: 22-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
```

REFERENCE/DOCKET NUMBER: 480052.409C2  
TELEPHONE: 206-622-4900  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 345 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..345  
US-08-725-969-13

Query Match 16.4%; Score 80; DB 2: Length 345;  
Best Local Similarity 100.0%; Pred. No. 1.3e-28;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 145 AACTGGGTGAATGTAATAGTGAATTTGAAAAAATGAAGATCTTATTCAATCTATGCAT 204  
Db 1 AACTGGGTGAATGTAATAGTGAATTTGAAAAAATGAAGATCTTATTCAATCTATGCAT 60

Qy 205 ATTGATGCTACTTTATATAC 224  
Db 61 ATTGATGCTACTTTATATAC 80

RESULT 41  
US-08-794-524-13  
; Sequence 13, Application US/08794524  
; Patent No. 5985262  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/794,524  
; FILING DATE: 03-FEB-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/393,305  
; FILING DATE: 22-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 480052.409C2  
; TELEPHONE: 206-622-4900  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 345 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS

LOCATION: 1..345  
US-08-794-524-13

Query Match 16.4%; Score 80; DB 2: Length 345;  
Best Local Similarity 100.0%; Pred. No. 1.3e-28;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 145 AACTGGGTGAATGTAATAGTGAATTTGAAAAAATGAAGATCTTATTCAATCTATGCAT 204  
Db 1 AACTGGGTGAATGTAATAGTGAATTTGAAAAAATGAAGATCTTATTCAATCTATGCAT 60

Qy 205 ATTGATGCTACTTTATATAC 224  
Db 61 ATTGATGCTACTTTATATAC 80

RESULT 42  
US-09-189-193-13  
; Sequence 13, Application US/09189193  
; Patent No. 6184359  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/189,193  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/393,305  
; FILING DATE: 22-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 480052.409C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-622-4900  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 345 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..345  
US-09-189-193-13

Query Match 16.4%; Score 80; DB 4: Length 345;  
Best Local Similarity 100.0%; Pred. No. 1.3e-28;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 145 AACTGGGTGAATGTAATAGTGAATTTGAAAAAATGAAGATCTTATTCAATCTATGCAT 204  
Db 1 AACTGGGTGAATGTAATAGTGAATTTGAAAAAATGAAGATCTTATTCAATCTATGCAT 60

QY 205 ATTGATGCTACTTTATATAC 224  
|||||  
Db 61 ATTGATGCTACTTTATATAC 80  
|||||

RESULT 43  
US-08-859-998-435  
; Sequence 435, Application US/08859998  
; Patent No. 5994076  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; APPLICANT: Jokhadze, George  
; APPLICANT: Bibilashvili, Robert  
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1375  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 2200 Sand Hill Road, Suite 100  
; CITY: Menlo Park  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; FILING DATE: 21-MAY-1997  
; APPLICATION NUMBER: US/08/859,998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Field, Bret E.  
; REGISTRATION NUMBER: 37,620  
; REFERENCE/DOCKET NUMBER: 09096/002001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-0875  
; TELEFAX: 415-854-0875  
; INFORMATION FOR SEQ ID NO: 435:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 32 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide primer  
US-08-859-998-435

Query Match 6.5%; Score 32; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 4.le-06;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TTGAGAGTATTTCATCCAGTCTACTTGTG 53  
|||||  
Db 1 TTGAGAGTATTTCATCCAGTCTACTTGTG 32  
|||||

RESULT 44  
US-08-859-998-436/c  
; Sequence 436, Application US/08859998  
; Patent No. 5994076  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; APPLICANT: Jokhadze, George  
; APPLICANT: Bibilashvili, Robert  
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL

; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1375  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 2200 Sand Hill Road, Suite 100  
; CITY: Menlo Park  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/859,998  
; FILING DATE: 21-MAY-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Field, Bret E.  
; REGISTRATION NUMBER: 37,620  
; REFERENCE/DOCKET NUMBER: 09096/002001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-322-5070  
; TELEFAX: 415-854-0875  
; INFORMATION FOR SEQ ID NO: 436:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 32 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide primer  
US-08-859-998-436

Query Match 6.5%; Score 32; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 4.le-06;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 347 TCCTAGCAACACAGTTTGTCTCTAATGGG 378  
|||||  
Db 32 TCCTAGCAACACAGTTTGTCTCTAATGGG 1  
|||||

RESULT 45  
US-09-225-928-435  
; Sequence 435, Application US/09225928  
; Patent No. 6352829  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; APPLICANT: Jokhadze, George  
; APPLICANT: Bibilashvili, Robert  
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1375  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 2200 Sand Hill Road, Suite 100  
; CITY: Menlo Park  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:

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;
; APPLICATION NUMBER: US/09/225,928
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 435:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
;
; US-09-225-928-435
;
; Query Match 6.5%; Score 32; DB 4; Length 32;
; Best Local Similarity 100.0%; Pred. No. 4.1e-06;
; Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 22 TTGAGAAGTATTTCATCCAGTCTACTTGTG 53
; | | | | | | | | | | | | | | | | | | | |
; DB 1 TTGAGAAGTATTTCATCCAGTCTACTTGTG 32
;
; RESULT 46
; US-09-225-928-436/c
; Sequence 436, Application US/09225928
; Patent No. 6352829
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; Johhadze, George
; Billashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,928
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 436:
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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
;
; US-09-225-928-436
;
; Query Match 6.5%; Score 32; DB 4; Length 32;
; Best Local Similarity 100.0%; Pred. No. 4.1e-06;
; Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 347 TCCTAGCAACAAACAGTTTCTTCTTAATGGG 378
; | | | | | | | | | | | | | | | | | | | |
; DB 32 TCCTAGCAACAAACAGTTTCTTCTTAATGGG 1
;
; RESULT 47
; US-08-962-503-2
; Sequence 2, Application US/08962503
; Patent No. 6087172
; GENERAL INFORMATION:
; APPLICANT: Veerapaneni, Dange
; APPLICANT: Hamanaka, Shoji
; APPLICANT: No. 6087172awa, Iwao
; TITLE OF INVENTION: RIBOZYMES TARGETED TO IL-15 MRNA
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/962,503
; FILING DATE: 31-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 09326/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; US-08-962-503-2
;
; Query Match 4.3%; Score 21; DB 3; Length 21;
; Best Local Similarity 57.1%; Pred. No. 0.58;
; Matches 12; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
;
; QY 59 TTCTAAACAGTCATTTCTTCTAA 79
; | | | | | | | | | | | | | | | | |
; DB 1 UUCUAAACAGCAUUUUUCAA 21
;
; RESULT 48
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US-08-962-503-4  
; Sequence 4, Application US/08962503  
; Patent No. 6087172  
; GENERAL INFORMATION:  
; APPLICANT: Veerapaneni, Dange  
; APPLICANT: Hamanaka, Shoji  
; APPLICANT: No. 6087172awa, Iwao  
; TITLE OF INVENTION: RIBOZYMES TARGETED TO IL-15 MRNA  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/962,503  
; FILING DATE: 31-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haile, Ph.D., Lisa A  
; REGISTRATION NUMBER: 38,347  
; REFERENCE/DOCKET NUMBER: 09326/002001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 619/678-5099  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA  
US-08-962-503-4

Query Match 4.3%; Score 21; DB 3; Length 21;  
Best Local Similarity 52.4%; Pred. No. 0.58;  
Matches 11; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 88 GGCATTTCATGCTCTCATTTG 108  
||||:||||:||||:|  
DB 1 GGCAUUCAGUCUUCAUUUG 21

RESULT 49  
US-08-962-503-10  
; Sequence 10, Application US/08962503  
; Patent No. 6087172  
; GENERAL INFORMATION:  
; APPLICANT: Veerapaneni, Dange  
; APPLICANT: Hamanaka, Shoji  
; APPLICANT: No. 6087172awa, Iwao  
; TITLE OF INVENTION: RIBOZYMES TARGETED TO IL-15 MRNA  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/962,503  
; FILING DATE: 31-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haile, Ph.D., Lisa A  
; REGISTRATION NUMBER: 38,347  
; REFERENCE/DOCKET NUMBER: 09326/002001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 619/678-5099  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA  
US-08-962-503-10

Query Match 4.3%; Score 21; DB 3; Length 21;  
Best Local Similarity 61.9%; Pred. No. 0.58;  
Matches 13; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 454 GTACATATTGTCCAATGTC 474  
|:|:|:|:|:|:|:|:|:|:|:|:|:|  
DB 1 GUACAUUUGUCCAAUUGUC 21

RESULT 50  
US-08-392-317B-10/c  
; Sequence 10, Application US/08392317B  
; Patent No. 5795966  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Paxton, Raymond  
; APPLICANT: Pettit, Dean  
; TITLE OF INVENTION: Antagonists of IL-15  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: Word for Windows 95, 7.0  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/392,317B  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Malaska, Stephen L.  
; REGISTRATION NUMBER: 32,655  
; REFERENCE/DOCKET NUMBER: 2831  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-587-0430  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; HYPOTHETICAL: NO  
US-08-392-317B-10

Query Match 4.3%; Score 21; DB 1; Length 36;  
Best Local Similarity 100.0%; Pred. No. 0.57;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

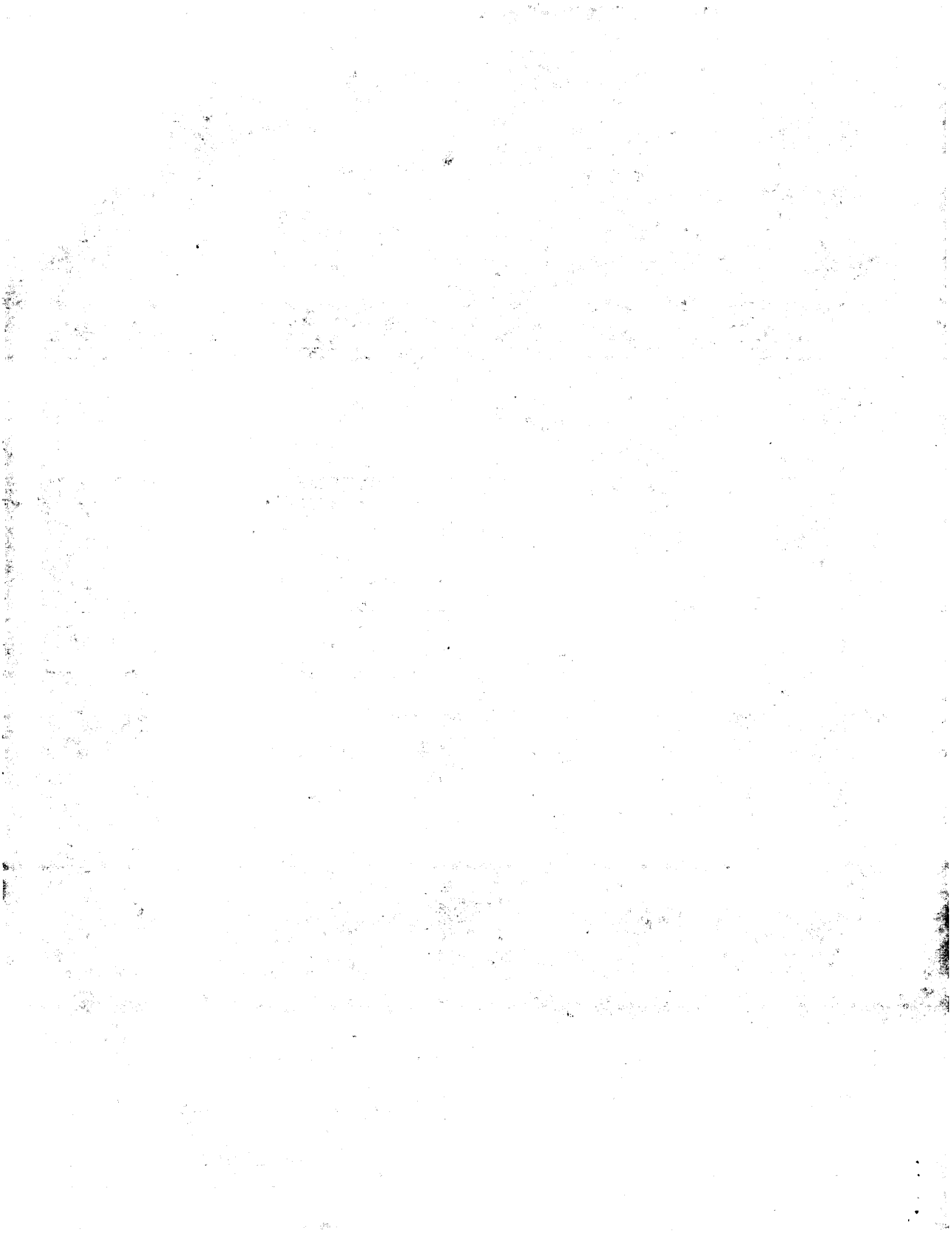
Qy 469 ATGTTTCATCAACACTTCTTGA 489

|||||

Db 36 ATGTTTCATCAACACTTCTTGA 16

Search completed: August 6, 2002, 21:31:16

Job time: 4613 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 6, 2002, 19:25:47 ; Search time 2365.28 Seconds  
(without alignments)  
2790.372 Million cell updates/sec

Title: US-09-724-841-1

Perfect score: 489

Sequence: 1 ATGAGAAATTCGAACACCA.....TGTTCACTCAACTTCTTGA 489

Scoring table:

OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 12

Total number of hits satisfying chosen parameters: 620075

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

EST: \*  
1: em\_estba: \*  
2: em\_esthum: \*  
3: em\_estin: \*  
4: em\_estmu: \*  
5: em\_estov: \*  
6: em\_estpl: \*  
7: em\_estro: \*  
8: em\_htc: \*  
9: gb\_estl: \*  
10: gb\_est2: \*  
11: gb\_htc: \*  
12: gb\_gss: \*  
13: em\_gss\_hum: \*  
14: em\_gss\_inv: \*  
15: em\_gss\_pln: \*  
16: em\_gss\_vrt: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	489	100.0	982	9	AL548180
2	350	71.6	509	9	AA463370
3	302	61.8	994	9	AL572832
4	261	53.4	800	10	EG184658
5	233	47.6	637	9	AI860008
6	191	39.1	756	10	BI832895
7	172	35.2	872	10	BI758686
8	137	28.0	471	10	N76741
9	82	16.8	494	9	AW804168
10	77	15.7	309	10	BF095213
11	72	14.7	483	9	AW804165
12	63	12.9	301	10	BF088290
13	55	11.2	474	10	N49734
14	54	11.0	278	9	BE177883
15	54	11.0	718	10	BI766231
16	52	10.6	550	10	BE698667
17	49	10.0	166	10	BF379349

18	37	7.6	817	10	BI756810
19	32	6.5	275	10	BF088272
20	30	6.1	564	9	AA863763
21	30	6.1	590	9	AA544986
22	30	6.1	430	9	BB661271
23	28	5.7	631	9	AA858938
24	26	5.3	429	9	AA863979
25	26	5.3	515	10	BF704348
26	23	4.7	405	9	AW121368
27	23	4.7	420	10	BE690327
28	23	4.7	434	9	AI503618
29	23	4.7	458	9	BB825167
30	23	4.7	509	9	AI120615
31	23	4.7	538	9	AI152482
32	22	4.5	652	9	BB664509
33	22	4.5	826	10	BI685688
34	21	4.3	560	9	AI161778
35	21	4.3	687	12	AG099196
36	21	4.3	690	9	AI596704
37	21	4.3	742	12	AQ935740
38	20	4.1	204	9	BB467257
39	20	4.1	224	9	BB213861
40	20	4.1	253	9	AI447397
41	20	4.1	286	9	BB141025
42	20	4.1	288	9	BB003966
43	20	4.1	294	9	BB006389
44	20	4.1	294	9	BB292315
45	20	4.1	295	9	BB135090
46	20	4.1	295	9	BB157192
47	20	4.1	307	4	BB714486
48	20	4.1	347	9	BB165365
49	20	4.1	370	9	AV660075
50	20	4.1	370	12	BB7338
51	20	4.1	444	10	H69259
52	20	4.1	453	12	B95318
53	20	4.1	456	12	A2931315
54	20	4.1	469	10	H53231
55	20	4.1	522	12	A2930291
56	20	4.1	526	10	H58906
57	20	4.1	602	10	BG565703
58	20	4.1	632	12	AG161012
59	20	4.1	644	9	AV650917
60	20	4.1	662	10	BF644753
61	20	4.1	665	9	AW950626
62	20	4.1	672	9	AV651015
63	20	4.1	687	9	AV651014
64	20	4.1	703	9	AV649004
65	20	4.1	709	10	BG292430
66	20	4.1	740	12	AQ449556
67	20	4.1	851	10	BI517849
68	20	4.1	960	10	BE571962
69	19	3.9	209	10	BE938076
70	19	3.9	213	9	AV369506
71	19	3.9	228	9	AV353802
72	19	3.9	231	9	AV363702
73	19	3.9	232	9	AV281576
74	19	3.9	237	9	BB071942
75	19	3.9	241	9	AV358985
76	19	3.9	250	9	AV311878
77	19	3.9	257	9	AV263140
78	19	3.9	258	9	AV272906
79	19	3.9	267	9	AV361979
80	19	3.9	281	9	AV362067
81	19	3.9	285	9	AV337803
82	19	3.9	287	9	AV137961
83	19	3.9	291	9	AV234777
84	19	3.9	291	9	BB068790
85	19	3.9	294	9	AV290821
86	19	3.9	301	9	BB397292
87	19	3.9	302	9	AV299788
88	19	3.9	303	9	AI180204
89	19	3.9	304	9	BB226778
90	19	3.9	329	9	BB244070

c 91	19	3.9	449	12	AZ651701	AZ651701 1M0522J06	c 164	18	3.7	274	9	BB397706	BB397706 BB397706
c 92	19	3.9	452	12	AZ441144	AZ441144 1M0232P14	c 165	18	3.7	275	9	AV222107	AV222107
c 93	19	3.9	460	10	BM201463	C0226A09-	c 166	18	3.7	277	9	AV091358	AV091358
c 94	19	3.9	492	10	BF590380	nab23h01.	c 167	18	3.7	277	9	AV266497	AV266497
c 95	19	3.9	511	9	BF757042	BF757042 BB757042	c 168	18	3.7	277	9	BB672231	BB672231
c 96	19	3.9	513	12	AZ306212	AZ306212 1M0007M12	c 169	18	3.7	277	12	AZ708418	RPCI-23-2
c 97	19	3.9	531	12	AZ844980	AZ844980 2M0144M24	c 170	18	3.7	278	9	AA549719	VK73b12.s
c 98	19	3.9	534	12	AZ955992	AZ955992 2M0222K18	c 171	18	3.7	281	9	AV298822	AV298822
c 99	19	3.9	537	9	AW647771	AW647771 EST326G225	c 172	18	3.7	281	9	BB227954	BB227954
c 100	19	3.9	593	12	AZ819331	AZ819331 2M0089G23	c 173	18	3.7	283	9	BB028006	BB028006
c 101	19	3.9	598	10	BF815372	BF815372 RCS-C1014	c 174	18	3.7	283	9	BB400981	BB400981
c 102	19	3.9	615	12	BH264776	BH264776 CH230-91E	c 175	18	3.7	283	9	BB401704	BB401704
c 103	19	3.9	626	12	AZ371503	AZ371503 1M0122P19	c 176	18	3.7	286	4	BB714578	BB714578 Mus muscu
c 104	19	3.9	648	9	AA874636	AA874636 vx81e08.r	c 177	18	3.7	287	12	AZ077601	RPCI-23-3
c 105	19	3.9	661	9	AL558400	AL558400 AL558400	c 178	18	3.7	288	9	AV306050	AV306050
c 106	19	3.9	701	10	BI250248	BI250248 602995039	c 179	18	3.7	288	9	BB385117	BB385117
c 107	19	3.9	709	12	AG070283	AG070283 Par trogl	c 180	18	3.7	289	9	AA591974	AA591974
c 108	19	3.9	745	9	AL558401	AL558401 AL558401	c 181	18	3.7	290	9	BB410080	BB410080
c 109	19	3.9	767	12	AG159240	AG159240 Pan trogl	c 182	18	3.7	292	9	AA558753	L0299E09-
c 110	19	3.9	797	12	BH203201	BH203201 Sml-581l1	c 183	18	3.7	294	9	AA220037	AA220037
c 111	19	3.9	819	12	AG112237	AG112237 Pan trogl	c 184	18	3.7	295	9	AA213941	u043h10.x
c 112	19	3.9	827	9	AV755697	AV755697 AV755697	c 185	18	3.7	297	9	AV299808	AV299808
c 113	19	3.9	835	12	AZ671617	AZ671617 ENFLY05TF	c 186	18	3.7	297	9	AV301759	AV301759
c 114	19	3.9	837	12	AZ670079	AZ670079 ENTMD67TF	c 187	18	3.7	297	10	BM196758	C0336F12-
c 115	19	3.9	884	12	AZ673472	AZ673472 ENTKG94TF	c 188	18	3.7	298	9	BB395777	BB395777
c 116	19	3.9	891	12	BH157193	BH157193 ENTRW47TR	c 189	18	3.7	298	10	BG229413	mab94h01.
c 117	19	3.9	911	12	AZ692138	AZ692138 ENTKY08TF	c 190	18	3.7	299	10	BM238574	K0519H02-
c 118	19	3.9	915	10	BF179198	BF179198 601807449	c 191	18	3.7	301	12	AZ893931	RPCI-24-1
c 119	19	3.9	946	12	BH163338	BH163338 ENTKU20TF	c 192	18	3.7	302	9	AV339738	AV339738
c 120	19	3.9	997	10	BG745910	BG745910 602724090	c 193	18	3.7	302	9	AA407893	EST02504
c 121	19	3.9	1152	10	BG198961	BG198961 RST18233	c 194	18	3.7	303	9	BB133104	BB133104
c 122	19	3.9	3317	11	AK016536	AK016536 Mus muscu	c 195	18	3.7	303	9	BE197021	BE197021
c 123	18	3.7	147	12	AQ995523	AQ995523 RPCI-23-3	c 196	18	3.7	303	10	BM293795	BM293795 C0271H07-
c 124	18	3.7	156	10	R29175	R29175 FI-283D-22	c 197	18	3.7	306	9	AA590190	AA590190
c 125	18	3.7	169	9	AA472866	AA472866 vd59d08.r	c 198	18	3.7	307	9	BB403122	BB403122
c 126	18	3.7	174	9	BB063147	BB063147 BB063147	c 199	18	3.7	311	9	AA117220	AA117220
c 127	18	3.7	175	9	AA574499	AA574499 vm29a05.r	c 200	18	3.7	311	9	AA1920451	AA1920451
c 128	18	3.7	178	9	AA275836	AA275836 AV275836	c 201	18	3.7	314	9	BB378197	BB378197
c 129	18	3.7	181	9	AA791987	AA791987 vm79e05.r	c 202	18	3.7	319	9	AA220041	AA220041
c 130	18	3.7	182	9	AA591844	AA591844 vk11h09.r	c 203	18	3.7	321	9	BB094072	BB094072
c 131	18	3.7	191	9	BB331755	BB331755 BB331755	c 204	18	3.7	321	10	BE595674	BE595674
c 132	18	3.7	195	10	BI126484	BI126484 1076P21P	c 205	18	3.7	322	10	BM202091	BM202091
c 133	18	3.7	196	9	AA608053	AA608053 v41e12.r	c 206	18	3.7	324	9	AA1840812	AA1840812
c 134	18	3.7	198	9	AA407298	AA407298 vf02c09.r	c 207	18	3.7	324	9	BB458691	BB458691
c 135	18	3.7	209	9	BB017128	BB017128 BB017128	c 208	18	3.7	324	10	BF012935	BF012935
c 136	18	3.7	214	9	AV273198	AV273198 AV273198	c 209	18	3.7	327	9	AA189942	AA189942
c 137	18	3.7	218	9	AA624833	AA624833 vn79h07.r	c 210	18	3.7	327	10	C79484	C79484
c 138	18	3.7	230	10	BF318887	BF318887 uy06e02.x	c 211	18	3.7	328	10	BM166474	BM166474
c 139	18	3.7	233	10	BE987320	BE987320 UI-M-CG0p	c 212	18	3.7	328	10	BF557546	BF557546
c 140	18	3.7	237	9	AV254443	AV254443 AV254443	c 213	18	3.7	330	9	AA964138	AA964138
c 141	18	3.7	239	9	AV257076	AV257076 AV257076	c 214	18	3.7	333	10	BM215604	BM215604
c 142	18	3.7	240	9	AU044544	AU044544 AU044544	c 215	18	3.7	333	10	T53024	T53024
c 143	18	3.7	240	9	AU072894	AU072894 AU072894	c 216	18	3.7	336	9	AA821796	AA821796
c 144	18	3.7	240	9	AU073785	AU073785 AU073785	c 217	18	3.7	337	9	AA474338	AA474338
c 145	18	3.7	242	9	AV228154	AV228154 AV228154	c 218	18	3.7	340	10	C80101	C80101
c 146	18	3.7	244	9	AA615220	AA615220 vn99c04.r	c 219	18	3.7	343	9	AA445092	AA445092
c 147	18	3.7	246	9	A1216676	A1216676 qg66g04.x	c 220	18	3.7	344	10	BM212341	BM212341
c 148	18	3.7	246	9	AA274060	AA274060 vb93d12.r	c 221	18	3.7	345	10	BM202714	BM202714
c 149	18	3.7	246	9	BB019486	BB019486 BB019486	c 222	18	3.7	348	9	AI922279	AI922279
c 150	18	3.7	252	9	AA162341	AA162341 ms28h11.r	c 223	18	3.7	350	9	AV260115	AV260115
c 151	18	3.7	252	9	AV273674	AV273674 AV273674	c 224	18	3.7	351	9	AA600650	AA600650
c 152	18	3.7	255	9	AA821844	AA821844 vp74g10.r	c 225	18	3.7	352	9	AU046265	AU046265
c 153	18	3.7	255	12	AQ266553	AQ266553 RPCI111-75	c 226	18	3.7	353	9	AA408333	AA408333
c 154	18	3.7	257	9	AV280365	AV280365 AV280365	c 227	18	3.7	353	9	AA467637	AA467637
c 155	18	3.7	264	9	AA823950	AA823950 vq93c10.r	c 228	18	3.7	355	10	BM211773	BM211773
c 156	18	3.7	266	9	AA875787	AA875787 uj19g12.x	c 229	18	3.7	357	9	AA617572	AA617572
c 157	18	3.7	266	9	AA575487	AA575487 vl94a11.r	c 230	18	3.7	359	10	BI450851	BI450851
c 158	18	3.7	268	10	BF011500	BF011500 ux82b08.x	c 231	18	3.7	359	12	AQ097232	AQ097232
c 159	18	3.7	272	9	AV298811	AV298811 AV298811	c 232	18	3.7	360	9	AI846846	AI846846
c 160	18	3.7	274	9	AV211972	AV211972 AV211972	c 233	18	3.7	360	12	BH286458	BH286458
c 161	18	3.7	274	9	AV228337	AV228337 AV228337	c 234	18	3.7	362	9	AA967691	AA967691
c 162	18	3.7	274	9	AV298540	AV298540 AV298540	c 235	18	3.7	362	9	AI850625	AI850625
c 163	18	3.7	274	9	AA562085	AA562085 SMOVAFCAP	c 236	18	3.7	362	10	BF456402	BF456402

237	18	3.7	365	9	AU020180	AU020180	310	18	3.7	420	10	BM211792	BM211792
c 238	18	3.7	366	9	BB792924	BB792924	311	18	3.7	421	10	BM211579	BM211579
c 239	18	3.7	367	9	AA607047	AA607047	312	18	3.7	423	9	AU046235	AU046235
c 240	18	3.7	368	9	AT171341	AT171341	c 313	18	3.7	423	9	AA472511	AA472511
c 241	18	3.7	369	9	AA574822	AA574822	c 314	18	3.7	423	9	AA607207	AA607207
c 242	18	3.7	369	9	AA5956148	AA5956148	315	18	3.7	423	10	BM195852	BM195852
c 243	18	3.7	369	9	AA5956148	AA5956148	316	18	3.7	427	10	BF018954	BF018954
c 244	18	3.7	369	10	BE956369	BE956369	317	18	3.7	428	9	AU044913	AU044913
245	18	3.7	370	10	BE690580	BE690580	318	18	3.7	428	9	AU045805	AU045805
246	18	3.7	371	10	C77835	C77835	319	18	3.7	428	9	BB787979	BB787979
247	18	3.7	371	10	BF455507	BF455507	320	18	3.7	428	10	C91313	C91313
248	18	3.7	372	9	A1931762	A1931762	c 321	18	3.7	429	9	AA183505	AA183505
c 249	18	3.7	372	12	AQ243976	AQ243976	c 322	18	3.7	429	9	BB725537	BB725537
250	18	3.7	374	9	AA884912	AA884912	323	18	3.7	429	12	AZ376171	AZ376171
c 251	18	3.7	378	9	AA414231	AA414231	c 324	18	3.7	430	9	AA118142	AA118142
c 252	18	3.7	379	9	BB729120	BB729120	c 325	18	3.7	430	9	AI836306	AI836306
253	18	3.7	379	10	BM196374	BM196374	326	18	3.7	430	10	AU020903	AU020903
254	18	3.7	380	9	AA409906	AA409906	327	18	3.7	431	10	BM206854	BM206854
c 255	18	3.7	381	9	AA667136	AA667136	328	18	3.7	432	9	AA956167	AA956167
c 256	18	3.7	381	9	AA590022	AA590022	329	18	3.7	432	9	AI427155	AI427155
257	18	3.7	381	10	BM244811	BM244811	330	18	3.7	432	9	AI597452	AI597452
258	18	3.7	382	9	AA894025	AA894025	c 331	18	3.7	432	9	AA154638	AA154638
c 259	18	3.7	387	9	AA022776	AA022776	c 332	18	3.7	432	10	BM388381	BM388381
c 260	18	3.7	388	9	AA624515	AA624515	c 333	18	3.7	432	12	AQ596799	AQ596799
261	18	3.7	388	10	BM201924	BM201924	c 334	18	3.7	433	10	BM211533	BM211533
262	18	3.7	389	12	AQ386064	AQ386064	335	18	3.7	434	9	BB777477	BB777477
c 263	18	3.7	391	9	BB812884	BB812884	336	18	3.7	434	12	AZ614281	AZ614281
c 264	18	3.7	391	9	BB816659	BB816659	337	18	3.7	434	10	BM202178	BM202178
265	18	3.7	392	10	C85299	C85299	c 338	18	3.7	436	9	AL023002	AL023002
c 266	18	3.7	392	10	BE282241	BE282241	339	18	3.7	437	12	AQ931776	AQ931776
267	18	3.7	393	10	BI180886	BI180886	c 340	18	3.7	437	12	BB689115	BB689115
c 268	18	3.7	393	10	BE996121	BE996121	341	18	3.7	439	9	BB689115	BB689115
c 269	18	3.7	394	9	AI152962	AI152962	c 342	18	3.7	440	9	BB727163	BB727163
c 270	18	3.7	394	9	BB737365	BB737365	343	18	3.7	441	9	AU015767	AU015767
c 271	18	3.7	394	9	BB776210	BB776210	344	18	3.7	441	12	AQ180103	AQ180103
272	18	3.7	394	12	AQ386547	AQ386547	345	18	3.7	441	10	BM212010	BM212010
c 273	18	3.7	396	9	BB679784	BB679784	346	18	3.7	442	10	BM213982	BM213982
c 274	18	3.7	398	9	AW557380	AW557380	347	18	3.7	442	10	BM207263	BM207263
c 275	18	3.7	398	9	BB734214	BB734214	348	18	3.7	444	10	BM244925	BM244925
c 276	18	3.7	400	9	AV435067	AV435067	349	18	3.7	444	10	BF465056	BF465056
c 277	18	3.7	400	10	BG091042	BG091042	c 350	18	3.7	446	9	BB815133	BB815133
278	18	3.7	401	10	BI813883	BI813883	351	18	3.7	447	9	AU016087	AU016087
279	18	3.7	403	9	AI835263	AI835263	352	18	3.7	447	9	AU018053	AU018053
280	18	3.7	403	9	AA212831	AA212831	c 353	18	3.7	447	9	BB726102	BB726102
281	18	3.7	403	9	AU044813	AU044813	354	18	3.7	447	12	AZ376943	AZ376943
282	18	3.7	405	9	AU020762	AU020762	c 355	18	3.7	449	9	AI931890	AI931890
c 283	18	3.7	405	9	BB688562	BB688562	356	18	3.7	450	9	AA561628	AA561628
c 284	18	3.7	405	10	R08563	R08563	c 357	18	3.7	450	9	AA561628	AA561628
c 285	18	3.7	405	9	BB730650	BB730650	c 358	18	3.7	451	10	BM236922	BM236922
c 286	18	3.7	408	9	BB740703	BB740703	c 359	18	3.7	451	10	BE333868	BE333868
287	18	3.7	408	10	W88449	W88449	c 360	18	3.7	455	10	BM207467	BM207467
c 288	18	3.7	409	9	BB679707	BB679707	361	18	3.7	455	10	BE859399	BE859399
c 289	18	3.7	409	9	AA607241	AA607241	c 362	18	3.7	456	9	AU020075	AU020075
c 290	18	3.7	410	9	AU019865	AU019865	c 363	18	3.7	456	10	BF016586	BF016586
c 291	18	3.7	410	9	BB775427	BB775427	364	18	3.7	457	9	AI874752	AI874752
c 292	18	3.7	410	9	AA624484	AA624484	365	18	3.7	457	9	BE200159	BE200159
c 293	18	3.7	411	9	BB740610	BB740610	366	18	3.7	458	9	AI574253	AI574253
c 294	18	3.7	413	9	AA467432	AA467432	367	18	3.7	459	10	BG141987	BG141987
c 295	18	3.7	414	9	BB671586	BB671586	368	18	3.7	460	9	AW542146	AW542146
c 296	18	3.7	414	9	AA623499	AA623499	c 369	18	3.7	462	9	AI847974	AI847974
c 297	18	3.7	415	9	AU038028	AU038028	c 370	18	3.7	462	9	BB729989	BB729989
c 298	18	3.7	415	9	BB728890	BB728890	c 371	18	3.7	464	10	BF452080	BF452080
c 299	18	3.7	415	10	C90402	C90402	372	18	3.7	465	10	BM201383	BM201383
300	18	3.7	416	9	AA511816	AA511816	c 373	18	3.7	466	9	AA727743	AA727743
c 301	18	3.7	417	9	AA540403	AA540403	374	18	3.7	466	9	BB782622	BB782622
c 302	18	3.7	418	9	AU019079	AU019079	c 375	18	3.7	467	9	AU045831	AU045831
c 303	18	3.7	418	9	BB686162	BB686162	c 376	18	3.7	468	9	AA823991	AA823991
c 304	18	3.7	418	9	BB773985	BB773985	377	18	3.7	469	9	AI849896	AI849896
c 305	18	3.7	418	9	BB778684	BB778684	378	18	3.7	469	10	BM201529	BM201529
c 306	18	3.7	419	9	BB727814	BB727814	379	18	3.7	470	9	AW520913	AW520913
c 307	18	3.7	419	10	C92187	C92187	c 380	18	3.7	470	10	BF426717	BF426717
c 308	18	3.7	420	9	BB778592	BB778592	c 381	18	3.7	471	9	BB726679	BB726679
c 309	18	3.7	420	9	BB789543	BB789543	382	18	3.7	472	10	BM108956	BM108956

383	18	3.7	472	10	BM211974	BM211974 C0815C09-	C 456	18	3.7	532	12	AQ580750
384	18	3.7	472	10	BE689558	BE689558 uw56a05.y	C 457	18	3.7	535	9	BB728402
385	18	3.7	473	9	AV649984	AV649984 AV649984	C 458	18	3.7	536	9	AI574187
386	18	3.7	475	12	AQ480622	AQ480622 RPCI-11-2	C 459	18	3.7	536	9	AW539336
387	18	3.7	476	10	BI445047	BI445047 dah8f109.	C 460	18	3.7	537	10	BM195875
388	18	3.7	476	9	AI839932	AI839932 UI-M-AH0-	C 461	18	3.7	537	10	BM217305
389	18	3.7	481	9	AA799615	AA799615 EST189112	C 462	18	3.7	537	10	BM235857
390	18	3.7	482	9	AI118098	AI118098 ui45b04.x	C 463	18	3.7	538	12	AQ940903
391	18	3.7	485	10	BF634279	BF634279 PM3-HT090	C 464	18	3.7	539	10	BM234992
392	18	3.7	485	12	AQ129107	AQ129107 HS_3032_B	C 465	18	3.7	539	12	TA307H04Q
393	18	3.7	486	10	BM200981	BM200981 C0218F12-	C 466	18	3.7	540	12	AZ022946
394	18	3.7	486	12	AZ151908	AZ151908 SP_0033_A	C 467	18	3.7	542	9	AA946354
395	18	3.7	487	12	AQ674710	AQ674710 HS_5485_B	C 468	18	3.7	545	10	BM214714
396	18	3.7	487	12	BM043470	BM043470 RPCI-24-3	C 469	18	3.7	545	10	BM273689
397	18	3.7	489	9	AI115232	AI115232 ui47g11.x	C 470	18	3.7	545	12	AZ816255
398	18	3.7	490	10	C77228	C77228 C77228 Mous	C 471	18	3.7	546	12	AQ047202
399	18	3.7	491	10	BM212590	BM212590 C0824A03-	C 472	18	3.7	547	10	BM214009
400	18	3.7	492	9	AI118515	AI118515 ue94a11.x	C 473	18	3.7	548	9	AW538613
401	18	3.7	492	10	BG511261	BG511261 sad15f03.	C 474	18	3.7	548	10	BM214667
402	18	3.7	492	10	BM198785	BM198785 C0407C07-	C 475	18	3.7	549	9	AW542231
403	18	3.7	492	10	BF707238	BF707238 282765 MA	C 476	18	3.7	549	10	BG973636
404	18	3.7	493	9	AI118113	AI118113 ui45c11.x	C 477	18	3.7	549	10	BM212709
405	18	3.7	493	9	BB775372	BB775372 BB775372	C 478	18	3.7	549	10	BM275035
406	18	3.7	493	10	BM196969	BM196969 C0340H08-	C 479	18	3.7	549	12	AQ664726
407	18	3.7	493	10	BM208542	BM208542 C0630C07-	C 480	18	3.7	551	10	BM222627
408	18	3.7	494	12	AZ896962	AZ896962 RPCI-24-1	C 481	18	3.7	552	10	BG602945
409	18	3.7	495	9	AI118544	AI118544 ue94d11.x	C 482	18	3.7	554	9	AU046092
410	18	3.7	495	9	BB740490	BB740490 BB740490	C 483	18	3.7	554	9	BB697241
411	18	3.7	495	10	BM120732	BM120732 L0943E04-	C 484	18	3.7	554	10	BM070007
412	18	3.7	497	9	AU020982	AU020982 A0202982	C 485	18	3.7	554	10	BM249894
413	18	3.7	498	9	AI9311734	AI9311734 ui64h08.x	C 486	18	3.7	554	12	AQ053708
414	18	3.7	498	10	BM197982	BM197982 C0352C12-	C 487	18	3.7	556	9	AW537428
415	18	3.7	498	10	BM205036	BM205036 C0277H12-	C 488	18	3.7	556	10	C75988
416	18	3.7	498	10	BM237256	BM237256 K0448C12-	C 489	18	3.7	556	10	C76526
417	18	3.7	499	10	BM196148	BM196148 C0323F02-	C 490	18	3.7	557	9	AW544791
418	18	3.7	499	10	BM234583	BM234583 K0402G10-	C 491	18	3.7	558	12	B65439
419	18	3.7	500	9	AU086794	AU086794 A0086794	C 492	18	3.7	559	10	BM203848
420	18	3.7	500	10	AA536918	AA536918 vj73h05.r	C 493	18	3.7	559	10	BM236811
421	18	3.7	500	10	BM207737	BM207737 C0617C02-	C 494	18	3.7	560	9	AU020808
422	18	3.7	500	10	BM235076	BM235076 K0411C08-	C 495	18	3.7	560	10	BM195303
423	18	3.7	501	9	AL024147	AL024147 w827b28	C 496	18	3.7	562	10	B1965650
424	18	3.7	501	10	BM231231	BM231231 K0307A09-	C 497	18	3.7	562	10	BE290472
425	18	3.7	502	10	BG156404	BG156404 saa74c11.	C 498	18	3.7	563	10	BM203747
426	18	3.7	502	10	BM206953	BM206953 C0605H04-	C 499	18	3.7	563	10	BM208834
427	18	3.7	502	10	BM213221	BM213221 C0833C08-	C 500	18	3.7	564	10	BM203839
428	18	3.7	502	10	BM213439	BM213439 C0836E02-	C 501	18	3.7	564	10	BM208730
429	18	3.7	503	10	BM236669	BM236669 K0439C03-	C 502	18	3.7	564	10	BM217133
430	18	3.7	503	10	BM230585	BM230585 K0825C02-	C 503	18	3.7	565	10	C76737
431	18	3.7	504	10	BM248830	BM248830 K0823A12-	C 504	18	3.7	566	10	BM205630
432	18	3.7	504	12	AQ188512	AQ188512 HS_3229_B	C 505	18	3.7	566	10	C76026
433	18	3.7	505	10	BM203149	BM203149 C0250A07-	C 506	18	3.7	566	12	AZ714866
434	18	3.7	505	10	BM212998	BM212998 C0830B12-	C 507	18	3.7	568	9	AV608082
435	18	3.7	508	9	BB691349	BB691349 BB691349	C 508	18	3.7	568	10	BM215373
436	18	3.7	509	10	BG276567	BG276567 uv06h04.y	C 509	18	3.7	568	10	BM217128
437	18	3.7	510	10	B1565107	B1565107 RH62779.5	C 510	18	3.7	569	10	BM214678
438	18	3.7	513	9	AA779991	AA779991 zj24c04.s	C 511	18	3.7	570	10	C76653
439	18	3.7	513	9	AW541128	AW541128 C0141D02-	C 512	18	3.7	570	12	AZ105435
440	18	3.7	514	10	BM203566	BM203566 C0256C12-	C 513	18	3.7	571	10	BM215943
441	18	3.7	514	12	AQ279658	AQ279658 CUIPI-E1-	C 514	18	3.7	571	10	BM216421
442	18	3.7	515	10	BI292847	BI292847 UI-R-DO0-	C 515	18	3.7	571	10	BM217218
443	18	3.7	516	9	AW543411	AW543411 C0169E10-	C 516	18	3.7	572	9	AU020795
444	18	3.7	518	9	AA870237	AA870237 vql3e03.r	C 517	18	3.7	572	12	AQ480604
445	18	3.7	521	10	C77244	C77244 C77244 Mous	C 518	18	3.7	573	9	AU016201
446	18	3.7	522	9	AW539575	AW539575 C0121E03-	C 519	18	3.7	573	10	C79641
447	18	3.7	522	9	AW551636	AW551636 L0202E02-	C 520	18	3.7	574	9	AA866248
448	18	3.7	523	10	BF467766	BF467766 UI-M-CC0-	C 521	18	3.7	574	9	AW912752
449	18	3.7	524	10	BM212134	BM212134 C0817F02-	C 522	18	3.7	575	9	AW538302
450	18	3.7	526	9	AL034996	AL034996 r8710a44	C 523	18	3.7	575	10	C80687
451	18	3.7	526	12	AQ97894	AQ97894 HS_5080_B	C 524	18	3.7	576	9	AU043131
452	18	3.7	526	12	AQ663497	AQ663497 HS_5470_A	C 525	18	3.7	576	10	BM114982
453	18	3.7	527	9	AV667301	AV667301 AV667301	C 526	18	3.7	576	10	BM117446
454	18	3.7	530	10	BM217301	BM217301 C0893H08-	C 527	18	3.7	577	10	C80439
455	18	3.7	531	12	BH594729	BH594729 BOHJU30TF	C 528	18	3.7	577	10	C81031

529	18	3.7	578	9	AW536305	G0102H06-	602	18	3.7	625	9	AW538382	AW538382	CO106H04-
530	18	3.7	578	9	AW542798	C0162A03-	603	18	3.7	626	9	AA891547	AA891547	EST195350
531	18	3.7	578	9	AW545501	C0194E02-	604	18	3.7	628	10	BM212729	BM212729	C0826A12-
532	18	3.7	578	10	BM212208	C0818F03-	c 605	18	3.7	629	10	BG641951	BG641951	pql1c.pk0
533	18	3.7	578	12	AQ344059	RPC111-12	606	18	3.7	629	10	C77452	C77452	C77452
534	18	3.7	579	9	AW545117	C0188H02-	607	18	3.7	630	9	AV647929	AV647929	C77452
535	18	3.7	580	9	AU014946	AU014946	608	18	3.7	630	9	AW543247	AW543247	AV647929
536	18	3.7	580	9	AU019399	AU019399	609	18	3.7	631	10	BM214099	BM214099	C0167E02-
537	18	3.7	580	10	C77885	C77885	610	18	3.7	631	10	AW556309	AW556309	C0846B02-
538	18	3.7	580	10	C79611	C79611	611	18	3.7	633	9	AW554681	AW554681	L0244A07-
539	18	3.7	581	10	C79992	C79992	612	18	3.7	634	9	BM206420	BM206420	C0297D02-
540	18	3.7	581	10	C80026	C80026	613	18	3.7	635	10	BM117976	BM117976	L0858H03-
541	18	3.7	581	10	C80784	C80784	614	18	3.7	639	10	BM213185	BM213185	C0832G07-
542	18	3.7	582	9	AV601815	AV601815	615	18	3.7	639	10	BF296518	BF296518	C0832G07-
543	18	3.7	583	10	C77105	C77105	616	18	3.7	640	10	AW554289	AW554289	038PBC02
544	18	3.7	584	10	BM210907	BM210907	617	18	3.7	641	9	BF226841	BF226841	L0250C12-
545	18	3.7	584	10	BM212987	BM212987	618	18	3.7	641	9	BF226841	BF226841	u216005.x
546	18	3.7	584	10	BM213717	BM213717	619	18	3.7	643	10	BG722010	BG722010	60269H780
547	18	3.7	584	10	C77287	C77287	620	18	3.7	644	10	BF295663	BF295663	026PBG04
548	18	3.7	585	10	BM118265	BM118265	621	18	3.7	651	10	AW537136	AW537136	G0112C09-
549	18	3.7	585	10	C76637	C76637	c 622	18	3.7	653	9	A1100779	A1100779	602886077
550	18	3.7	586	10	BM211029	BM211029	623	18	3.7	655	12	A2939870	A2939870	2M0199J06
551	18	3.7	586	12	A2523793	A2523793	624	18	3.7	655	12	BF19393	BF19393	RH50424.5
552	18	3.7	587	9	A1177032	EST220639	625	18	3.7	659	10	BM232406	BM232406	K0322G09-
553	18	3.7	587	9	AV592641	AV592641	626	18	3.7	665	10	BM234598	BM234598	K0433B01-
554	18	3.7	587	9	AW545182	C0189F03-	627	18	3.7	666	10	BM246185	BM246185	K0734F07-
555	18	3.7	588	9	AW543110	C0165G07-	628	18	3.7	668	10	BE373132	BE373132	601224560
556	18	3.7	589	9	AW545261	C0191E08-	629	18	3.7	668	12	A2841032	A2841032	2M0138017
557	18	3.7	589	10	BM211553	BM211553	630	18	3.7	669	9	AI747287	AI747287	u114e09.x
558	18	3.7	591	12	AQ268847	AQ268847	631	18	3.7	675	12	AQ279923	AQ279923	CITB1-EI-
559	18	3.7	593	10	C79006	C79006	632	18	3.7	676	9	AI747565	AI747565	u120c11.x
560	18	3.7	596	9	AW539717	AW539717	633	18	3.7	676	10	BI660658	BI660658	603303769
561	18	3.7	599	9	AI931829	AI931829	634	18	3.7	678	9	AW536293	AW536293	G0102G03-
562	18	3.7	599	10	C79899	C79899	635	18	3.7	678	12	AQ986462	AQ986462	RPCT-23-3
563	18	3.7	601	10	BM206814	BM206814	636	18	3.7	679	12	BH028386	BH028386	RPCT-24-3
564	18	3.7	601	10	C80230	C80230	637	18	3.7	680	9	AI649101	AI649101	uK25q03.x
565	18	3.7	602	9	AJ396846	AJ396846	638	18	3.7	680	12	AG148608	AG148608	PaD_trsgl
566	18	3.7	603	9	AI747387	AI747387	639	18	3.7	685	10	BM214339	BM214339	C0849B10-
567	18	3.7	605	10	C80357	C80357	640	18	3.7	686	10	BG597144	BG597144	EST495822
568	18	3.7	606	12	BH050025	BH050025	641	18	3.7	696	10	BE370804	BE370804	601219190
569	18	3.7	607	9	AW542707	AW542707	642	18	3.7	697	9	AW546385	AW546385	L0007E12-
570	18	3.7	609	9	AW542900	AW542900	643	18	3.7	698	9	AW552386	AW552386	L0211A04-
571	18	3.7	609	9	AW551806	AW551806	644	18	3.7	703	12	BH595374	BH595374	BOHBB31TF
572	18	3.7	611	12	AQ037516	AQ037516	645	18	3.7	705	10	BF321411	BF321411	uz61h08.x
573	18	3.7	612	10	BF449868	BF449868	646	18	3.7	707	10	BM247579	BM247579	K0804A09-
574	18	3.7	613	12	A2453878	A2453878	647	18	3.7	707	12	AQ899446	AQ899446	HS_2014_A
575	18	3.7	614	9	AI648012	AI648012	648	18	3.7	707	12	AQ643626	AQ643626	RPCT193-Dp
576	18	3.7	615	10	BM247847	BM247847	c 649	18	3.7	714	9	AU219388	AU219388	AU219388
577	18	3.7	615	10	BM249828	BM249828	650	18	3.7	714	9	AW261730	AW261730	um91f02.x
578	18	3.7	616	10	BG976190	BG976190	651	18	3.7	714	10	BG074109	BG074109	H3131A03-
579	18	3.7	616	10	BM199794	BM199794	652	18	3.7	715	9	AW536818	AW536818	G0109B06-
580	18	3.7	616	10	BM244971	BM244971	653	18	3.7	718	10	BM212954	BM212954	C0829F01-
581	18	3.7	616	10	BM246673	BM246673	c 654	18	3.7	726	10	BF160457	BF160457	601768429
582	18	3.7	616	10	BM250705	BM250705	655	18	3.7	730	9	AW107844	AW107844	um23q03.x
583	18	3.7	616	10	BE692767	BE692767	656	18	3.7	730	10	BE273845	BE273845	601104341
584	18	3.7	618	9	AW539635	AW539635	657	18	3.7	739	9	BE055345	BE055345	GA_Ea000
585	18	3.7	619	9	AW539701	AW539701	658	18	3.7	740	9	AI596268	AI596268	uK24C02.x
586	18	3.7	619	9	AW539781	AW539781	659	18	3.7	741	9	AW146135	AW146135	um37f08.x
587	18	3.7	619	9	AW539802	AW539802	660	18	3.7	741	10	BM211217	BM211217	C0802E02-
588	18	3.7	619	12	BH301289	BH301289	c 661	18	3.7	750	10	BI520192	BI520192	603071440
589	18	3.7	620	9	AW541851	AW541851	662	18	3.7	751	12	BH573707	BH573707	BOHCU72TF
590	18	3.7	620	10	BM213687	BM213687	663	18	3.7	754	9	AW536140	AW536140	G0101A08-
591	18	3.7	620	10	BM214263	BM214263	664	18	3.7	754	10	BE096436	BE096436	601502370
592	18	3.7	620	10	BM235649	BM235649	c 665	18	3.7	757	12	BH560224	BH560224	BOGZWLTF
593	18	3.7	620	12	BH430568	BH430568	666	18	3.7	759	12	CNS02C9N	CNS02C9N	AL190868
594	18	3.7	621	9	AW545352	AW545352	667	18	3.7	760	10	BG064775	BG064775	H3023G01-
595	18	3.7	621	12	AQ240058	AQ240058	668	18	3.7	767	9	AI747083	AI747083	u109c12.x
596	18	3.7	622	10	BM207038	BM207038	669	18	3.7	767	12	BH556210	BH556210	BOHKV48TF
597	18	3.7	622	10	BM226678	BM226678	670	18	3.7	769	12	B21922	B21922	F4P15-T7 IG
598	18	3.7	622	10	BM248555	BM248555	671	18	3.7	774	9	A1327279	A1327279	mo64f05.x
599	18	3.7	623	10	BM226214	BM226214	672	18	3.7	776	10	BG064772	BG064772	H3023F10-
600	18	3.7	624	10	BM211156	BM211156	673	18	3.7	778	9	AI746330	AI746330	u105e11.x
601	18	3.7	624	12	BH615724	BH615724	c 674	18	3.7	778	10	BI454836	BI454836	603172359

675	18	3.7	778	12	AQ796876	AQ796876 nbxb0071G	C 748	17	3.5	271	12	BH143445	BH143445 TDGEA14TH
676	18	3.7	784	9	A1158885	A1158885 ui42b10.x	C 749	17	3.5	273	9	AV040912	AV040912
677	18	3.7	785	9	A1158885	A1158885 ue97c02.x	C 750	17	3.5	273	9	AA344119	AA344119 EST49991
678	18	3.7	790	10	BG064774	BG064774 H3023F12-	C 751	17	3.5	273	10	BI484000	BI484000 R667008.5
679	18	3.7	790	10	BM206985	BM206985 C0606B04-	C 752	17	3.5	274	10	BE925249	BE925249 CM4-AN008
680	18	3.7	793	9	A1596224	A1596224 uk23f07.x	C 753	17	3.5	276	9	AI909191	AI909191 IL-BT201-
681	18	3.7	793	9	A1649095	A1649095 uk25f07.x	C 754	17	3.5	276	9	BE824318	BE824318 GM70002B
682	18	3.7	795	10	BG064773	BG064773 H3023F11-	C 755	17	3.5	279	12	AZ868439	AZ868439 2M0180112
683	18	3.7	800	10	BG410034	BG410034 S10-7-A5	C 756	17	3.5	279	12	AV260465	AV260465 AV260465
684	18	3.7	813	12	BH537808	BH537808 BOHPB08TR	C 757	17	3.5	281	9	AV798655	AV798655 RC2-UM005
685	18	3.7	815	9	A1987784	A1987784 um06h12.x	C 758	17	3.5	282	9	AA226442	AA226442 NC18006.s
686	18	3.7	820	12	AQ247270	AQ247270 HS_2064_A	C 759	17	3.5	283	9	BB065754	BB065754 BB065754
687	18	3.7	831	9	A1747459	A1747459 ul15h03.x	C 760	17	3.5	283	12	AQ986268	AQ986268 RPCI-23-2
688	18	3.7	835	12	AQ746923	AQ746923 HS_5538_A	C 761	17	3.5	284	9	AA343616	AA343616 EST49426
689	18	3.7	836	9	AW105920	AW105920 um28h05.x	C 762	17	3.5	284	12	AQ527922	AQ527922 RPCI-11-3
690	18	3.7	838	9	AW108233	AW108233 um27g02.x	C 763	17	3.5	288	9	BB249039	BB249039 BB249039
691	18	3.7	841	9	A1746528	A1746528 ul08b06.x	C 764	17	3.5	291	10	BI026450	BI026450 CM4-MT028
692	18	3.7	861	12	AQ750054	AQ750054 HS_5574_A	C 765	17	3.5	291	10	BI594660	BI594660 AS_NC_19E
693	18	3.7	863	10	BG622794	BG622794 602647582	C 766	17	3.5	293	9	AW569223	AW569223 s164d04.y
694	18	3.7	874	12	CNS01XDI	AL171567 Tetraodon	C 767	17	3.5	294	12	AQ789234	AQ789234 HS_3113_B
695	18	3.7	879	9	A1596038	A1596038 uk22a08.x	C 768	17	3.5	298	9	AV134103	AV134103 AV134103
696	18	3.7	885	12	AQ878812	AQ878812 HS_3135_A	C 769	17	3.5	299	9	AV047271	AV047271 AV047271
697	18	3.7	886	12	BH181333	AL618283 T7 end of	C 770	17	3.5	300	9	AA343501	AA343501 EST49372
698	18	3.7	886	12	CNS07MZD	AW108145 um26h09.x	C 771	17	3.5	302	10	M77939	M77939 EST01523 Fe
699	18	3.7	890	9	AW108145	AW108145 um26h09.x	C 772	17	3.5	307	9	AV710185	AV710185 AV710185
700	18	3.7	895	10	BF683994	BF683994 602141327	C 773	17	3.5	307	9	BE165968	BE165968 MR3-HT048
701	18	3.7	923	10	BF583473	BF583473 602097491	C 774	17	3.5	307	10	Z45258	Z45258 HSC2KH091 n
702	18	3.7	934	12	BH146654	BH146654 ENQL55TR	C 775	17	3.5	308	9	AV100794	AV100794 AV100794
703	18	3.7	935	12	AZ204912	AZ204912 SP_0097_B	C 776	17	3.5	310	9	BE150312	BE150312 QV4-HT026
704	18	3.7	940	9	AW279338	AW279338 GA_Ea002	C 777	17	3.5	311	12	BH584386	BH584386 BOHHX20TF
705	18	3.7	943	10	B1662923	B1662923 603286676	C 778	17	3.5	312	9	BB058327	BB058327 BB058327
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707	18	3.7	996	12	CNS04RLL	AL130405 Tetraodon	C 780	17	3.5	313	10	T36119	T36119 EST96907 Hu
708	18	3.7	1017	12	CNS07CEW	AL439086 T3 end of	C 781	17	3.5	315	10	BE102135	BE102135 UI-R-BT1-
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## ALIGNMENTS

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DEFINITION prime, mRNA sequence.
AL548180
VERSION AL548180.1 GI:12882943
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 982)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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/note="Vector: pCMVSPORT 6; Site:1. NotI; 1st strand cDNA
was primed with a NotI-oligo(df) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
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Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 275 a 208 c 214 g 284 t 1 others
ORIGIN
Query Match 100.0%; Score 489; DB 9; Length 982;
Best Local Similarity 100.0%; Pred. No. 4.4e-239; Indels 0; Gaps 0;
Matches 489; Conservative 0; Mismatches 0;
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Db 358 ATGAGAAATTTTGGAAACACATTTGAGAAAGTATTTCATCCAGTGTCTACTTGTGTTTACTT 417
Qy 61 CTAAACAGTCAATTTTCTAACTGAAGCTGGCATTCATGCTTCTTCATTTGGGCTGTTTCACT 120
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Qy 121 GCAGGGCTTCCTAAACAGAGCCCACTGGGTGAATGTAATAAGTATTTGAAAAAAATTT 180
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Db 718 AGTTTGTCTTCTTAATGGGAATGTAACAGATCTGGATGCAAGAGATGTGAGGAACTGGAG 777
Qy 421 GAAAAAATATTTAAAGATTTTTCGAGAGTTCCTTGTACATATTTGTCCAATGTTTCATCAAC 480
Db 778 GAAAAAATATTTAAAGATTTTTCGAGAGTTCCTTGTACATATTTGTCCAATGTTTCATCAAC 837
Qy 481 ACTTCTTGA 489
Db 838 ACTTCTTGA 846
RESULT 2
AL5463370 509 bp mRNA linear EST 10-JUN-1997
LOCUS AL5463370
DEFINITION zyx97d12.r1 Soares_NHMPUL_S1 Homo sapiens cDNA clone IMAGE:811703 5,
similar to SW:ILL15_HUMAN P40933 INTERLEUKIN-15 PRECURSOR ;, mRNA
sequence.
ACCESSION AL5463370
VERSION AL5463370.1 GI:2188254
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 509)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.,
Schellensberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wyllie
,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
```

Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Possible reversed clone: similarity on wrong strand  
Seq primer: -28m13 rev2 ET from Amersham  
High quality sequence stop: 416.

#### FEATURES

source

1. .509  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="IMAGE:811703"  
/tissue\_type="Soares\_NhHMPu\_S1"  
/tissue\_type="Pooled human melanocyte, fetal heart, and pregnant uterus"  
/lab\_host="DH10B"  
/note="Organ: mixed (see below); Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site1: Not I; Site2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NBHM, pregnant uterus NBHPU, and fetal heart NBH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."  
149 a 91 c 108 g 161 t

#### BASE COUNT

ORIGIN

Query Match 71.6%; Score 350; DB 9; Length 509;  
Best Local Similarity 99.8%; Pred. No. 5.3e-168;  
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACACATTTGAGAGTATTTCATCCAGTGCTACTTGTTTACTT 60  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 61 CTAACAGTCATTTTCTAACTGAAGTGGCATTCATGCTCTTTCATTTTGGCTGTTTCAGT 120  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 165 CTAACAGTCATTTTCTAACTGAAGTGGCATTCATGCTCTTTCATTTTGGCTGTTTCAGT 224  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 121 GCAGGCTTCCTAAACAGAGCCAACTGGTGAATGTAATAAGTGATTTGAAAAAAT 180  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 225 GCAGGCTTCCTAAACAGAGCCAACTGGTGAATGTAATAAGTGATTTGAAAAAAT 284  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 181 GAAGATCTTATTCATCTATGCATATTGATGCTACTTTATATACGGAAGTGATGTCAC 240  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 285 GAAGATCTTATTCATCTATGCATATTGATGCTACTTTATATACGGAAGTGATGTCAC 344  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 241 CCCAGTTGCAAGTAACAGCAATGAAGTCTTCTCTTGGAGTTACAAGTTATTTTCACTT 300  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 345 CCCAGTTGCAAGTAACAGCAATGAAGTCTTCTCTTGGAGTTACAAGTTATTTTCACTT 404  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 301 GAGTCGGAGATCCAGTATTCATGATACAGTAGAAAACTGATCATCTCAGCAACAAC 360  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 405 GAGTCGGAGATCCAGTATTCATGATACAGTAGAAAACTGATCATCTCAGCAACAAC 464  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 361 AGTTTCTCTTCTAATGGGAATGTAACAGAAATCTGGATGCAA 401  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 465 AGTTTCTCTTCTAATGGGAATGTAACAGAAATCTGGATGCAA 505  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

#### RESULT 3

AL572832/c

LOCUS

DEFINITION

AL572832

prime, mRNA sequence.

AL572832

AL572832.1 GI:12931481

KEYWORDS

EST.

SOURCE

human.

994 bp mRNA linear EST 16-FEB-2001

AL572832 LTI\_NFL006\_PL2 Homo sapiens cDNA clone CS0D1034T009 3

prime, mRNA sequence.

AL572832

AL572832.1 GI:12931481

KEYWORDS

EST.

SOURCE

human.

#### ORGANISM

Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

#### REFERENCE

1 (bases 1 to 994)

AUTHORS

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE

Full-length cDNA libraries and normalization

JOURNAL

Unpublished (2001)

COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers

1. .994

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="LTI\_NFL006\_PL2"

/tissue\_type="placenta"

/note="Vector: pCMVSPORT 6; Site1: NotI; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and

cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed by

a division of Invitrogen 9800 Medical Center Drive

Rockville, Maryland 20850, USA Fax : (1) 301 610 8371

Email : filang@lifetech.com URL :

http://fulllength.invitrogen.com"

BASE COUNT 333 a 186 c 154 g 316 t 5 others

ORIGIN

Query Match 61.8%; Score 302; DB 9; Length 994;  
Best Local Similarity 100.0%; Pred. No. 1.8e-143;  
Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 TTATTCATCTATGTCATATTGATGCTACTTTATATACGGAAGTGTTCACCCAGTT 247  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 861 TTATTCATCTATGTCATATTGATGCTACTTTATATACGGAAGTGTTCACCCAGTT 802  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 248 GCAAGTAACAGCAATGAAGTGTCTCTCTGGAGTTACAAGTTATTTCACTTGAGTCCG 307  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 801 GCAAGTAACAGCAATGAAGTGTCTCTCTGGAGTTACAAGTTATTTCACTTGAGTCCG 742  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 308 GAGATCCAAGTATTCATGATACAGTAGAAAATCTGATCATCTCAGCAACAACAGTTGT 367  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 741 GAGATCCAAGTATTCATGATACAGTAGAAAATCTGATCATCTCAGCAACAACAGTTGT 682  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 368 CTTCTAATGGGAATGTAACAGAAATCTGGATGCAAAAGATGTGAGGAATGAGGAGAAAAA 427  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 681 CTTCTAATGGGAATGTAACAGAAATCTGGATGCAAAAGATGTGAGGAATGAGGAGAAAAA 622  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 428 ATATTAAAGAAATTTTGGCAGAGTTTGTACATATTCTCCAAATGTTTCATCAACACTTCT 487  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 621 ATATTAAAGAAATTTTGGCAGAGTTTGTACATATTCTCCAAATGTTTCATCAACACTTCT 562  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 488 GA 489  
Db ||  
QY 561 GA 560  
Db ||

#### RESULT 4

BG184658

LOCUS

DEFINITION

RST3720 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.

ACCESSION

BG184658

VERSION

BG184658.1 GI:13706473

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 800)

AUTHORS	Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.		REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 637)		
	Creation of genome-wide protein expression libraries using random activation of gene expression			NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .		
	Nat. Biotechnol. 19 (5), 440-445 (2001)			National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
	21227151			Unpublished (1997)		
JOURNAL MEDLINE COMMENT	Contact: Scott J. Cain		JOURNAL COMMENT	Contact: Robert Strausberg, Ph.D.		
	Athersys, Inc.			Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a>		
	3201 Carnegie Ave, Cleveland, OH 44115, USA			Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.		
	Tel: 216 431 9900			cDNA Library Preparation: Life Technologies, Inc.		
TITLE	Fax: 216 361 9596		FEATURES	DNA Sequencing by: Washington University Genome Sequencing Center		
	Email: <a href="mailto:scain@atersys.com">scain@atersys.com</a>			Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://www-bio.llnl.gov/bbrp/image/image.html">www-bio.llnl.gov/bbrp/image/image.html</a>		
	High quality sequence stop: 444.			Insert Length: 3944 Std Error: 0.00		
	Location/Qualifiers			Seq primer: -40UP from Gibco		
FEATURES source	1. .800		BASE COUNT	207 a 111 c 91 g 227 t 1 others		
	/organism="Homo sapiens"			ORIGIN		
	/db_xref="taxon:9606"			Query Match		
	/clone_lib="Athersys RAGE Library"			Best Local Similarity 47.6%; Score 233; DB 9; Length 637;		
FEATURES source	/cell_line="Htl080"		QY	257 CAGCAATGAAGTGCTTCTCTGGAGTTACAAAGTTATTTCACCTTCAGTCCGAGATGCAA 316		
	/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is Htl080, since a random activation method was used, these sequence tags are not necessarily expressed in Htl080 under normal circumstances."			Db 570 CAGCAATGAAGTGCTTCTCTGGAGTTACAAAGTTATTTCACCTTCAGTCCGAGATGCAA 511		
	expressed in Htl080 under normal circumstances."			QY 317 GTATTTCATGATCAGTAGAAAATCTGATCATCTAGCAACAACAGTTGTGTTCTTAATG 376		
	235 a 151 c 165 g 247 t 2 others			Db 510 GTATTTCATGATCAGTAGAAAATCTGATCATCTAGCAACAACAGTTGTGTTCTTAATG 451		
BASE COUNT	53.4%; Score 261; DB 10; Length 800;		QY	377 GGAATGTAACAGAAATCTGGATGCAAGAAGATGTGAGAACTGGAGAAAATAATATAAG 436		
	Best Local Similarity 99.7%; Pred. No. 1.6e-122;			Db 450 GGAATGTAACAGAAATCTGGATGCAAGAAGATGTGAGAACTGGAGAAAATAATATAAG 391		
	Matches 311; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			QY 437 AATTTTTCAGAGCTTTGTGACATATTGTCCAAATGTTTCATCAACACTTCTTTGA 489		
	Query Match			Db 390 AATTTTTCAGAGCTTTGTGACATATTGTCCAAATGTTTCATCAACACTTCTTTGA 338		
BASE COUNT	53.4%; Score 261; DB 10; Length 800;		QY	437 AATTTTTCAGAGCTTTGTGACATATTGTCCAAATGTTTCATCAACACTTCTTTGA 489		
	Best Local Similarity 99.7%; Pred. No. 1.6e-122;			Db 390 AATTTTTCAGAGCTTTGTGACATATTGTCCAAATGTTTCATCAACACTTCTTTGA 338		
	Matches 311; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			RESULT 6		
	Query Match			BI832895		
BASE COUNT	53.4%; Score 261; DB 10; Length 800;		QY	301 GAGTCCGGAGAT 312		
	Best Local Similarity 99.7%; Pred. No. 1.6e-122;			Db 565 GAGTCCGGAGAT 576		
	Matches 311; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			LOCUS		
	Query Match			BI832895		
BASE COUNT	53.4%; Score 261; DB 10; Length 800;		QY	301 GAGTCCGGAGAT 312		
	Best Local Similarity 99.7%; Pred. No. 1.6e-122;			Db 565 GAGTCCGGAGAT 576		
	Matches 311; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			DEFINITION		
	Query Match			BI832895		
BASE COUNT	53.4%; Score 261; DB 10; Length 800;		QY	301 GAGTCCGGAGAT 312		
	Best Local Similarity 99.7%; Pred. No. 1.6e-122;			Db 565 GAGTCCGGAGAT 576		
	Matches 311; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			ACCESSION		
	Query Match			BI860008		
BASE COUNT	53.4%; Score 261; DB 10; Length 800;		QY	301 GAGTCCGGAGAT 312		
	Best Local Similarity 99.7%; Pred. No. 1.6e-122;			Db 565 GAGTCCGGAGAT 576		
	Matches 311; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			VERSION		
	Query Match			BI860008		
BASE COUNT	53.4%; Score 261; DB 10; Length 800;		QY	301 GAGTCCGGAGAT 312		
	Best Local Similarity 99.7%; Pred. No. 1.6e-122;			Db 565 GAGTCCGGAGAT 576		
	Matches 311; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			KEYWORDS		
	Query Match			EST.		
BASE COUNT	53.4%; Score 261; DB 10; Length 800;		QY	301 GAGTCCGGAGAT 312		
	Best Local Similarity 99.7%; Pred. No. 1.6e-122;			Db 565 GAGTCCGGAGAT 576		
	Matches 311; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			ORGANISM		
	Query Match			Homo sapiens		
BASE COUNT	53.4%; Score 261; DB 10; Length 800;		QY	301 GAGTCCGGAGAT 312		
	Best Local Similarity 99.7%; Pred. No. 1.6e-122;			Db 565 GAGTCCGGAGAT 576		
	Matches 311; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			REFERENCE		
	Query Match			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
BASE COUNT	53.4%; Score 261; DB 10; Length 800;		QY	301 GAGTCCGGAGAT 312		
	Best Local Similarity 99.7%; Pred. No. 1.6e-122;			Db 565 GAGTCCGGAGAT 576		
	Matches 311; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			AUTHORS		
	Query Match			NIH-MGC <a href="http://mgc.ncbi.nlm.nih.gov/">http://mgc.ncbi.nlm.nih.gov/</a> .		
BASE COUNT	53.4%; Score 261; DB 10; Length 800;		QY	301 GAGTCCGGAGAT 312		
	Best Local Similarity 99.7%; Pred. No. 1.6e-122;			Db 565 GAGTCCGGAGAT 576		
	Matches 311; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			TITLE		
	Query Match			National Institutes of Health, Mammalian Gene Collection (MGC)		
BASE COUNT	53.4%; Score 261; DB 10; Length 800;		QY	301 GAGTCCGGAGAT 312		
	Best Local Similarity 99.7%; Pred. No. 1.6e-122;			Db 565 GAGTCCGGAGAT 576		
	Matches 311; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			JOURNAL		
	Query Match			Unpublished (1999)		

## COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM11557 row: k column: 20  
High quality sequence stop: 756.  
Location/Qualifiers  
source  
1. .756  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5221771"  
/clone\_lib="NIH\_MGC\_120"  
/lab\_host="DH10B"  
/note="Organ: pooled pancreas and spleen; Vector: PCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source anonymous pool of 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH\_MGC Library."  
BASE COUNT 247 a 115 c 143 g 251 t  
ORIGIN

Query Match 39.1%; Score 191; DB 10; Length 756;  
Best Local Similarity 100.0%; Pred. No. 1e-86;  
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 174 AAAAATTGAAGCTTATTCATCATGATTCATGCTACTTATATATACGGAAGTGA 233  
|||||  
Db 1 AAAAATTGAAGCTTATTCATCATGATTCATGCTACTTATATATACGGAAGTGA 60  
|||||

QY 234 TGTTCACCCAGTTGCGAAGTACAGCAATGAAGTGTCTTCTTGGAGTTACAAAGTTAT 293  
|||||  
Db 61 TGTTCACCCAGTTGCGAAGTACAGCAATGAAGTGTCTTCTTGGAGTTACAAAGTTAT 120  
|||||

QY 294 TTCACTTGAGTCCGAGATGCAAGTATTCATGATACAGTAGAGAAATCTGATCATCCTAGC 353  
|||||  
Db 121 TTCACTTGAGTCCGAGATGCAAGTATTCATGATACAGTAGAGAAATCTGATCATCCTAGC 180  
|||||

QY 354 AAACAACAGTT 364  
|||||  
Db 181 AAACAACAGTT 191  
|||||

## RESULT 7

BI758686  
LOCUS BI758686 872 bp mRNA linear EST 25-SEP-2001  
DEFINITION 603024240F1 NIH\_MGC\_114 Homo sapiens cDNA clone IMAGE:5194977 5', mRNA sequence.  
ACCESSION BI758686  
VERSION BI758686.1 GI:15750264  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 872)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

## FEATURES

source  
1. .872  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5194977"  
/clone\_lib="NIH\_MGC\_114"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: PCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH\_MGC Library."  
BASE COUNT 200 a 222 c 227 g 223 t  
ORIGIN

Query Match 35.2%; Score 172; DB 10; Length 872;  
Best Local Similarity 100.0%; Pred. No. 5.2e-77;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACCAACATTTGAGAAGTATTTCCATCCAGTGTACTGTGTTTACTT 60  
|||||  
Db 592 ATGAGAAATTCGAAACCAACATTTGAGAAGTATTTCCATCCAGTGTACTGTGTTTACTT 651  
|||||

QY 61 CTAAACAGCTATTTTCTAACTGCACTGGCATTCATGTCTTCATTTTGGCTGTGTTTCACT 120  
|||||  
Db 652 CTAAACAGCTATTTTCTAACTGCACTGGCATTCATGTCTTCATTTTGGCTGTGTTTCACT 711  
|||||

QY 121 CGAGGGCTTCTAAACAGAGACCACTGGGTGAATGTAAATGAAGTATTGA 172  
|||||  
Db 712 CGAGGGCTTCTAAACAGAGACCACTGGGTGAATGTAAATGAAGTATTGA 763  
|||||

## RESULT 8

BI76741  
LOCUS N76741 471 bp mRNA linear EST 02-APR-1996  
DEFINITION Y282g12.r1 Soares\_multiple\_sclerosis\_2bNHMSP Homo sapiens cDNA clone IMAGE:289606 5', similar to SW:IL15\_HUMAN P40933 INTERLEUKIN-15 PRECURSOR ;, mRNA sequence.  
ACCESSION N76741  
VERSION N76741.1 GI:1239319  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 471)  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT Contact: Willson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: reverse ET

## FEATURES

source  
1. .872  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5194977"  
/clone\_lib="NIH\_MGC\_114"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: PCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH\_MGC Library."  
BASE COUNT 200 a 222 c 227 g 223 t  
ORIGIN

Query Match 35.2%; Score 172; DB 10; Length 872;  
Best Local Similarity 100.0%; Pred. No. 5.2e-77;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACCAACATTTGAGAAGTATTTCCATCCAGTGTACTGTGTTTACTT 60  
|||||  
Db 592 ATGAGAAATTCGAAACCAACATTTGAGAAGTATTTCCATCCAGTGTACTGTGTTTACTT 651  
|||||

QY 61 CTAAACAGCTATTTTCTAACTGCACTGGCATTCATGTCTTCATTTTGGCTGTGTTTCACT 120  
|||||  
Db 652 CTAAACAGCTATTTTCTAACTGCACTGGCATTCATGTCTTCATTTTGGCTGTGTTTCACT 711  
|||||

QY 121 CGAGGGCTTCTAAACAGAGACCACTGGGTGAATGTAAATGAAGTATTGA 172  
|||||  
Db 712 CGAGGGCTTCTAAACAGAGACCACTGGGTGAATGTAAATGAAGTATTGA 763  
|||||

## RESULT 8

BI76741  
LOCUS N76741 471 bp mRNA linear EST 02-APR-1996  
DEFINITION Y282g12.r1 Soares\_multiple\_sclerosis\_2bNHMSP Homo sapiens cDNA clone IMAGE:289606 5', similar to SW:IL15\_HUMAN P40933 INTERLEUKIN-15 PRECURSOR ;, mRNA sequence.  
ACCESSION N76741  
VERSION N76741.1 GI:1239319  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 471)  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT Contact: Willson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: reverse ET

High quality sequence stop: 296.

FEATURES  
source  
1. 471  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="GDB:3905446"  
/db\_xref="taxon:9606"  
/clone\_lib="IMAGE:289606"  
/clone\_lib="Soares\_multiple\_sclerosis\_2NbHMSp"  
/sex="male"  
/tissue\_type="multiple sclerosis lesions"  
/dev\_stage="Age 46"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="vector: p7T3D (Pharmacia) with a modified  
polylinker V.TYPE: phagemid; Site.1: Not I; Site.2: Eco RI  
; 1st strand cDNA was primed with a Not I - oligo(dT)  
primer [5].  
TGTACCAATCTGAAGTGGGCGCGCATTTTTTTTTTTTTTTT 3'],  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified p7T3 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Soares and M.Patima Bonaldo. RNA from 4 multiple sclerosis  
lesions from one patient was kindly provided by Dr. Kevin  
G. Becker (NINDS/NIH). "

BASE COUNT 161 a 68 c 83 g 154 t 5 others  
ORIGIN

Query Match 28.0%; Score 137; DB 10; Length 471;  
Best Local Similarity 100.0%; Pred. No. 4.2e-59;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 AAATCTGATCTACCAACACACTTGTCTTCTTAATGGGAATGTACAGAACTCG 394  
|||||  
Db 38 AAATCTGATCTACCAACACACTTGTCTTCTTAATGGGAATGTACAGAACTCG 97  
|||||  
QY 395 GATGCAAGAATGTGAGGAAGTGGAGGAAAAAATATTAAAGAAATTTTGCAGAGTTTG 454  
|||||  
Db 98 GATGCAAGAATGTGAGGAAGTGGAGGAAAAAATATTAAAGAAATTTTGCAGAGTTTG 157  
|||||

QY 455 TACATATTGTCAAATG 471  
|||||  
Db 158 TACATATTGTCAAATG 174  
|||||

RESULT 9  
AW804168/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 494)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Negai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.

REFERENCE  
AUTHORS  
TITLE  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil

JOURNAL  
MEDLINE  
COMMENT  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-IL2-UT0071-050  
900-144-B03&t3=2000-09-05&t4=1)

Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-PM4-UM0088-050  
400-001-d12&t3=2000-04-05&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 494.

FEATURES  
source  
1. 494  
Location/Qualifiers

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="UM0088"  
/dev\_stage="Adult"  
/note="Organ: uterus; Vector: puc18; Site.1: SmaI; Site.2:  
SmaI; A mini-library was made by cloning products derived  
from ORESTES PCR (U.S. Letters Patent application No. 196  
,716 - Ludwig Institute for Cancer Research) profiles  
into the puc 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions. "

BASE COUNT 174 a 91 c 69 g 160 t  
ORIGIN

Query Match 16.8%; Score 82; DB 9; Length 494;  
Best Local Similarity 100.0%; Pred. No. 5.5e-31;  
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 408 TGAGGAAGTGGAGGAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTGTCCA 467  
|||||  
Db 494 TGAGGAAGTGGAGGAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTGTCCA 435  
|||||

QY 468 AATGTTTCATCAACACTTCTTGA 489  
|||||  
Db 434 AATGTTTCATCAACACTTCTTGA 413  
|||||

RESULT 10  
BF095213  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 309)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Negai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.

REFERENCE  
AUTHORS  
TITLE  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil

JOURNAL  
MEDLINE  
COMMENT  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-IL2-UT0071-050  
900-144-B03&t3=2000-09-05&t4=1)

Seq primer: puc 18 forward  
High quality sequence stop: 309.  
Location/Qualifiers  
1. .309

#### FEATURES

source  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="UT0071"  
/dev\_stage="Adult"

/note="Organ: uterus\_tumor; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
BASE COUNT 110 a 48 c 55 g 96 t  
ORIGIN

Query Match 15.7%; Score 77; DB 10; Length 309;  
Best Local Similarity 100.0%; Pred. No. 2.1e-28;  
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 387 AGAATCGGATGCAAGATGTCGAGAACTGGAGGAGGAAAAATATTAAAGAAATTTTGCA 446  
|||||  
Db 79 AGAATCGGATGCAAGATGTCGAGAACTGGAGGAGGAAAAATATTAAAGAAATTTTGCA 138  
|||||  
QY 447 GAGTTTGTACATATTG 463  
|||||  
Db 139 GAGTTTGTACATATTG 155  
|||||

#### RESULT 11

AW804165/c  
LOCUS  
PM4-UM0088-050400-001-cl1 UM0088 Homo sapiens cDNA, mRNA linear EST 16-MAY-2000  
DEFINITION  
AW804165  
ACCESSION  
AW804165.1 GI:7856035  
VERSION  
KEYWORDS  
SOURCE  
human.

#### ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 483)

DIAS Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663

#### TITLE

JOURNAL  
MEDLINE  
COMMENT  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-PM4-UM0088-050  
400-001-cl1&t3=2000-04-05&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 483.

#### FEATURES

source  
Location/Qualifiers  
1. .483  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="UM0088"

/dev\_stage="Adult"

/note="Organ: uterus; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
BASE COUNT 175 a 87 c 67 g 154 t  
ORIGIN

Query Match 14.7%; Score 72; DB 9; Length 483;  
Best Local Similarity 100.0%; Pred. No. 7.2e-26;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 418 GAGGAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTGTCACAAATGTTCAIC 477  
|||||  
Db 483 GAGGAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTGTCACAAATGTTCAIC 424  
|||||  
QY 478 AACACTTCTTGA 489  
|||||  
Db 423 AACACTTCTTGA 412  
|||||

#### RESULT 12

BF088290/c

LOCUS

DEFINITION

BF088290

ACCESSION

VERSION

KEYWORDS

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 301)

DIAS Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

CONTACT: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-CM1-HT0875-060

900-385-g04&t3=2000-09-06&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 301.

Location/Qualifiers

1. .301

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="HT0875"

/dev\_stage="Adult"

/note="Organ: head\_neck; Vector: puc18; Site\_1: SmaI;

Site\_2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

```
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      96 a      56 c      48 g      101 t
ORIGIN

Query Match      12.9%; Score 63; DB 10; Length 301;
Best Local Similarity 100.0%; Pred. No. 3e-21;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 427 AATATTAAAGATTTTGCAGAGTTTGTACATATTTGCCAAATGTTCAACACTTCT 486
|||||
Db 286 AATATTAAAGATTTTGCAGAGTTTGTACATATTTGCCAAATGTTCAACACTTCT 227

QY 487 TGA 489
|||
Db 226 TGA 224

RESULT 13
N49734/c
LOCUS      N49734      474 bp      mRNA      linear      EST 14-FEB-1996
DEFINITION yz06b12.s1 Soares_multiple_sclerosis_2NBH MSP Homo sapiens cDNA
            clone IMAGE:282239 3' similar to SW:IL15_HUMAN P40933
INTERLEUKIN-15 PRECURSOR ; mRNA sequence.
ACCESSION  N49734      GI:1190900
VERSION     EST.
KEYWORDS    human.
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 474)
AUTHORS     Hillier,L., Clark,N., Dubucque,T., Ellistson,K., Hawkins,M., Holman
            ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
            Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
            ,R., Williamson,A., Wohldmann,P. and Wilson,R.
            The WashU-Merck EST Project
            Unpublished (1995)
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: ml3 -40 forward
            High quality sequence stop: 263.
FEATURES     source
            1..474
                /organism="Homo sapiens"
                /db_xref="GDB:3900767"
                /db_xref="taxon:9606"
                /clone="IMAGE:282239"
                /clone_lib="Soares_multiple_sclerosis_2NBH MSP"
                /sex="male"
                /tissue_type="multiple sclerosis lesions"
                /dev_stage="Age 46"
                /lab_host="DH10B (ampicillin resistant)"
                /note="vector: pT73D (Pharmacia) with a modified
                polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco RI
                ; 1st strand cDNA was primed with a Not I - oligo(dT)
                primer [5'
                TGTACCAATCTGAAGTGGGAGCGCGCATTTTCTTTTCTTTTCTTTT 3'],
                double-stranded cDNA was size selected, ligated to Eco RI
                adapters (Pharmacia), digested with Not I and cloned into
                the Not I and Eco RI sites of a modified pT73 vector
                (Pharmacia). Library went through one round of
                normalization to a Cot = 5. Library constructed by Bento
                Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis
                lesions from one patient was kindly provided by Dr. Kevin
                G. Becker (NINDS/NIH)."
```

```
BASE COUNT      160 a      81 c      67 g      161 t      5 others
ORIGIN

Query Match      11.2%; Score 55; DB 10; Length 474;
Best Local Similarity 100.0%; Pred. No. 3.5e-17;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 435 AGAATTTTTCAGAGTTTGTACATATTTGTCCAAATGTTCAACACTTCTTGA 489
|||||
Db 367 AGAATTTTTCAGAGTTTGTACATATTTGTCCAAATGTTCAACACTTCTTGA 313

RESULT 14
BE177883
LOCUS      BE177883      278 bp      mRNA      linear      EST 22-JUN-2000
DEFINITION RC3-HT06000-170300-011-e04 HT06000 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BE177883
VERSION     BE177883.1 GI:8657035
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 278)
AUTHORS     Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
            Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
            20202663
            Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-RC3-HT06000-170
            300-011-e04&t3=2000-03-17&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 9
            High quality sequence stop: 278.
FEATURES     source
            1..278
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_lib="HT06000"
                /dev_stage="Adult"
                /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                Site_2: SmaI; A mini-library was made by cloning products
                derived from ORESTES PCR (U.S. Letters Patent application
                No. 196,716 - Ludwig Institute for Cancer Research)
                profiles into the pUC 18 vector. Reverse transcription of
                tissue mRNA and cDNA amplification were performed under
                low stringency conditions."
                low stringency conditions."
BASE COUNT      75 a      50 c      54 g      98 t      1 others
ORIGIN

Query Match      11.0%; Score 54; DB 9; Length 278;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTTCGAACACACATTTTGAGAAGTATTTCCATCCAGTCTACTGTGT 54
|||||
```

Db 216 ATGAGAATTTCGAACACACATTGAGAGTATTTCATCCAGTGTCTACTTGTGT 269

RESULT 15  
LOCUS BI766231 718 bp mRNA linear EST 25-SEP-2001  
DEFINITION 603052877F1 NTH\_MGC\_122 Homo sapiens cDNA clone IMAGE:5202523 5',  
mRNA sequence.  
ACCESSION BI766231  
VERSION BI766231.1 GI:15757809  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 718)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
Tissue procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILLNL at:  
<http://image.llnl.gov>  
Plate: LLAM11507 row: 1 column: 20  
High quality sequence stop: 717.

FEATURES  
source  
1..718  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5202523"  
/clone\_lib="NTH\_MGC\_122"  
/lab\_host="DH10B"  
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;  
Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source  
anonymous pool of 24 week female lung, 16 week female  
spleen, and 20-22 week male spleens. Library is oligo-dT  
primed and directionally cloned (EcoRV site is destroyed  
upon cloning). Average insert size 1.4 kb, insert size  
range 1-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 026. Note:  
this is a NIH-MGC Library."  
BASE COUNT 144 a 184 c 188 g 201 t 1 others  
ORIGIN

Query Match 11.0%; Score 54; DB 10; Length 718;  
Best Local Similarity 100.0%; Pred. No. 1.1e-16;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAATTTCGAACACACATTGAGAGTATTTCATCCAGTGTCTACTTGTGT 54  
|||||  
Db 620 ATGAGAATTTCGAACACACATTGAGAGTATTTCATCCAGTGTCTACTTGTGT 673  
|||||

RESULT 16  
LOCUS BE598667 550 bp mRNA linear EST 11-SEP-2000  
DEFINITION RC2-UT0023-290700-011-b01 UT0023 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BE598667  
VERSION BE598667.1 GI:10085736  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 550)  
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare  
, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=4t2-RC2-UT0023-290>)  
700-011-b01&t3=2000-07-29&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 7  
High quality sequence stop: 548.  
FEATURES  
source  
1..550  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="UT0023"  
/dev\_stage="Adult"  
/note="Organ: uterus tumor; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."  
BASE COUNT 184 a 75 c 104 g 186 t 1 others  
ORIGIN

Query Match 10.6%; Score 52; DB 10; Length 550;  
Best Local Similarity 100.0%; Pred. No. 1.2e-15;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 TTGCTTCTAATGGGAATGTACAGAACTCGATCGAAGAATGTGAGGAAC 415  
|||||  
Db 10 TTGCTTCTAATGGGAATGTACAGAACTCGATCGAAGAATGTGAGGAAC 61  
|||||

RESULT 17  
LOCUS BF379349 166 bp mRNA linear EST 27-NOV-2000  
DEFINITION RC2-UT0023-110800-015-g08\_1 UT0023 Homo sapiens cDNA, mRNA  
sequence.  
ACCESSION BF379349  
VERSION BF379349.1 GI:11368474  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 166)  
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare  
, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663

COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC2&t2=RC2-UT0023-  
110800-015-g08\_1&t3=2000-08-11&t4=1)  
Seq primer: puc 18 forward.

FEATURES

source

1. 166

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="UT0023"  
/dev\_stage="Adult"

/note="Organ: uterus\_tumor; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

60 a 26 c 33 g 47 t

BASE COUNT  
ORIGIN

Query Match

Best Local Similarity 10.0%; Score 49; DB 10; Length 166;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 364

TTGCTCTTAATGGGAATACACGAATCTGGATGCAAGATGTGAGG 412

Db 51

TTGCTCTTAATGGGAATTAACGAATCTGGATGCAAGATGTGAGG 99

RESULT 18

BI756810

LOCUS 603024487F1 NIH\_MGC\_114 Homo sapiens cDNA clone IMAGE:5194964 5',  
mRNA sequence.

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 817)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Sequencing by: the I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLML1487 row: n column: 21

High quality sequence start: 5

High quality sequence stop: 711.

Location/Qualifiers

1. .817

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="IMAGE:5194964"

/clone\_lib="NIH\_MGC\_114"

FEATURES

source

/lab\_host="DH10B"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: EcoRV (destroyed); RNA source anonymous pool of 6  
male brains, age range 23-27 yo. Library is oligo-dT  
primed and directionally cloned (EcoRV site is destroyed  
upon cloning). Average insert size 1.5 kb, insert size  
range 1-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 019. Note:  
this is a NIH\_MGC Library."

186 a 215 c 209 g 206 t

BASE COUNT  
ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 5.4e-08; Length 817;

Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 82

GAAGCTGCATTCATGCTCTTCATTTGGGCTGTTTCA 118

Db 651

GAAGCTGCATTCATGCTCTTCATTTGGGCTGTTTCA 687

RESULT 19

BF088272/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 275)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-CM1-HT0875-060

900-385-a05&t3=2000-09-06&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 4

High quality sequence stop: 275.

Location/Qualifiers

1. .275

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="HT0875"

/dev\_stage="Adult"

/note="Organ: head\_neck; Vector: puc18; Site\_1: SmaI;

Site\_2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

[illegible]

## RESULT 22

BB661271 631 bp mRNA linear EST 26-OCT-2001  
 LOCUS BB661271 RIKEN full-length enriched, 0 day neonate kidney Mus  
 DEFINITION musculus cDNA clone D63003E03 5', mRNA sequence.  
 BB661271  
 ACCESSION BB661271.1 GI:16495050  
 VERSION  
 KEYWORDS  
 SOURCE house mouse.

## ORGANISM

Mus musculus  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

## REFERENCE

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,  
 Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda  
 ,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,  
 Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki  
 ,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,  
 Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,  
 Muramatsu,M. and Hayashizaki,Y.  
 RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

## TITLE

## JOURNAL

## COMMENT

Unpublished (2001)  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center(GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gsc.riken.go.jp,  
 URL:http://genome.gsc.riken.go.jp/  
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh  
 ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)  
 wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,  
 Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura  
 ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and  
 Hayashizaki,Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)  
 Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara  
 ,Y. and Hayashizaki,Y.  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa  
 ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and  
 Hayashizaki,Y.  
 Computational Analysis of Full-Length Mouse cDNAs Compared with  
 Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)  
 Please visit our web site (http://genome.gsc.riken.go.jp) for  
 further details.  
 e mouse tissues.

## FEATURES

## source

1. 631  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone="D63003E03"  
 /clone\_lib="RIKEN full-length enriched, 0 day neonate  
 kidney"  
 /tissue\_type="kidney"  
 /dev\_stage="0 day neonate"  
 /lab\_host="DH10B"  
 /note="Site\_1: Sali; Site\_2: BamHI; cDNA library was  
 prepared and sequenced in Mouse Genome Encyclopedia  
 Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in  
 RIKEN, Division of Experimental Animal Research in Riken

contributed to prepare mouse tissues. 1st strand cDNA was  
 primed with a primer [5'  
 GAGAGAGAGCGCGCACTCGAGTTTTTTTTTTTNN 3'], cDNA was  
 prepared by using trehalose thermo-activated reverse  
 transcriptase and subsequently enriched for full-length by  
 cap-trapper. Second strand cDNA was prepared with the  
 primer adapter of sequence [5'  
 GAGAGAGATTCTCGATTAAATTAATCCCCCCCCCC 3']. cDNA  
 was cleaved with BamHI and XhoI. Vector: a modified  
 pBluescript KS(+) after bulk excision from Lambda FLC I."  
 BASE COUNT 169 a 146 c 173 t  
 ORIGIN

Query Match 6.1%; Score 30; DB 9; Length 631;  
 Best Local Similarity 100.0%; Pred.No.0.00021;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 85 GCTGGCATTTCATCTTCATTTTGGGCTGT 114

|||||

Db 480 GCTGGCATTTCATCTTCATTTTGGGCTGT 509

## RESULT 23

## AA858938/c

## LOCUS

DEFINITION AA858938 430 bp mRNA linear EST 03-JUL-1999  
 UI-R-A0-aj-a-01-0-UI.s3 UI-R-A0 Rattus norvegicus cDNA clone  
 UI-R-A0-aj-a-01-0-UI 3' similar to gb|U69272|RN069272 Rattus  
 norvegicus Interleukin-15 mRNA, complete cds, mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

AA858938.1 GI:4229212  
 EST.  
 SOURCE Norway rat.  
 ORGANISM Rattus norvegicus  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## COMMENT

1 (bases 1 to 430)  
 Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 Genome Res. 6 (9), 791-806 (1996)  
 97044477  
 On Mar 10, 1998 this sequence version replaced gi:2948289.  
 Contact: Soares, MB  
 Program for Rat Gene Discovery and Mapping  
 University of Iowa  
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: msoares@blue.weeg.uiowa.edu  
 The sequence tag present in the cDNA between the NotI site and the  
 oligo-dr track served to identify it as a clone from the normalized  
 ph.D. Clone distribution. cDNA Library Preparation: M. Fatima Bonaldo,  
 Genetics This clone is also available through the I.M.A.G.E.  
 Consortium at LLNL (info@image.llnl.gov). IMAGE ID-1767474 The  
 following repetitive elements were found in this cDNA sequence:  
 1-24, >AT-rich#Low\_complexity  
 Seq primer: M13 Forward  
 POLYA=No.  
 Location/Qualifiers  
 1..430  
 /organism="Rattus norvegicus"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /clone="UI-R-A0-aj-a-01-0-UI"  
 /clone\_lib="UI-R-A0"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /note="vector: pVT3D-Pac (Pharmacia) with a modified  
 polylinker; Site\_1: Not I; Site\_2: Eco RI; This library  
 consists of a mixture of individually tagged normalized

## FEATURES

## source

1..430  
 Location/Qualifiers  
 /organism="Rattus norvegicus"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /clone="UI-R-A0-aj-a-01-0-UI"  
 /clone\_lib="UI-R-A0"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /note="vector: pVT3D-Pac (Pharmacia) with a modified  
 polylinker; Site\_1: Not I; Site\_2: Eco RI; This library  
 consists of a mixture of individually tagged normalized

5.38; Score 26; DB 10; Length 515;

Best Local Similarity 100.0%; Pred. No. 0.024; Mismatches 0; Indels 0; Gaps 0;  
Matches 26; Conservative 0;  
Qy 388 GAATCTGGATGCAAGAATGTGAGGA 413  
|||||  
Db 413 GAATCTGGATGCAAGAATGTGAGGA 388

RESULT 26  
AW121368/c  
LOCUS  
DEFINITION  
UI-M-BH2.2-aom-e-04-0-UI.s1 NIH\_BMAP\_M\_S3.2 Mus musculus cDNA clone  
UI-M-BH2.2-aom-e-04-0-UI 3', mRNA sequence.  
ACCESSION  
AW121368  
VERSION  
AW121368.1 GI:6096701  
KEYWORDS  
EST.  
SOURCE  
house mouse.  
ORGANISM  
Mus musculus  
REFERENCE  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 405)  
Bonaldo,M.F., Lennon,G. and Soares,M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
9704477  
Contact: Chin, H  
National Institute of Mental Health  
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
20892-9643, USA  
Tel: 301 443 1706  
Fax: 301 443 9890  
Email: m82@mail.nih.gov

The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a bonafide poly A  
tail. The sequence tag present in the cDNA between the NotI site  
and the oligo-dT track served to identify it as a clone from the  
normalized pineal glands library cDNA Library preparation: M.B.  
Soares Lab Clone distribution: NIH BMAP cDNA clones will be made  
available by the means that is soon to be determined. When NIH  
determines the means for distribution of the BMAP cDNA clones, this  
record will be updated accordingly when that means is determined.  
Seq primer: M13 Forward  
POLYA=Yes.

FEATURES  
Source  
1. 405  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UI-M-BH2.2-aom-e-04-0-UI"  
/clone\_lib="NIH\_BMAP\_M\_S3.2"  
/dev\_stages="27-32 days"  
/lab\_host="DH10B (Life Technologies)"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; The  
NIH\_BMAP\_M\_S3.2 library is a subtracted library of a  
series, ultimately derived from a mixture of individually  
tagged normalized libraries from ten regions of the mouse  
brain (cerebellum, brain stems, olfactory bulbs,  
hypothalamus, cortex, amygdala, basal ganglia, pineal  
gland, striatum, hippocampus) after a series of  
subtractions to reduce the representation of cDNAs from  
which ESTs had already been generated. The following  
serially subtracted libraries were generated in this  
process: NIH\_BMAP\_M\_S3.2, NIH\_BMAP\_M\_S2, NIH\_BMAP\_M\_S1.  
The subtracted library (NIH\_BMAP\_M\_S3.2) was constructed  
as follows: PCR amplified cDNA inserts from NIH\_BMAP\_M\_S2  
clones from which 3' ESTs had been derived was used as a  
driver in a hybridization with the NIH\_BMAP\_M\_S2 library  
in the form of single-stranded circles. The remaining  
single-stranded circles (subtracted library) was purified  
by hydroxyapatite column chromatography, converted to

double-stranded circles and electroporated into DH10B  
bacteria (Life Technologies) to generate the  
NIH\_BMAP\_M\_S3.2 library. This procedure has been  
previously described (Bonaldo, Lennon and Soares, Genome  
Research 6:791-806, 1996)  
TAG\_LIB=NIH\_BMAP\_M\_S3.2  
TAG\_TISSUE=pineal-glands  
TAG\_SEQ=CAACAC"

BASE COUNT 119 a 73 g 130 t  
ORIGIN  
Query Match 4.7%; Score 23; DB 9; Length 405;  
Best Local Similarity 100.0%; Pred. No. 0.82;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 460 ATTGTCCAAATGTTTCATCAACAC 482  
|||||  
Db 329 ATTGTCCAAATGTTTCATCAACAC 307

RESULT 27  
BE690327/c  
LOCUS  
DEFINITION  
BE690327.1  
ACCESSION  
BE690327  
VERSION  
BE690327.1 GI:10077951  
KEYWORDS  
EST.  
SOURCE  
house mouse.  
ORGANISM  
Mus musculus  
REFERENCE  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 420)  
NCI-CCRP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
MGI:1386283

Seq primer: -40RP from Gibco  
High quality sequence stop: 367.  
FEATURES  
Location/Qualifiers  
1. 420  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3466923"  
/clone\_lib="Soares\_mammary\_gland\_NNLMG"  
/sex="female (lactating)"  
/tissue\_type="mammary gland"  
/lab\_host="DH10B"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; 1st strand cDNA was prepared from mammary  
gland tissue from a lactating female, and was then primed  
with a Not I - oligo(dT) primer. Double-stranded cDNA was  
ligated to Eco RI adaptors (Pharmacia), digested with Not  
I and cloned into the Not I and Eco RI sites of the  
modified pT7T3 vector. Library is normalized. Library  
was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 126 a 87 c 86 g 121 t  
ORIGIN  
Query Match 4.7%; Score 23; DB 10; Length 420;  
Best Local Similarity 100.0%; Pred. No. 0.82;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 460 ATTGTCCAAATGTTTCATCAACAC 482  
|||||

Db 304 ATTGTCCAAATGTTTCATCAACAC 282

RESULT 28  
AI503618/c  
LOCUS  
DEFINITION  
IMAGE:948935 3' similar to gb:U14332 Mus musculus interleukin 15 (MOUSE); mRNA sequence.

ACCESSION  
AI503618  
VERSION  
AI503618.1 GI:4401469  
KEYWORDS  
EST.  
SOURCE  
house mouse.  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
1 (bases 1 to 434)  
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL  
Unpublished (1997)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
This clone is available royalty-free through LNL; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
MGI:545791  
This clone was previously sequenced on the 5' end only, this new data is from the 3' end  
High quality sequence stop: 379.

FEATURES  
Source  
Location/Qualifiers  
1..434  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone\_image="948935"  
/clone\_lib="Soares\_mammary\_gland\_NbMMG"  
/sex="male"  
/tissue\_type="mammary gland"  
/dev\_stage="4 weeks"  
/lab\_host="DH10B"  
/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia RI) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(df) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCGCAATGGTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."

BASE COUNT  
131 a 89 c 87 g 125 t 2 others

Query Match 4.7%; Score 23; DB 9; Length 434;  
Best Local Similarity 100.0%; Pred. No. 0.81;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 460 ATTGTCCAAATGTTTCATCAACAC 482  
|||||  
Db 315 ATTGTCCAAATGTTTCATCAACAC 293  
|||||

RESULT 29  
BB825167  
LOCUS  
DEFINITION  
IMAGE:948935 3' similar to gb:U14332 Mus musculus interleukin 15 (MOUSE); mRNA sequence.

ACCESSION  
BB825167  
VERSION  
BB825167.1 GI:17003410  
KEYWORDS  
EST.

SOURCE  
ORGANISM  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
1 (bases 1 to 458)  
Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,Y., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.  
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. 2001)  
Unpublished (2001)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: [genome-res@gsc.riken.go.jp](mailto:genome-res@gsc.riken.go.jp),  
URL:<http://genome.gsc.riken.go.jp/>,  
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
wagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.  
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES  
source  
Location/Qualifiers  
1..458  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="G830036M09"  
/clone\_lib="RIKEN full-length enriched, mammary gland RCB-0526 Jyg-MC(A) cDNA"  
/tissue\_type="mammary gland"  
/cell\_line="RCB-0526 Jyg-MC(A)"  
137 a 89 c 95 g 137 t

BASE COUNT  
137 a 89 c 95 g 137 t

Query Match 4.7%; Score 23; DB 9; Length 458;  
Best Local Similarity 100.0%; Pred. No. 0.81;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 460 ATTGTCCAAATGTTTCATCAACAC 482  
|||||  
Db 146 ATTGTCCAAATGTTTCATCAACAC 168  
|||||

RESULT 30  
A1120615  
LOCUS  
DEFINITION  
IMAGE:1399363 5' similar to gb:U14332 Mus musculus interleukin 15 (MOUSE); mRNA sequence.

```

ACCESSION      A1120615
VERSION        A1120615.1  GI:3520939
KEYWORDS
SOURCE         house mouse.
ORGANISM       Mus musculus
REFERENCE
AUTHORS       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 509)
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE         The WashU-HMI Mouse EST Project
JOURNAL       Unpublished (1996)
COMMENT       Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:911079
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 361.
Location/Qualifiers
1..509
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:139363"
/clone_lib="Soares_mammary_gland_NbMMG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia
) with a modified polylinker; Site.1: Not I; Site.2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5'
TGTTCACCAATGTAAGTGGAGCGCGCGAATGTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."
BASE COUNT    171 a 108 c 96 g 134 t
ORIGIN
Query Match      4.7%; Score 23; DB 9; Length 509;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 460 ATTGTCCAAATGTTTCATCAACAC 482
|||||
DB 404 ATTGTCCAAATGTTTCATCAACAC 426

RESULT 31
LOCUS      A1152482/c
DEFINITION ud83409 rl Soares_mammary_gland_NMLMG Mus musculus cDNA clone
IMAGE:1477457 5' similar to gb:U14332 Mus musculus interleukin 15
(MOUSE);, mRNA sequence.
ACCESSION  A1152482
VERSION    A1152482.1  GI:3680951
KEYWORDS
SOURCE     house mouse.
ORGANISM   Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 652)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Haru,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toyota,T.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 538)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE         The WashU-HMI Mouse EST Project
JOURNAL       Unpublished (1996)
COMMENT       Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:925813
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 326.
Location/Qualifiers
1..538
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:1477457"
/clone_lib="Soares_mammary_gland_NMLMG"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
/note="vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized. Library."
BASE COUNT    163 a 108 c 103 g 163 t 1 others
ORIGIN
Query Match      4.7%; Score 23; DB 9; Length 538;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 460 ATTGTCCAAATGTTTCATCAACAC 482
|||||
DB 319 ATTGTCCAAATGTTTCATCAACAC 297

RESULT 32
LOCUS      BB664509/c
DEFINITION BB664509 RIKEN full-length enriched, 0 day neonate lung Mus
musculus cDNA clone E030042P04 5', mRNA sequence.
ACCESSION  BB664509
VERSION    BB664509.1  GI:16498263
KEYWORDS
SOURCE     house mouse.
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 652)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Haru,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toyota,T.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

```

JOURNAL  
COMMENT

Unpublished (2001)  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center(GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gsc.riken.go.jp,  
 URL: http://genome.gsc.riken.go.jp/  
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh  
 , M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)  
 wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,  
 Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura  
 , S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and  
 Hayashizaki, Y.

RIKEN Integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)  
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara  
 , Y. and Hayashizaki, Y.  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa  
 , K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and  
 Hayashizaki, Y.  
 Computational Analysis of Full-Length Mouse cDNAs Compared with  
 Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)  
 Please visit our web site (http://genome.gsc.riken.go.jp) for  
 further details.

FEATURES  
source

Location/Qualifiers  
 1. .652  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone\_lib="E030042P04"  
 /clone\_lib="RIKEN full-length enriched, 0 day neonate  
 lung"  
 /tissue\_type="lung"  
 /dev\_stage="0 day neonate"  
 /lab\_host="DH10B"  
 /note="Site\_1: SalI; Site\_2: BamHI; cDNA library was  
 prepared and sequenced in Mouse Genome Encyclopedia  
 Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in  
 RIKEN Division of Experimental Animal Research in Riken  
 contributed to prepare mouse tissues. 1st strand cDNA was  
 primed with a primer [5'  
 GAGAGAGAGCGCGCGCACTCGAGTGTGTTTTTTTTTTTNN 3'], cDNA was  
 prepared by using trehalose thermo-activated reverse  
 transcriptase and subsequently enriched for full-length by  
 cap-trapper. Second strand cDNA was prepared with the  
 primer adapter of sequence [5'  
 GAGAGAGATCTCGAGTGTGTTAAATATCCCCCCCCCC 3']. cDNA  
 was cleaved with BamHI and XhoI. Vector: a modified  
 pBluescript KS(+) after bulk excision from Lambda FLC I."  
 165 a 130 c 118 g 239 t

BASE COUNT  
ORIGIN

Query Match 4.5%; Score 22; DB 9; Length 652;  
 Best Local Similarity 100.0%; Pred. No. 2.6;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 417 GGAGGAAAAAATATTAAGAA 438  
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 Db 624 GGAGGAAAAAATATTAAGAA 603

## RESULT 33

BI685688  
 LOCUS  
 DEFINITION 603309529f1 NCI\_CGAP\_Mam6 Mus musculus cDNA clone IMAGE:5345382 5',  
 mRNA sequence.  
 ACCESSION BI685688  
 VERSION BI685688  
 KEYWORDS EST. GI:15648316  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 826)  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: cgaps-r@mail.nih.gov  
 Tissue Procurement: Jeffrey Green M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLML1877 row: j column: 07  
 High quality sequence stop: 826.  
 Location/Qualifiers  
 1. .826  
 /organism="Mus musculus"  
 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone\_lib="IMAGE:5345382"  
 /clone\_lib="NCI\_CGAP\_Mam6"  
 /sex="female, virgin"  
 /tissue\_type="infiltrating ductal carcinoma"  
 /dev\_stage="5 months"  
 /lab\_host="DH10B"  
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site\_1: SalI;  
 Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
 Library constructed by Life Technologies. Investigator  
 providing samples: Jeffrey Green, M.D., NIH"

FEATURES  
source

Location/Qualifiers  
 1. .826  
 /organism="Mus musculus"  
 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone\_lib="IMAGE:5345382"  
 /clone\_lib="NCI\_CGAP\_Mam6"  
 /sex="female, virgin"  
 /tissue\_type="infiltrating ductal carcinoma"  
 /dev\_stage="5 months"  
 /lab\_host="DH10B"  
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site\_1: SalI;  
 Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
 Library constructed by Life Technologies. Investigator  
 providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT 212 a 218 c 174 g 222 t  
 ORIGIN

Query Match 4.5%; Score 22; DB 10; Length 826;  
 Best Local Similarity 100.0%; Pred. No. 2.5;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 GCTGGCATTTCATCTTCATTT 106  
 |||||||  
 Db 565 GCTGGCATTTCATCTTCATTT 586

## RESULT 34

BI161778  
 LOCUS  
 DEFINITION A006P680 Hybrid aspen plasmid library Populus tremula x Populus  
 tremuloides cDNA 5', mRNA sequence.  
 ACCESSION BI161778  
 VERSION BI161778  
 KEYWORDS EST. GI:3853063  
 SOURCE Populus tremula x Populus tremuloides.  
 ORGANISM Populus tremula x Populus tremuloides  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.  
 1 (bases 1 to 560)

## REFERENCE

AUTHORS Sterky, F., Regan, S., Karlsson, J., Hertzberg, M., Rohde, A., Holmberg  
 , A., Amini, B., Bhalerao, R., Larsson, M., Villarreal, R., Van Montagu  
 , M., Sandberg, G., Olsson, O., Teeri, T., Boerjan, W., Gustafsson, P.,  
 Uhlen, M., Sundberg, B. and Lundberg, J.

TITLE Gene discovery in the wood-forming tissues of poplar: Analysis of  
JOURNAL 5,692 expressed sequence tags  
MEDLINE Proc. Natl. Acad. Sci. U.S.A. 95 (22), 13330-13335 (1998)  
COMMENT 99007314  
Contact: Sterky F  
Department of Biotechnology  
Royal Institute of Technology (KTH)  
Teknikringen 34, S-100 44 STOCKHOLM, Sweden  
Tel: +46 8 790 8287  
Fax: +46 8 24 54 52  
Email: fredrik@biochem.kth.se  
PCR PRIMERS  
FORWARD: AAAGGGGATGTGCTGCAAGGG  
BACKWARD: CTTCCCGCTGCTATGTGTGTG  
Seq primer: CGTTGTAACGACGCCAG  
High quality sequence stop: 560.

FEATURES  
source  
1..560  
/organism="Populus tremula x Populus tremuloides"  
/db\_xref="taxon:47664"  
/clone\_lib="Hybrid aspen plasmid library"  
/tissue\_type="Cambial region"  
/dev\_stage="1.5 m actively growing tree"  
/lab\_host="E.coli"  
/note="Vector: pBluescript SK; Site\_1: SalI; Site\_2: NotI;  
Cambial region tissues, including developing xylem, the  
meristematic cambial zone and the developing and mature  
phloem, was harvested from 1.5 m actively growing trees.  
cDNA was prepared and cloned into lambda gt22a. DNA was  
isolated and subcloned into pBluescript SK using SalI and  
NotI restriction enzymes."  
173 a 76 c 176 g 133 t 2 others

BASE COUNT 173 a 76 c 176 g 133 t 2 others  
ORIGIN

Query Match 4.3%; Score 21; DB 9; Length 560;  
Best Local Similarity 100.0%; Pred. No. 8.4;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TTGAGAAGTATTTCCATCCAG 42  
|||||  
Db 389 TTGAGAAGTATTTCCATCCAG 409  
|||||

RESULT 35  
AG099196  
LOCUS Pan troglodytes DNA, clone: PTB-101G10.R, genomic survey sequence.  
DEFINITION AG099196  
ACCESSION AG099196  
VERSION AG099196.1 GI:16719713  
KEYWORDS GSS; GSS (genome survey sequence).  
SOURCE Pan troglodytes male lymphoblast DNA, clone\_lib:PTB Chimpanzee Male  
BAC Library clone:PTB-101G10.R.

ORGANISM  
Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
1 (sites)  
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Totoki,Y., Watanabe,H. and Sakaki,Y.  
BAC end sequenced of Library PTB  
Unpublished  
2 (bases 1 to 687)  
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Totoki,Y., Watanabe,H. and Sakaki,Y.  
Direct Submission  
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-chou,Tsrumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail:chimbpes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/  
Tel:81-45-503-9111, Fax:81-45-503-9170)  
Clones are derived from the chimpanzee BAC library PTB This BAC end  
was generated during the R&D process and may have higher chance of  
clone tracking errors.

TITLE Gene discovery in the wood-forming tissues of poplar: Analysis of  
JOURNAL 5,692 expressed sequence tags  
MEDLINE Proc. Natl. Acad. Sci. U.S.A. 95 (22), 13330-13335 (1998)  
COMMENT 99007314  
Contact: Sterky F  
Department of Biotechnology  
Royal Institute of Technology (KTH)  
Teknikringen 34, S-100 44 STOCKHOLM, Sweden  
Tel: +46 8 790 8287  
Fax: +46 8 24 54 52  
Email: fredrik@biochem.kth.se  
PCR PRIMERS  
FORWARD: AAAGGGGATGTGCTGCAAGGG  
BACKWARD: CTTCCCGCTGCTATGTGTGTG  
Seq primer: CGTTGTAACGACGCCAG  
High quality sequence stop: 560.

FEATURES  
source  
1..560  
/organism="Populus tremula x Populus tremuloides"  
/db\_xref="taxon:47664"  
/clone\_lib="Hybrid aspen plasmid library"  
/tissue\_type="Cambial region"  
/dev\_stage="1.5 m actively growing tree"  
/lab\_host="E.coli"  
/note="Vector: pBluescript SK; Site\_1: SalI; Site\_2: NotI;  
Cambial region tissues, including developing xylem, the  
meristematic cambial zone and the developing and mature  
phloem, was harvested from 1.5 m actively growing trees.  
cDNA was prepared and cloned into lambda gt22a. DNA was  
isolated and subcloned into pBluescript SK using SalI and  
NotI restriction enzymes."  
173 a 76 c 176 g 133 t 2 others

BASE COUNT 173 a 76 c 176 g 133 t 2 others  
ORIGIN

Query Match 4.3%; Score 21; DB 9; Length 560;  
Best Local Similarity 100.0%; Pred. No. 8.4;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TTGAGAAGTATTTCCATCCAG 42  
|||||  
Db 389 TTGAGAAGTATTTCCATCCAG 409  
|||||

RESULT 35  
AG099196  
LOCUS Pan troglodytes DNA, clone: PTB-101G10.R, genomic survey sequence.  
DEFINITION AG099196  
ACCESSION AG099196  
VERSION AG099196.1 GI:16719713  
KEYWORDS GSS; GSS (genome survey sequence).  
SOURCE Pan troglodytes male lymphoblast DNA, clone\_lib:PTB Chimpanzee Male  
BAC Library clone:PTB-101G10.R.

ORGANISM  
Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
1 (sites)  
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Totoki,Y., Watanabe,H. and Sakaki,Y.  
BAC end sequenced of Library PTB  
Unpublished  
2 (bases 1 to 687)  
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Totoki,Y., Watanabe,H. and Sakaki,Y.  
Direct Submission  
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-chou,Tsrumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail:chimbpes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/  
Tel:81-45-503-9111, Fax:81-45-503-9170)  
Clones are derived from the chimpanzee BAC library PTB This BAC end  
was generated during the R&D process and may have higher chance of  
clone tracking errors.

PRIMERS  
Sequencing: M13Rev  
LIBRARY Vector : pKS145  
R.Site 1 : SacI  
R.Site 2 : SacI.  
Location/Qualifiers  
1..687  
/organism="Pan troglodytes"  
/db\_xref="taxon:9598"  
/clone="PTB-101G10.R"  
/sex="male"  
/cell\_type="lymphoblast"  
/clone\_lib="PTB Chimpanzee Male BAC Library"  
289 a 115 c 121 g 160 t 2 others

BASE COUNT 289 a 115 c 121 g 160 t 2 others  
ORIGIN

Query Match 4.3%; Score 21; DB 12; Length 687;  
Best Local Similarity 100.0%; Pred. No. 8.3;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 TGTATAAGTGATTTCAGAAA 176  
|||||  
Db 527 TGTATAAGTGATTTCAGAAA 547  
|||||

RESULT 36  
A1596704  
LOCUS vk38h11.yl Soares\_mammary\_gland\_NDMG Mus musculus cDNA clone  
DEFINITION IMAGE:948933 5' similar to gb:U14332 Mus musculus interleukin 15  
(MOUSE);, mRNA sequence.  
A1596704 690 bp mRNA linear EST 21-APR-1999  
A1596704.1 GI:4605752  
EST.  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 690)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
MGI:545789  
This read is a RESEQUENCE of a previously sequenced mouse clone  
This read has been verified (found to hit its original self in the  
correct orientation)  
Seq primer: -40RP from Gibco  
High quality sequence stop: 466.  
Location/Qualifiers  
1..690  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:948933"  
/clone\_lib="Soares\_mammary\_gland\_NDMG"  
/sex="male"  
/tissue\_type="mammary gland"  
/dev\_stage="4 weeks"  
/lab\_host="DH10B"  
/notes="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia  
) with a modified polylinker; Site\_1: Not I; Site\_2: Eco  
RI; 1st strand cDNA was primed with a Not I - Oligo(dT)  
primer [5'  
TGTACCAATCTCAAGTGGAGCGCCGGAATGGTGTGTGTGTGTGTGTGTGTGT  
T 3'] double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into



contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'  
 GAGAGAGAGCGCGCACTGAGTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'  
 GAGAGAGATCTCGATTAAATTAATATCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I." 46 c 37 g 73 t

BASE COUNT 48 a 46 c 37 g 73 t  
 ORIGIN

Query Match 4.1%; Score 20; DB 9; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 TGAAGCTGGCATTCATGTCT 100

Db 95 TGAAGCTGGCATTCATGTCT 114

RESULT 39

BB213861

LOCUS

DEFINITION BB213861 RIKEN full-length enriched, adult male aorta and vein Mus musculus cDNA clone A530014K14 3' similar to S59342 nuclear pore complex glycoprotein p62, mRNA sequence.

ACCESSION BB213861

VERSION BB213861.1

KEYWORDS GI:8878814

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 224)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, F., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTs (Konno, H., et al.)

Unpublished (2000)

CONTACT: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@sc.riken.go.jp,

URL: http://genome.gsc.riken.go.jp/

Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoaka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Thermotabilization and thermoactivation of thermolabile enzymes by

trehalose and its application for the synthesis of full length

cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh, M., Katsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,

Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

Automated filtration-based high-throughput plasmid preparation

system. Genome Res. 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,

19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES  
 source

Location/Qualifiers

1..224

/organism="Mus musculus"

/db\_xref="taxon:10090"

/clone="A530014K14"

/clone.lib="RIKEN full-length enriched, adult male aorta

and vein"

/sex="male"

/tissue\_type="aorta and vein"

/dev\_host="adult"

/lab\_host="DHI0B"

/note="Site\_1: Sali; Site\_2: BamHI; cDNA library was

prepared and sequenced in Mouse Genome Encyclopedia

Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in

RIKEN. Division of Experimental Animal Research in Riken

contributed to prepare mouse tissues. 1st strand cDNA was

primed with a primer [5'

GAGAGAGAGGATCCCAAGCTCTTTTTTTTTTTVN 3'], cDNA was

prepared by using trehalose thermo-activated reverse

transcriptase and subsequently enriched for full-length by

cap-trapper. cDNA went through one round of normalization

to Rot = 20.0 and subtraction to Rot = 459.0. Second

strand cDNA was prepared with the primer adapter of

sequence [5' GAGAGAGATCTCGATTAAATTAATATCCCCCCCCCC

3']. cDNA was cleaved with XhoI and BamHI. Vector: a

modified pBluescript KS(+) after bulk excision from Lambda

FLC I."

BASE COUNT 51 a 51 c 38 g 84 t

ORIGIN

Query Match 4.1%; Score 20; DB 9; Length 224;

Best Local Similarity 100.0%; Pred. No. 29;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 TGAAGCTGGCATTCATGTCT 100

Db 119 TGAAGCTGGCATTCATGTCT 138

RESULT 40

AI447397/c

LOCUS

DEFINITION

AI447397

AI447397

AI447397.1

GI:4303701

KEYWORDS

SOURCE

ORGANISM

Mus musculus

house mouse.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 253)

NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

This clone was previously sequenced on the 5' end only, this new

data is from the 3' end

High quality sequence stop: 247.

Location/Qualifiers

1..253

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="IMAGE:583435"

/clone\_lib="Soares\_thymus\_2NbMT"  
 /sex="male"  
 /tissue\_type="Thymus"  
 /dev\_stage="4 weeks"  
 /lab\_host="DH10B"

/note="Vector: p7T3D-Pac (Pharmacia) with a modified polylinker. Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCGTCTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Patima Bonaldo."

55 a 36 c 22 g 140 t

BASE COUNT  
 ORIGIN

Query Match 4.1%; Score 20; DB 9; Length 253;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 424 AAAAATATTAAAGATTTT 443

Db 176 AAAAATATTAAAGATTTT 157

RESULT 41

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BBI41025 286 bp mRNA linear EST 28-JUN-2000  
 BBI41025 RIKEN full-length enriched, adult female vagina Mus  
 musculus cDNA clone 993003P08 3' similar to S59342 nuclear pore  
 complex glycoprotein p62, mRNA sequence.

BBI41025.1 GI:8795962

EST.

house mouse

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

(bases 1 to 286)

Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci

,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,

Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,

Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,

Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.

, Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.

, Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata

,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.

, Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya

,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.

, Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino

,M., Muramatsu,M. and Hayashizaki,Y.

RIKEN Mouse ESTs (Konno,H., et al.)

Unpublished (2000)

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@sc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp/

N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Thermotabilization and thermoactivation of the thermolabile enzymes by

trehalose and its application for the synthesis of full length

Automated filtration-based high-throughput plasmid preparation  
 system. Genome Res. 9 (5), 463-470 (1999)  
 Carninci,P. and Hayashizaki,Y.  
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
 19-44 (1999)  
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for  
 further details.

FEATURES  
 source

1. 286  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone="993003P08"  
 /clone\_lib="RIKEN full-length enriched, adult female  
 vagina"  
 /sex="female"  
 /tissue\_type="vagina"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"

/note="Site\_1: SalI; Site\_2: BamHI; cDNA library was  
 prepared and sequenced in Mouse Genome Encyclopedia  
 Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in  
 RIKEN. Division of Experimental Animal Research in Riken  
 contributed to prepare mouse tissues. 1st strand cDNA was  
 primed with a primer [5'  
 GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTCTT 3'], cDNA was  
 prepared by using trehalose thermo-activated reverse  
 transcriptase and subsequently enriched for full-length by  
 cap-trapper. cDNA went through one round of normalization  
 to Rot = 10.0 and subtraction to Rot = 185.0. Second  
 strand cDNA was prepared with the primer adaptor of  
 sequence [5' GAGAGAGATCTCGAGTAAATTAATATCCCTCCCCC  
 3']. cDNA was cleaved with XhoI and BamHI. Vector: a  
 modified pBluescript KS(+) after bulk excision from Lambda  
 FLC I."

BASE COUNT 67 a 62 c 53 g 103 t 1 others  
 ORIGIN

Query Match 4.1%; Score 20; DB 9; Length 286;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 TGAAGCTGGCATTCATGCT 100

Db 184 TGAAGCTGGCATTCATGCT 203

RESULT 42

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BB003966 288 bp mRNA linear EST 22-JUN-2000  
 BB003966 RIKEN full-length enriched, 10 day neonate skin Mus  
 musculus cDNA clone 4732457L13 3' similar to S59342 nuclear pore  
 complex glycoprotein p62, mRNA sequence.

BB003966.1 GI:8093414

EST.

house mouse

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

(bases 1 to 288)

Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci

,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,

Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,

Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,

Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.

, Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.

, Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata

,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.

, Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya

,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.

, Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino

M., Muramatsu, M. and Hayashizaki, Y.  
 RIKEN Mouse ESTs (Konno, H., et al.)  
 Unpublished (2000)  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan  
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 Fax: 81-45-503-9216  
 Email: genome-res@sc.riken.go.jp,  
 URL: http://genome.gsc.riken.go.jp/  
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki  
 N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Thermotabilization and thermoactivation of thermostable enzymes by  
 trehalose and its application for the synthesis of full length  
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
 Itoh, M., Katsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,  
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki  
 Y. and Hayashizaki, Y.  
 Automated filtration-based high-throughput plasmid preparation  
 system. Genome Res. 9 (5), 463-470 (1999)  
 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
 19-44 (1999)  
 Please visit our web site (http://genome.rtc.riken.go.jp) for  
 further details.  
 Location/Qualifiers  
 1. .288  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="4732457L13"  
 /clone\_lib="RIKEN full-length enriched, 10 day neonate  
 skin"  
 /sex="mixed"  
 /tissue\_type="skin"  
 /dev\_stage="10 days neonate"  
 /lab\_host="DH10B"  
 /note="Site 1: Sali; Site 2: BamHI; cDNA library was  
 prepared and sequenced in Mouse Genome Encyclopedia  
 Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in  
 RIKEN. Division of Experimental Animal Research in Riken  
 contributed to prepare mouse tissues. 1st strand cDNA was  
 primed with a primer [5'  
 GAGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTTTCTTNN 3'], cDNA was  
 prepared by using trehalose thermo-activated reverse  
 transcriptase and subsequently enriched for full-length by  
 cap-trapper. cDNA went through one round of normalization  
 to Rot = 10.0 and subtraction to Rot = 100.0. Second  
 strand cDNA was prepared with the primer adapter of  
 sequence [5' GAGAGAGATCTCGAGTTAAATTAATTCCTCCCCCCCC  
 3']. cDNA was cloned into the XhoI and BamHI sites.  
 Vector: a modified pBluescript KS(+) after bulk excision  
 from Lambda FLC I"  
 63 a 67 c 56 g 102 t  
 BASE COUNT  
 ORIGIN  
 Query Match 4.1%; Score 20; DB 9; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 81 TGAAGCTGCATTCATGTCT 100  
 Db 183 TGAAGCTGCATTCATGTCT 202  
 RESULT 43  
 BB006389  
 LOCUS BB006389 294 bp mRNA linear EST 22-JUN-2000  
 DEFINITION BB006389 RIKEN full-length enriched, 10 day neonate skin Mus

TITLE  
 JOURNAL  
 COMMENT

musculus cDNA clone 4732471F04 3' similar to S59342 nuclear pore  
 complex glycoprotein p62, mRNA sequence.  
 BB006389 GI:8095787  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 house mouse.  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 294)  
 Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci  
 P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,  
 Hirozane, T., Ishii, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,  
 Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,  
 Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,  
 Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,  
 Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata  
 Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.,  
 Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya  
 T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I.,  
 Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino  
 M., Muramatsu, M. and Hayashizaki, Y.  
 RIKEN Mouse ESTs (Konno, H., et al.)  
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 The Institute of Physical and Chemical Research (RIKEN)  
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 Email: genome-res@sc.riken.go.jp,  
 URL: http://genome.gsc.riken.go.jp/  
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki  
 N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Thermotabilization and thermoactivation of thermostable enzymes by  
 trehalose and its application for the synthesis of full length  
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
 Itoh, M., Katsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,  
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki  
 Y. and Hayashizaki, Y.  
 Automated filtration-based high-throughput plasmid preparation  
 system. Genome Res. 9 (5), 463-470 (1999)  
 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
 19-44 (1999)  
 Please visit our web site (http://genome.rtc.riken.go.jp) for  
 further details.  
 Location/Qualifiers  
 1. .294  
 /organism="Mus musculus"  
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 skin"  
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 /lab\_host="DH10B"  
 /note="Site 1: Sali; Site 2: BamHI; cDNA library was  
 prepared and sequenced in Mouse Genome Encyclopedia  
 Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in  
 RIKEN. Division of Experimental Animal Research in Riken  
 contributed to prepare mouse tissues. 1st strand cDNA was  
 primed with a primer [5'  
 GAGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTTTCTTNN 3'], cDNA was  
 prepared by using trehalose thermo-activated reverse  
 transcriptase and subsequently enriched for full-length by  
 cap-trapper. cDNA went through one round of normalization  
 to Rot = 10.0 and subtraction to Rot = 100.0. Second  
 strand cDNA was prepared with the primer adapter of  
 sequence [5' GAGAGAGATCTCGAGTTAAATTAATTCCTCCCCCCCC  
 3']. cDNA was cloned into the XhoI and BamHI sites.  
 Vector: a modified pBluescript KS(+) after bulk excision  
 from Lambda FLC I"  
 63 a 67 c 56 g 102 t  
 BASE COUNT  
 ORIGIN  
 Query Match 4.1%; Score 20; DB 9; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 81 TGAAGCTGCATTCATGTCT 100  
 Db 183 TGAAGCTGCATTCATGTCT 202  
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 BB006389  
 LOCUS BB006389 294 bp mRNA linear EST 22-JUN-2000  
 DEFINITION BB006389 RIKEN full-length enriched, 10 day neonate skin Mus

sequence [5' GAGAGAGAGATTCTCGAGTAAATTAATTCGCCGCCGCCGCC  
3']. cDNA was cloned into the XhoI and BamHI sites.  
Vector: a modified pBluescript KS(+) after bulk excision

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ORIGIN

Query Match      4.1%; Score 20; DB 9; Length 294;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT	44
LOCUS	BB292315
DEFINITION	BB292315 RIKEN full-length enriched, 9.5 days embryo parthenogenote Mus musculus cDNA clone B130010r22 3', similar to S59342 nuclear pore complex glycoprotein p62, mRNA sequence.

VERSION	GI:8992807	ORGANISM
KEYWORDS		
SOURCE		
REFERENCE		
AUTHORS		
TITLE		
BB292315.1	GI:8992807	house mouse.
EST.		mus musculus
Mus musculus		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
1 (bases 1 to 294)		
Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci		
P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,		
Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,		
Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,		
Kiyosawa,H., Kojiwa,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.		
Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.		
Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata		
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Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tomimaga,N., Toya		
T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.		
Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino		
M., Muramatsu,M. and Hayashizaki,Y.		
RIKEN Mouse ESTs (Konno,H., et al.)		

CONTACT: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,  
URL: <http://genome.gsc.riken.go.jp/>  
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasakawa, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Thermotabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. *Proc. Natl. Acad. Sci. U.S.A.* 95 (2), 520-524 (1998)  
Itoh, M., Kicsuna, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.  
Automated filtration-based high-throughput plasmid preparation system. *Genome Res.* 9 (5), 463-470 (1999)  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning. *Methods Enzymol.* 303, 19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

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FEATURES
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/site="Site.1: Salt; Site.2: BamHI: cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGGAGAGAGAGATCCAGAGCTCTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of subtraction to
rot = 225.0. Second strand cDNA was prepared with the
primer adapter of sequence [5',
GAGGAGAGATCTCGATTATTAATTAATCCCCCCCCCCC 3']. cDNA
was cleaved with XhoI and BamHI. Vector: a modified
pBluescript KS(+) after bulk excision from Lambda FLC I.".
60 a 91 c 46 g 97 t

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BASE COUNT	ORIGIN	60 a	91 c	46 g	97 t

Query Match	4.1%	Score 20;	DB 9;
Best Local Similarity	100.0%;	Pred. No. 29;	Length 294;
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;
		Gaps 0;	

Qy	81	TGAAGCTGGCATTTCATGTCT	100
Dδ	191	TGAAGCTGGCATTTCATGTCT	210

RESULT	45
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LOCUS	BB135090
DEFINITION	295 bp mRNA linear EST 28-JUN-2000
	BB135090 RIKEN full-length enriched, adult male bone Mus musculus
	CDNA clone 983012A02 3' similar to S59342 nuclear pore complex
	glycoprotein p62, mRNA sequence.

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE
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BB135090.1	1	GI:8790027	house mouse	<i>Eukaryota; Metazoa;</i>	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
EST.	1				1 (bases 1 to 295)

REFERENCE AUTHORS	TITLE
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 295)	
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shbata, K., Shibata Y., Shigenoto, Y., Shingawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya T., Tsunoda, Y., Watehiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino M., Muramatsu, M. and Hayashizaki, Y.	
RIKEN Mouse ESTs (Konno, H., et al.)	

TITLE  
COMMENT

Muramatsu, M., and Hayashizaki, Y.  
RIKEN Mouse ESTs (Konno, H., et al.)  
Unpublished (2000)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
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, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Thermostabilization and thermoactivation of thermolabile enzymes by  
trehalose and its application for the synthesis of full length  
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
Itoh, M., Kitsunai, F., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,  
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki  
Y. and Hayashizaki, Y.  
Automated filtration-based high-throughput plasmid preparation  
system. Genome Res. 9 (5), 463-470 (1999)  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
19-44 (1999)  
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further details.

## FEATURES

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Location/Qualifiers  
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/organism="Mus musculus"  
/db\_xref="taxon:10090"  
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/lab\_host="DH10B"  
/note="Site\_1: Sali; Site\_2: BamHI; cDNA library was  
prepared and sequenced in Mouse Genome Encyclopedia  
Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN. Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer [5'  
GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTNN 3'], cDNA was  
prepared by using trehalose thermo-activated reverse  
transcriptase and subsequently enriched for full-length by  
cap-trapper. cDNA went through one round of normalization  
to Rot = 10.0 and subtraction to Rot = 185.0. Second  
strand cDNA was prepared with the primer adapter of  
sequence [5' GAGAGAGATCTCGAGTTAATTAATATCCCCCCCCC  
3']. cDNA was cleaved with XhoI and BamHI. Vector: a  
modified pBluescript KS(+) after bulk excision from Lambda  
FLC I."

## BASE COUNT

ORIGIN

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## Query Match

Best Local Similarity 4.1%; Score 20; DB 9; Length 295;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 TGAAGCTGGCATTCATGTCT 100

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Db 190 TGAAGCTGGCATTCATGTCT 209

## RESULT 46

BB157192

LOCUS

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musculus cDNA clone A130035D04 3' similar to S59342 nuclear pore

complex glycoprotein p62, mRNA sequence.

BB157192

BB157192.1 GI:8813122

EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 295)  
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci  
P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,  
Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,  
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,  
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.

, Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,  
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Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino  
M., Muramatsu, M. and Hayashizaki, Y.  
RIKEN Mouse ESTs (Konno, H., et al.)  
Unpublished (2000)

## TITLE

JOURNAL

COMMENT

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gs.riken.go.jp

URL: <http://genome.gsc.riken.go.jp/>

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Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki  
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Automated filtration-based high-throughput plasmid preparation  
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Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
19-44 (1999)  
Please visit our web site (<http://genome.rtc.riken.go.jp>) for  
further details.

## FEATURES

source

Location/Qualifiers

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/organism="Mus musculus"

/db\_xref="taxon:10090"

/clone="A130035D04"

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prepared and sequenced in Mouse Genome Encyclopedia

Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in

RIKEN. Division of Experimental Animal Research in Riken

contributed to prepare mouse tissues. 1st strand cDNA was

primed with a primer [5'  
GAGAGAGAGATCCAGAGCTCTTTTCTTTTNN 3'], cDNA was

prepared by using trehalose thermo-activated reverse

transcriptase and subsequently enriched for full-length by

cap-trapper. cDNA went through one round of normalization

to Rot = 10.0 and subtraction to Rot = 185.0. Second

strand cDNA was prepared with the primer adapter of

sequence [5' GAGAGAGATCTCGAGTTAATTAATATCCCCCCCCC

3']. cDNA was cleaved with XhoI and BamHI. Vector: a

modified pBluescript KS(+) after bulk excision from Lambda  
FLC I."

BASE COUNT 64 a 71 c 55 g 105 t

ORIGIN

Query Match 4.1%; Score 20; DB 9; Length 295;

Best Local Similarity 100.0%; Pred. No. 29;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 TGAAGCTGGCATTCATGTCT 100

|||||

Db 190 TGAAGCTGGCATTCATGTCT 209

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RESULT 47
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XX BB714486;
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SV BB714486.1
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09-OCT-2001 (Rel. 69, Created)
DT 09-OCT-2001 (Rel. 69, Last updated, Version 1)
XX
DE Mus musculus 9.5 days embryo parthenogenote cDNA, RIKEN full-length
DE enriched library, clone: B130060L02, 3' end partial sequence.
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KW EST (expressed sequence tag).
XX
OS Mus musculus (house mouse)
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OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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[1]
RA Akimura T., Arakawa T., Carninci P., Furuno M., Hanagaki T., Hayatsu N.,
RA Hiramoto K., Hirozane T., Imotani K., Ishii Y., Ito M.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Matsuyama T., Nakamura M.,
RA Nishi K., Nomura K., Numasaki R., Okazaki Y., Okido T., Saito R., Sakai C.,
RA Sakai K., Sakazume N., Sasaki D., Sato K., Shibata K., Shingawa A.,
RA Shiraki T., Sogabe Y., Suzuki H., Tagawa A., Takahashi F.,
RA Takaku-Akahira S., Tanaka T., Tomaru A., Toya T., Watahiki A.,
RA Yasunishi A., Muramatsu M., Hayashizaki Y.;
RA Submitted (28-SEP-2001) to the EMBL/GenBank/DBJ databases.
RL Yoshihide Hayashizaki, The Institute of Physical and Chemical Research
RL (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic
RL Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho,
RL Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
RL (E-mail: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/,
RL Tel: 81-45-503-9222, Fax: 81-45-503-9216)
XX
[2]
RA Akimura T., Arakawa T., Carninci P., Furuno M., Hanagaki T., Hayatsu N.,
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RA Yasunishi A., Muramatsu M., Hayashizaki Y.;
RA "RIKEN Encyclopedia of Mouse Full-length cDNAs";
RA Unpublished.
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[3]
RA Konno H., Fukunishi Y., Shibata K., Itoh M., Carninci P., Sugahara Y.,
RA Hayashizaki Y.;
RA "Computer-based methods for the mouse full-length cDNA encyclopedia:
RA real-time sequence clustering for construction of a nonredundant cDNA
RA library";
RA Genome Res. 11:281-289(2001).
XX
[4]
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RA "Normalization and subtraction of cap-trapper-selected cDNAs to prepare
RA full-length cDNA libraries for rapid discovery of new genes";
RA Genome Res. 10:1617-1630(2000).
XX
[5]
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N.,
RA Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R.,
RA Matsumoto H., Sakauechi S., Ikegami T., Kashiwagi K., Fujiwaki S.,
RA Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y.,
RA Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y.,

```

```

RA Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RA "RIKEN integrated sequence analysis (RISA) system-384-format sequencing
RA pipeline with 384 multipillar sequencer";
RA Genome Res. 10:1757-1771(2000).
XX
CC Please visit our web site (http://genome.gsc.riken.go.jp/) for
CC further details.
CC cDNA library was prepared and sequenced in Mouse Genome
CC Encyclopedia Project of Genome Exploration Research Group in Riken
CC Genomic Sciences Center and Genome Science Laboratory in RIKEN.
CC Division of Experimental Animal Research in Riken contributed to
CC prepare mouse tissues.
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FH 1. .307
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 199 TGAAGTCGTCATTCATGTC 218
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RESULT 48
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DEFINITION BB165365 RIKEN full-length enriched, 16 days neonate thymus Mus
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complex glycoprotein p62, mRNA sequence.
ACCESSION BB165365.1 GI:8821306
VERSION BB165365.1
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 347)
Konno H., Aizawa K., Akahira S., Akiyama J., Arakawa T., Carninci
P., Endo T., Fukuda S., Fukunishi Y., Hara A., Hayatsu N.,
Hirozane T., Hori F., Ishii Y., Ishikawa J., Ishikawa T., Itoh M.,
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Kiyosawa H., Kojima Y., Kondo S., Koya S., Kurihara C., Kusakabe M.,
Matsuyama T., Miki R., Mizuno F., Nakamura M., Oda H., Okazaki Y.,
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Y., Shigemoto Y., Shinagawa A., Shiraki T., Sogabe Y., Sugahara Y.,
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T., Tsurumoto Y., Watahiki A., Watanabe S., Yamamura T., Yamanaka I.,
Yano R., Yasunishi A., Yokota T., Yoshida K., Yoshiki A., Yoshino
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RIKEN Mouse ESTs (Konno H., et al.)
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Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.go.jp,

```

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REFERENCE BB165365
AUTHORS Konno H., Aizawa K., Akahira S., Akiyama J., Arakawa T., Carninci
P., Endo T., Fukuda S., Fukunishi Y., Hara A., Hayatsu N.,
Hirozane T., Hori F., Ishii Y., Ishikawa J., Ishikawa T., Itoh M.,
Izawa M., Kadota K., Kagawa I., Kai C., Kawai J., Kikuchi N.,
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Matsuyama T., Miki R., Mizuno F., Nakamura M., Oda H., Okazaki Y.,
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Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.go.jp,

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Db 31 TGAGGAACTGGAGGAAAAA 12

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384	16	3.3	1385	21	AA076806	Human ORFX ORF2361	457	16	3.3	2978	22	AAH159540	Chromosome 13q31-q
385	16	3.3	1408	17	AA078258	Survival motor neu	458	16	3.3	3001	21	AAH51765	S. epidermidis gen
386	16	3.3	1408	17	AA078260	Survival motor neu	459	16	3.3	3054	22	AAH54843	Human immune/haema
387	16	3.3	1437	22	AAH33683	Human colon cancer	460	16	3.3	3072	22	AAH69732	Human polynucleoti
388	16	3.3	1449	23	AA087551	DNA encoding novel	461	16	3.3	3101	22	AA159541	Original F-MuV/H-M
389	16	3.3	1488	19	AAV40767	C. felis esterase	462	16	3.3	3126	21	AAA36741	F-MuV/H-MV nucleot
390	16	3.3	1518	19	AAV20910	Helicobacter pylor	463	16	3.3	3126	21	AAA36742	S. epidermidis gen
391	16	3.3	1567	22	AAH76720	Human muscle BOP P	464	16	3.3	3126	21	AAH54548	Human polynucleoti
392	16	3.3	1574	21	AAH72392	Human nucleic acid	465	16	3.3	3149	22	AAH161108	Human EF-chiral ca
393	16	3.3	1590	19	AAV40743	C. felis esterase,	466	16	3.3	3181	22	AAH27594	Borrelia burgdorfe
394	16	3.3	1590	19	AAV40743	C. felis esterase,	467	16	3.3	3203	20	AAH20283	B. burgdorferi ant
395	16	3.3	1611	22	AAH160346	Ctenocephalides fe	468	16	3.3	3257	20	AAH16632	Human survival mot
396	16	3.3	1650	19	AAV40741	Human polynucleoti	469	16	3.3	3273	17	AAH18868	TMF gene. Homo sa
397	16	3.3	1650	19	AAV40742	C. felis esterase,	470	16	3.3	3279	14	AAQ49397	Human ovarian tumo
398	16	3.3	1656	21	AAH51261	Arabidopsis thalia	471	16	3.3	3282	24	ABK09761	Microspore-specifi
399	16	3.3	1662	22	AAH158560	Human polynucleoti	472	16	3.3	3293	11	AAQ05753	Brassica napus mic
400	16	3.3	1677	21	AA043066	Arabidopsis thalia	473	16	3.3	3293	18	AAH48862	B. burgdorferi ant
401	16	3.3	1734	23	AAH73869	DNA encoding novel	474	16	3.3	3354	20	AAH16631	Drosophila melanog
402	16	3.3	1751	22	AAK94218	Human full-length	475	16	3.3	3717	23	ABL19425	Staphylococcus aur
403	16	3.3	1780	19	AAH14142	H. pylori GHPO 358	476	16	3.3	3754	18	AAH74869	Drosophila melanog
404	16	3.3	1792	19	AAV40739	C. felis esterase,	477	16	3.3	3756	23	ABL11738	S. epidermidis gen
405	16	3.3	1792	19	AAV40740	C. felis esterase,	478	16	3.3	3774	22	AAH54262	Corn cellulose syn
406	16	3.3	1792	22	AAH21168	Ctenocephalides fe	479	16	3.3	3786	21	AAH58262	Putative TBP inter
407	16	3.3	1810	18	AAH54043	Helicobacter CP2 a	480	16	3.3	3787	22	ABA01228	DNA encoding a mai
408	16	3.3	1814	22	AAH85083	Human immune/haema	481	16	3.3	3813	21	AAZ99509	DNA encoding a mai
409	16	3.3	1824	14	AAQ45502	Sequence encoding	482	16	3.3	3813	21	AAZ99524	S. epidermidis gen
410	16	3.3	1834	22	AAH86012	Human GPR19 coding	483	16	3.3	3900	22	AAH54813	Drosophila melanog
411	16	3.3	1836	22	AAH08248	Human interferon-L	484	16	3.3	3974	23	ABL21565	Drosophila melanog
412	16	3.3	1837	22	AAH33504	Human colon cancer	485	16	3.3	4065	23	ABL11085	Drosophila melanog
413	16	3.3	1862	22	AAH18068	Human cDNA sequenc	486	16	3.3	4150	23	ABL03866	Drosophila melanog
414	16	3.3	1867	13	AAQ20377	Sequence of 67 kD	487	16	3.3	4287	23	ABL23481	Encodes E-cadherin
415	16	3.3	1868	22	AAH16590	Human cDNA sequenc	488	16	3.3	4333	12	AAQ11563	Drosophila melanog
416	16	3.3	1871	22	AAH64770	Human secreted pro	489	16	3.3	4525	23	ABL12092	Human immune/haema
417	16	3.3	1918	21	AAH49850	Arabidopsis thalia	490	16	3.3	4583	22	AAH67070	Human polynucleoti
418	16	3.3	1919	21	AAH39478	Arabidopsis thalia	491	16	3.3	4628	22	AAI59328	Human nervous syst
419	16	3.3	1996	22	AAH29614	Human endocrine po	492	16	3.3	4688	22	AAI18600	Human expressed po
420	16	3.3	2023	22	AAH18308	Human cDNA sequenc	493	16	3.3	4688	22	AAI19654	Human immune/haema
421	16	3.3	2107	19	AAH14514	H. pylori GHPO 126	494	16	3.3	4688	22	AAH83279	Human immune/haema
422	16	3.3	2152	24	AAH62474	CNA sequence #261	495	16	3.3	4707	15	AAQ66294	Deep Vent DNA poly
423	16	3.3	2177	22	AAH64716	Human immune/haema	496	16	3.3	4707	18	AAH70813	Deep Vent DNA poly
424	16	3.3	2177	22	AAH64717	Human immune/haema	497	16	3.3	4707	20	AAV68142	DNA polymerase gen
425	16	3.3	2201	22	AAH17312	Human cDNA sequenc	498	16	3.3	4734	23	ABL15322	Drosophila melanog
426	16	3.3	2266	22	AAH07317	Human pancreatic c	499	16	3.3	4968	23	ABL13204	Drosophila melanog
427	16	3.3	2266	22	AAH90476	Human digestive sy	500	16	3.3	5243	19	AAV65691	Fowlpox Virus vect
428	16	3.3	2308	22	AAH15944	Human cDNA sequenc	501	16	3.3	5275	20	AAZ10632	Splice variant ZAP
429	16	3.3	2319	22	AAH17550	Human cDNA sequenc	502	16	3.3	5474	24	ABL33271	Human immune syste
430	16	3.3	2359	22	AAH16114	Human polynucleoti	503	16	3.3	5475	19	AAV17777	Tomato Prf cDNA.
431	16	3.3	2359	23	AAH23986	Drosophila melanog	504	16	3.3	5641	22	AAH73449	Human immune/haema
432	16	3.3	2423	23	ABL07666	Drosophila melanog	505	16	3.3	5724	23	AAH79698	DNA encoding novel
433	16	3.3	2434	24	AAH199300	Mouse ischaemic co	506	16	3.3	5800	23	AAH79721	DNA encoding novel
434	16	3.3	2453	21	AAH14857	Human cDNA sequenc	507	16	3.3	5804	18	AAV74560	Staphylococcus aur
435	16	3.3	2484	21	AAH36995	Arabidopsis thalia	508	16	3.3	6013	24	AAH61323	Human gene regulat
436	16	3.3	2486	22	AAH159497	Human polynucleoti	509	16	3.3	6073	23	ABL33543	Human immune syste
437	16	3.3	2592	23	ABL14427	Drosophila melanog	510	16	3.3	6195	23	ABL14426	Drosophila melanog
438	16	3.3	2618	23	ABL25136	Drosophila melanog	511	16	3.3	6260	23	ABL02590	Drosophila melanog
439	16	3.3	2686	23	AAH73640	DNA encoding novel	512	16	3.3	6362	23	ABL19982	Drosophila melanog
440	16	3.3	2697	22	AAH94734	Human full-length	513	16	3.3	6447	22	ABA15828	Human nervous syst
441	16	3.3	2697	22	AAH14522	Human cDNA sequenc	514	16	3.3	6643	22	AAH84930	Human immune/haema
442	16	3.3	2761	22	AAH32786	Human secreted pro	515	16	3.3	6659	21	AAZ38662	DNA encoding a CON
443	16	3.3	2763	16	AAH15167	Methylthioadenosin	516	16	3.3	6802	22	AAH46282	Tumour suppressor
444	16	3.3	2763	16	AAQ92813	Human MTase. Homo	517	16	3.3	6802	24	AAH61068	Human gene regulat
445	16	3.3	2763	18	AAH85305	Human methylchoad	518	16	3.3	6882	20	AAZ10631	Splice variant ZAP
446	16	3.3	2763	20	AAH20866	Human MTase DNA.	519	16	3.3	6929	22	AAH27479	Rice photosensitiv
447	16	3.3	2763	22	AAH86091	Methylthioadenosin	520	16	3.3	6930	22	AAH27477	Rice photosensitiv



667	15	3.1	303	20	AAx04039	Human secreted pro	740	15	3.1	436	20	AAV90509	EST clone DW665.
668	15	3.1	316	20	AAV87934	EST clone FG625.	741	15	3.1	443	21	AAV59994	Human secreted pro
669	15	3.1	323	16	AAT26444	Human gene signatu	742	15	3.1	443	21	AAI88197	Human polynucleoti
670	15	3.1	326	22	AAC86756	Probe for DNA enco	743	15	3.1	443	22	AAH98725	Human EST-derived
671	15	3.1	331	20	AAV90700	Nucleotide sequenc	744	15	3.1	444	22	AAI87083	Human polynucleoti
672	15	3.1	341	22	AAI35200	Human musculoskele	745	15	3.1	445	22	AAF68101	Human lung tumour
673	15	3.1	343	23	ABL22103	Drosophila melanog	746	15	3.1	447	22	AAC86750	DNA encoding a Can
674	15	3.1	344	22	AAI87125	Human polynucleoti	747	15	3.1	447	22	AAS23431	Candida albicans e
675	15	3.1	345	21	AAC65305	Arabidopsis SCL ES	748	15	3.1	448	22	AAI81871	Human polynucleoti
676	15	3.1	346	20	AAx20065	Enterococcus faeca	749	15	3.1	451	23	AAx74824	DNA encoding novel
677	15	3.1	349	21	AAC32941	Human secreted pro	750	15	3.1	452	22	ABAS7711	Human foetal liver
678	15	3.1	353	22	AAK39414	Human immune/haema	751	15	3.1	452	22	AAI16622	Human breast cance
679	15	3.1	355	21	AACU5088	Human secreted pro	752	15	3.1	452	22	AAK05772	Human brain expres
680	15	3.1	359	20	AAV86907	EST clone BA79. H	753	15	3.1	452	22	AAK31396	Human bone marrow
681	15	3.1	366	14	AAQ60392	Human brain expres	754	15	3.1	452	22	AAI37289	Probe #5975 used t
682	15	3.1	367	22	AAI90999	Human polynucleoti	755	15	3.1	453	24	ABK16175	Human lung tumour
683	15	3.1	372	21	AAC04478	Human secreted pro	756	15	3.1	460	22	ABA42863	Human breast cell
684	15	3.1	383	22	AAF93349	cDNA encoding SRT	757	15	3.1	460	22	ABA53286	Human foetal liver
685	15	3.1	385	22	AAF65251	Novel human polynu	758	15	3.1	460	22	AAx23059	Probe #1525 for ge
686	15	3.1	388	22	AAI07719	Human breast cance	759	15	3.1	460	22	AAx39558	cDNA encoding nove
687	15	3.1	389	22	ABA19046	Human nervous syst	760	15	3.1	460	22	AAK01544	Human brain expres
688	15	3.1	393	16	AAT19086	Human gene signatu	761	15	3.1	460	22	AAK26989	Human bone marrow
689	15	3.1	394	22	AAI25465	Human breast cance	762	15	3.1	460	22	AAK88897	Human digestive sy
690	15	3.1	398	20	AAx41303	Human secreted pro	763	15	3.1	461	22	AAK82855	Human immune/haema
691	15	3.1	399	21	AAC18429	Human secreted pro	764	15	3.1	462	22	AAI36085	Human musculoskele
692	15	3.1	399	22	AAH52505	S. epidermidis ope	765	15	3.1	463	22	ABA54340	Human foetal liver
693	15	3.1	399	22	AAH52670	Human foetal liver	766	15	3.1	463	22	AAI12643	Probe #2576 for ge
694	15	3.1	400	22	ABA59166	Human foetal liver	767	15	3.1	469	22	AAH29331	Drosophila melanog
695	15	3.1	400	22	ABA27936	Probe #6402 for ge	768	15	3.1	470	22	AAH93301	Plasmodium falcipla
696	15	3.1	400	22	AAI32273	Human breast cance	769	15	3.1	473	22	ABA54307	Human foetal liver
697	15	3.1	400	22	AAK07356	Human brain expres	770	15	3.1	473	22	ABA24066	Probe #2532 for ge
698	15	3.1	400	22	AAK33123	Human bone marrow	771	15	3.1	473	22	AAK31276	Human bone marrow
699	15	3.1	400	22	AAI16338	Probe #6271 for ge	772	15	3.1	473	22	AAI33958	Probe #2644 used t
700	15	3.1	400	22	AAI38919	Probe #7605 used t	773	15	3.1	474	22	AAH87814	Peppermint plant o
701	15	3.1	401	22	AAK95389	Human neuregulin g	774	15	3.1	476	22	ABA57451	Human foetal liver
702	15	3.1	401	22	AAK96882	Human neuregulin g	775	15	3.1	476	22	ABA26952	Probe #5418 for ge
703	15	3.1	403	22	ABA13248	Human nervous syst	776	15	3.1	476	22	AAK05489	Human brain expres
704	15	3.1	404	22	AAI81699	Human polynucleoti	777	15	3.1	476	22	AAK31090	Human bone marrow
705	15	3.1	406	22	AAF66420	Novel human polynu	778	15	3.1	476	22	AAI36999	Probe #5685 used t
706	15	3.1	409	22	AAK64354	Novel human polynu	779	15	3.1	478	22	AAI91262	Human polynucleoti
707	15	3.1	413	20	AAx30334	DNA encoding a hum	780	15	3.1	478	22	AAx82617	DNA encoding novel
708	15	3.1	413	22	AAx40007	Genomic sequence #	781	15	3.1	481	22	ABA42474	Human breast cance
709	15	3.1	413	22	AAK91424	Human digestive sy	782	15	3.1	481	22	ABA52904	Human foetal liver
710	15	3.1	415	22	ABA26636	Probe #5102 for ge	783	15	3.1	481	22	ABA22685	Probe #1151 for ge
711	15	3.1	415	22	AAI14827	Human breast cance	784	15	3.1	481	22	AAK01152	Human brain expres
712	15	3.1	415	22	AAK30644	Human bone marrow	785	15	3.1	481	22	AAK26614	Human bone marrow
713	15	3.1	416	22	AAx35167	Human cardiovascular	786	15	3.1	481	22	AAI11242	Probe #1175 for ge
714	15	3.1	418	22	AAI84862	Human polynucleoti	787	15	3.1	481	22	AAI32507	Probe #1193 used t
715	15	3.1	420	21	AAC24192	Human secreted pro	788	15	3.1	481	22	AAI01158	Probe #1149 used t
716	15	3.1	421	22	ABA45920	Human breast cell	789	15	3.1	489	17	AAT34476	Neurite cDNA clone
717	15	3.1	421	22	ABA56446	Human foetal liver	790	15	3.1	489	20	AAZ09873	Human neurite cDNA
718	15	3.1	421	22	ABA26081	Probe #4547 for ge	791	15	3.1	491	22	AAH10670	Human cDNA clone (
719	15	3.1	421	22	AAI81436	Human polynucleoti	792	15	3.1	492	22	AAH12488	Human cDNA clone (
720	15	3.1	421	22	AAI88933	Human polynucleoti	793	15	3.1	508	22	AAI22143	Human breast cance
721	15	3.1	421	22	AAK30119	Human bone marrow	794	15	3.1	520	22	AAI86602	Human polynucleoti
722	15	3.1	421	22	AAI14714	Probe #4647 for ge	795	15	3.1	526	22	ABA61356	Human foetal liver
723	15	3.1	421	22	AAI36083	Probe #4769 used t	796	15	3.1	526	22	AAK09655	Human brain expres
724	15	3.1	421	22	AAI04520	Probe #4511 used t	797	15	3.1	526	22	AAK35546	Human bone marrow
725	15	3.1	422	23	AAx83209	DNA encoding novel	798	15	3.1	526	22	AAI41261	Probe #9947 used t
726	15	3.1	423	22	AAK61409	Human immune/haema	799	15	3.1	528	20	AAx84705	Human metastatic m
727	15	3.1	426	20	AAZ52927	Human prostate tum	800	15	3.1	534	22	ABA61780	Human foetal liver
728	15	3.1	426	22	AAH36570	Human colon cancer	801	15	3.1	534	22	AAI20615	Human breast cance
729	15	3.1	429	22	AAF64745	Novel human polynu	802	15	3.1	534	22	AAI41699	Probe #10385 used
730	15	3.1	430	22	AAK75228	Human immune/haema	803	15	3.1	534	22	AAx55814	Streptococcus pneu
731	15	3.1	430	22	AAK75229	Human immune/haema	804	15	3.1	541	21	AAx44053	Human secreted exp
732	15	3.1	432	20	AAx20064	Enterococcus faeca	805	15	3.1	545	22	AAF93437	Umbilical vein end
733	15	3.1	432	22	AAK66597	Novel human polynu	806	15	3.1	547	21	AAC94803	Cat flea hindgut a
734	15	3.1	434	22	ABA43324	Human breast cell	807	15	3.1	550	21	AAC94970	Cat flea hindgut a
735	15	3.1	434	22	ABA53767	Human foetal liver	808	15	3.1	552	21	AAI11673	Aspergillus niger
736	15	3.1	434	22	ABA23514	Probe #1980 for ge	809	15	3.1	553	21	AAC98315	Human colon cancer
737	15	3.1	434	22	AAI12062	Probe #1995 for ge	810	15	3.1	553	21	AAC54988	Arabidopsis thalia
738	15	3.1	434	22	AAI33396	Probe #2082 used t	811	15	3.1	556	20	AAx21045	Polynucleotide seq
739	15	3.1	434	22	AAI01984	Probe #1975 used t	812	15	3.1	557	22	AAS31032	Human diagnostic a

c 813	15	3.1	558	22	ABA60948	Human foetal liver	886	15	3.1	763	21	AAF09113	Fusarium venenatum
c 814	15	3.1	558	22	AAK09238	Human brain expres	c 887	15	3.1	766	22	AAH94026	Human foetal cDNA,
c 815	15	3.1	558	22	AAK35128	Human bone marrow	c 888	15	3.1	787	20	AAZ17095	Human gene express
c 816	15	3.1	558	22	AAI40845	Probe #9531 used t	c 889	15	3.1	787	20	AAZ17096	Human gene express
c 817	15	3.1	560	21	AAK57590	Human OREF ORF1345	890	15	3.1	789	21	AAC37646	Arabidopsis thalia
c 818	15	3.1	561	22	AAI44483	Probe #13169 used	c 891	15	3.1	791	20	AAZ17080	Human gene express
c 819	15	3.1	563	19	AAK14583	H. pylori GHPO 167	c 892	15	3.1	791	20	AAZ17093	Human gene express
c 820	15	3.1	581	21	AAF09240	Fusarium venenatum	c 893	15	3.1	791	22	AAH01670	Campylobacter rect
c 821	15	3.1	586	22	AAH29657	Drosophila melanog	c 894	15	3.1	794	21	AAH01670	DNA encoding a mur
c 822	15	3.1	594	22	ABA60763	Human foetal liver	c 895	15	3.1	794	21	AAH01670	DNA encoding a mur
c 823	15	3.1	594	22	ABA28813	Probe #7279 for ge	896	15	3.1	795	23	AAH01670	Streptococcus pneu
c 824	15	3.1	594	22	AAK34940	Human brain expres	c 897	15	3.1	795	23	AAH01670	Streptococcus pneu
c 825	15	3.1	594	22	AAK34940	Human brain expres	c 898	15	3.1	797	22	AAH01670	Human cDNA 5'-end
c 826	15	3.1	594	22	AAH01082	Probe #9342 used t	c 899	15	3.1	797	22	AAH01670	Human cDNA clone r
c 827	15	3.1	594	22	AAH01082	Human cDNA clone (	900	15	3.1	810	22	AAH01670	Human neuroblastom
c 828	15	3.1	594	24	AAH01082	Human G protein-co	c 901	15	3.1	821	22	AAH01670	Human cDNA clone (
c 829	15	3.1	598	21	AAH01082	Human lung tumour-	c 902	15	3.1	825	22	AAH01670	Human polynucleoti
c 830	15	3.1	598	23	AAH01082	Human lung tumour-	c 903	15	3.1	827	22	AAH01670	Human olfactory re
c 831	15	3.1	600	22	AAH01082	Human brain expres	c 904	15	3.1	828	22	AAH01670	Human cDNA clone (
c 832	15	3.1	600	22	AAH01082	Human brain thiole	c 905	15	3.1	830	22	AAH01670	Human breast cance
c 833	15	3.1	602	21	AAH01082	Human colon cancer	c 906	15	3.1	833	23	AAH01670	DNA encoding novel
c 834	15	3.1	605	22	AAH01082	Human cDNA encodin	907	15	3.1	837	22	AAH01670	Human nervous syst
c 835	15	3.1	607	21	AAH01082	Arabidopsis thalia	908	15	3.1	845	21	AAH01670	Arabidopsis thalia
c 836	15	3.1	630	22	AAH01082	Human cDNA clone (	909	15	3.1	851	21	AAH01670	Human cancer assoc
c 837	15	3.1	637	18	AAH01082	DNA encoding a Sta	c 910	15	3.1	851	21	AAH01670	Human colon cancer
c 838	15	3.1	639	22	AAH01082	S. epidermidis ope	c 911	15	3.1	852	21	AAH01670	Human colon cancer
c 839	15	3.1	643	21	AAH01082	Human pancreatic c	c 912	15	3.1	853	21	AAH01670	Arabidopsis thalia
c 840	15	3.1	644	21	AAH01082	Arabidopsis thalia	c 913	15	3.1	859	22	AAH01670	Arabidopsis thalia
c 841	15	3.1	645	21	AAH01082	Arabidopsis thalia	c 914	15	3.1	875	23	AAH01670	Human breast cance
c 842	15	3.1	646	21	AAH01082	Arabidopsis thalia	c 915	15	3.1	886	21	AAH01670	DNA encoding novel
c 843	15	3.1	651	21	AAH01082	Arabidopsis thalia	c 916	15	3.1	886	21	AAH01670	Arabidopsis thalia
c 844	15	3.1	652	23	AAH01082	Arabidopsis thalia	c 917	15	3.1	890	22	AAH01670	Human protein enco
c 845	15	3.1	655	21	AAH01082	DNA encoding novel	c 918	15	3.1	897	23	AAH01670	Human protein enco
c 846	15	3.1	656	21	AAH01082	Human secreted exp	c 919	15	3.1	900	21	AAH01670	Drosophila melanog
c 847	15	3.1	657	11	AAH01082	Human secreted exp	c 920	15	3.1	942	22	AAH01670	Arachidonic acid m
c 848	15	3.1	657	11	AAH01082	Cucumber Mosaic Vi	c 921	15	3.1	943	21	AAH01670	Human Par-4 DNA.
c 849	15	3.1	657	21	AAH01082	Neisseria gonorrh	c 922	15	3.1	945	21	AAH01670	Soybean AX5 promot
c 850	15	3.1	657	21	AAH01082	Neisseria meningit	c 923	15	3.1	952	22	AAH01670	Human immune/haema
c 851	15	3.1	657	21	AAH01082	Neisseria meningit	c 924	15	3.1	952	22	AAH01670	Human olfactory re
c 852	15	3.1	657	21	AAH01082	Neisseria meningit	c 925	15	3.1	954	23	AAH01670	DNA encoding novel
c 853	15	3.1	657	21	AAH01082	Neisseria meningit	c 926	15	3.1	979	23	AAH01670	Human GGT5 related
c 854	15	3.1	660	21	AAH01082	Aspergillus oryzae	c 927	15	3.1	993	21	AAH01670	Human GGT5 related
c 855	15	3.1	661	22	AAH01082	Human musculoskele	c 928	15	3.1	999	21	AAH01670	Human bone marrow
c 856	15	3.1	664	22	AAH01082	Drosophila melanog	c 929	15	3.1	1001	21	AAH01670	Murine TRX2m poly
c 857	15	3.1	668	22	AAH01082	Human polynucleoti	c 930	15	3.1	1001	21	AAH01670	Human immune/haema
c 858	15	3.1	693	21	AAH01082	Neisseria meningit	c 931	15	3.1	1001	21	AAH01670	Arabidopsis thalia
c 859	15	3.1	699	21	AAH01082	Neisseria meningit	c 932	15	3.1	1001	21	AAH01670	Arabidopsis thalia
c 860	15	3.1	699	21	AAH01082	Neisseria meningit	c 933	15	3.1	1001	21	AAH01670	Arabidopsis thalia
c 861	15	3.1	699	21	AAH01082	Neisseria meningit	c 934	15	3.1	1001	21	AAH01670	Human GGT5 related
c 862	15	3.1	699	21	AAH01082	Neisseria meningit	c 935	15	3.1	1001	21	AAH01670	Human GGT5 related
c 863	15	3.1	708	20	AAH01082	Human gene express	c 936	15	3.1	1019	22	AAH01670	Human bone marrow
c 864	15	3.1	709	22	AAH01082	Human breast cance	c 937	15	3.1	1021	22	AAH01670	Human bone marrow
c 865	15	3.1	720	19	AAH01082	Clone R2.1 from mu	c 938	15	3.1	1026	22	AAH01670	Murine TRX2m poly
c 866	15	3.1	723	21	AAH01082	Arabidopsis thalia	c 939	15	3.1	1033	21	AAH01670	Human immune/haema
c 867	15	3.1	726	23	AAH01082	DNA encoding novel	c 940	15	3.1	1034	23	AAH01670	Arabidopsis thalia
c 868	15	3.1	728	23	AAH01082	DNA encoding novel	c 941	15	3.1	1034	23	AAH01670	DNA encoding novel
c 869	15	3.1	731	22	AAH01082	Human cDNA clone (	c 942	15	3.1	1056	23	AAH01670	DNA encoding novel
c 870	15	3.1	734	22	AAH01082	Human cDNA clone (	c 943	15	3.1	1064	21	AAH01670	Human secreted pro
c 871	15	3.1	736	22	AAH01082	Human cDNA clone (	c 944	15	3.1	1072	20	AAH01670	Human secreted pro
c 872	15	3.1	737	21	AAH01082	Human cDNA clone (	c 945	15	3.1	1076	22	AAH01670	Human prostate tum
c 873	15	3.1	737	22	AAH01082	Human OREF ORF2993	c 946	15	3.1	1076	22	AAH01670	Human polynucleoti
c 874	15	3.1	738	20	AAH01082	Human gene expres	c 947	15	3.1	1089	23	AAH01670	DNA encoding novel
c 875	15	3.1	741	22	AAH01082	Human gene expres	c 948	15	3.1	1093	15	AAH01670	DNA encoding novel
c 876	15	3.1	747	20	AAH01082	Human cDNA clone (	c 949	15	3.1	1098	22	AAH01670	Human hepatic pare
c 877	15	3.1	747	21	AAH01082	Yeast surface disp	c 950	15	3.1	1100	21	AAH01670	Human immune/haema
c 878	15	3.1	747	21	AAH01082	Human colon cancer	c 951	15	3.1	1101	21	AAH01670	Neisseria meningit
c 879	15	3.1	752	20	AAH01082	Single chain r-cel	c 952	15	3.1	1101	21	AAH01670	Neisseria meningit
c 880	15	3.1	752	20	AAH01082	Human secreted pro	c 953	15	3.1	1102	20	AAH01670	DNA encoding novel
c 881	15	3.1	754	20	AAH01082	Human colon cancer	c 954	15	3.1	1106	20	AAH01670	Stealth virus nucl
c 882	15	3.1	754	20	AAH01082	Human gene expres	c 955	15	3.1	1107	22	AAH01670	Extended human sec
c 883	15	3.1	754	20	AAH01082	Human gene expres	c 956	15	3.1	1107	22	AAH01670	Neisseria gonorrhe
c 884	15	3.1	755	20	AAH01082	Human gene expres	c 957	15	3.1	1112	21	AAH01670	Human secreted pro
c 885	15	3.1	755	20	AAH01082	Human gene expres	c 958	15	3.1	1116	21	AAH01670	Arabidopsis thalia
			758	20	AAH01082	Human gene expres				1116	21	AAH01670	Arabidopsis thalia
										1117	21	AAH01670	Arabidopsis thalia
										1118	21	AAH01670	Arabidopsis thalia
										1126	22	AAH01670	Human foetal cDNA,
										1129	20	AAH01670	Human secreted pro
										1147	22	AAH01670	Human secreted pro
										1161	21	AAH01670	Human prothymosin
										1170	19	AAH01670	H. pylori cellular
										1209	22	AAH01670	Human immune/haema
										1231	18	AAH01670	Arabidopsis thalia

959	15	3.1	1231	21	AAC65282	Arabidopsis SCLa3
c 960	15	3.1	1237	21	AAC35953	Arabidopsis thalia
961	15	3.1	1251	24	ABI99464	Mouse ischaemic co
962	15	3.1	1272	20	AAV74302	Human plasma carbo
963	15	3.1	1273	22	ABA19162	Human nervous syst
c 964	15	3.1	1277	21	AAC46092	Arabidopsis thalia
965	15	3.1	1281	22	ABA19161	Human nervous syst
966	15	3.1	1282	22	AAF32798	Human secreted pro
c 967	15	3.1	1290	23	AAS23364	E. coli DNA for ce
c 968	15	3.1	1296	20	AAO1298	E. coli DAP aminot
969	15	3.1	1321	21	AAC47718	Zea mays DNA fragm
970	15	3.1	1323	20	AAV90860	Nucleotide sequenc
971	15	3.1	1327	22	AAS26504	Human cDNA encodin
972	15	3.1	1329	22	AAF79877	Chlamydomophila pneu
c 973	15	3.1	1333	10	AAH91328	E.coli Bio A gene.
974	15	3.1	1334	22	AAF79876	Chlamydomophila pneu
975	15	3.1	1341	22	AAD08117	Human CHLd5 protei
c 976	15	3.1	1352	22	AAS39721	Genomic sequence #
c 977	15	3.1	1352	22	AAK84207	Human immune/haema
c 978	15	3.1	1352	22	AAK84209	Human immune/haema
c 979	15	3.1	1354	22	AAK84208	Human immune/haema
980	15	3.1	1372	7	AAH60166	Sequence encoding
c 981	15	3.1	1372	21	AAC44910	Arabidopsis thalia
982	15	3.1	1385	23	AAS72610	DNA encoding novel
c 983	15	3.1	1400	22	AAS01017	Maize disease resi
984	15	3.1	1421	19	AAV32665	Caenorhabditis ele
985	15	3.1	1421	21	AAC36608	Arabidopsis thalia
986	15	3.1	1422	22	AAO3825	Human reproductive
c 987	15	3.1	1423	10	AAH90249	Cucumber mosaic vi
c 988	15	3.1	1426	18	AAH72272	Cucumber mosaic vi
989	15	3.1	1431	20	AAV08821	Gene No. 11 encodi
c 990	15	3.1	1460	22	AAH15490	Human cDNA sequenc
c 991	15	3.1	1464	22	AAH46190	Serine protease 15
c 992	15	3.1	1476	22	AAS44589	Human full-length
993	15	3.1	1484	21	AAC77846	Human cancer assoc
c 994	15	3.1	1485	22	AAH26555	Human breast cance
c 995	15	3.1	1491	23	AAS82735	DNA encoding novel
996	15	3.1	1496	22	AAD08116	Human chordin-like
997	15	3.1	1500	22	AAC55304	Human brain thlore
998	15	3.1	1512	22	AAD04000	Human protein tyro
999	15	3.1	1534	21	AAC59668	Human secreted pro
c1000	15	3.1	1539	22	AAH61030	Human polynucleoti

RESULT 1

AAT00526

ID

AAT00526 standard; cDNA; 489 BP.

AC

AAT00526;

AC

XX

02-FEB-1996 (first entry)

DT

XX

Human interleukin-15 precursor.

DE

XX

Interleukin-15; epithelium-derived T-cell factor; T lymphocyte; ss.

XX

XX

Homo sapiens.

OS

XX

Key

FT

XX

CDS

FT

XX

Location/Qualifiers

FT

XX

1..489

FT

XX

/\*tag= a

FT

XX

/note= "Claimed"

FT

XX

misc\_feature

FT

XX

145..489

FT

XX

/\*tag= b

FT

XX

/note= "Claimed"

FT

XX

WO9527722-A.

PN

XX

19-OCT-1995.

PD

XX

XX

PF	06-APR-1994;	94WO-US03793..
XX		
PR	06-APR-1994;	94WO-US03793.
XX		
PA	(IMMV ) IMMUNEX CORP.	
XX		
PI	Anderson DM, Eisenman JR, Fung V, Grabstein KH;	
PI	Rauch C;	
XX		
DR	WPI: 1995-373556/48.	
DR	P-PSDB; AAR83438.	
XX		
PT	Isolated DNA encoding polypeptide with mammalian IL-15 activity - which stimulates proliferation and differentiation of T cells, used for treating carcinoma(s), melanomas, etc. and viral infections	
PT		
XX		
PS	Claim 36; Page 28-29; 48pp; English.	
XX		
CC	A simian species of IL-15 (sIL-15) was purified and its AA sequence and cDNA sequence analysed (see AAR83309, AAR83436, AAT00524, AAT00525). Both the simian and the human ORFs encode a precursor polypeptide (AAR83436, AAR83438). The precursor polypeptides each comprise a 48-AA leader sequence and a sequence encoding mature simian or human IL-15 polypeptides. The active simian and human IL-15 polypeptides are disclosed in AAR83309 & AAR83310 respectively. The invention also comprises other mammalian IL-15, including human IL-15, that hybridise to probes defined by AAR83438. A plasmid contg. a recombinant clone of human IL-15 cDNA was deposited with ATCC on Feb. 19 1993 under ATCC 69245. The deposit was named 141-hETF. AAR83435 is a mammalian mature IL-15 polypeptide. It is a generic sequence which encompasses both AAR83309 (simian) and AAR83310 (human) IL-15 mature polypeptides.	
XX		
SQ	Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;	

Query Match 100.0%; Score 489; DB 16; Length 489;

Best Local Similarity 100.0%; Pred. No. 2.4e-229;

Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1

ATCAGAAATTCGAAACACACATTTGAGAGTATTTCATCCAGTCAGTCTACTGTGTTTACTT

60

Db

1

atgagaattctgaaccacattgtgagaagtatttccatccagtcgactgtgttcaatt

60

QY

61

CTAAACAGTCATTTCTAACTGAAGCTGGCATTCTCTTCATTTTGGGCTGTTTCAGT

120

Db

61

ctaaacagtcatttttctaactgaagctggcattcatgtcttcaattttggcgtttcagt

120

QY

121

GCAGGCTTCCTTAAACAGAACCCAACTGGTGAATGTAAATAGTGATTTGAAAAAATT

180

Db

121

gcagggtcttctaaacagagccaaactgggtgaatgtaataagtgatttgaaaaaatt

180

QY

181

GAAGATCTTATTCAATCTATGCATATTGATGCTACTTATATACGGAAGATGATGTTAC

240

Db

181

gaagatcttattcaatctatgcataattgatgtactttatatacaggaagtgtatcacc

240

QY

241

CCCAGTTGCAAAAGTAACAGCAATGAAGTCTTCTCTTGGAGTTACAAGTTATTTTCACTT

300

Db

241

cccagttgcaaaagtaacagcaaatgaagtcttctcttgaggattacaagttattcaatt

300

QY

301

GAGTCGGGAGATGCAAGTATTTCATGATACAGTAGAGAAATCTGATCATCTCTAGCAACAAC

360

Db

301

gagtcgggagatgcaagtatttcattgatacagtagaataatctgatcatctctagcaacaac

360

QY

361

AGTTTGTCTTCTTAATGGGAATGTAAACAGAACTCTGGATGCAAGAATGTGAGGAACATGGAG

420

Db

361

agtttgtcttcttaaatgggaatgttaacagaactctggatgcaagaaactgtgaggaactggag

420

QY

421

GAAGAAATATTAAAGAATTTTTCGAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC

480

Db

421

gaagaaatattaaagaatttttgcagagattttgtacatatgttccaaatgttccaaatcaac

480

QY

481

ACTTCTTGA 489

## ALIGNMENTS

RESULT	1
AAAT00526	
ID	AAAT00526 standard; cDNA; 489 BP.
XX	
AC	AAAT00526;
XX	
DT	02-FEB-1996 (first entry)
XX	
DE	Human interleukin-15 precursor.
XX	
KW	Interleukin-15; epithelium-derived T-cell factor; T lymphocyte; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Location/Qualifiers
CDS	1..489
FT	/*tag= a
FT	/note= "claimed"
FT	145..489
FT	/*tag= b
FT	/note= "claimed"
XX	
PN	WO9527722-A.
XX	
PD	19-OCT-1995.
XX	



PS Chalm 1; Fig 1; 35pp; English.

XX The simian ETF (epithelium derived T cell factor) was isolated from  
 CC African green monkey CV1/EBNA cell conditioned medium. The N-  
 CC terminal sequence of the purified sETF was determined and then PCR  
 CC primers were designed based on the sequence information. A 92 bp  
 CC fragment was amplified from CV1/EBNA DNA and was used as a probe to  
 CC screen a CV1/EBNA cDNA library for the full-length sETF coding  
 CC sequence (i.e. the present sequence). Mature sETF induces  
 CC proliferation and/or differentiation of precursor or mature T cells  
 CC and is useful for promoting long-term in vitro culture of  
 CC T-lymphocytes and T-cell lines. It is used for treating  
 CC gastrointestinal diseases including peptic ulcer, colitis and  
 CC malignancy and for treating HIV infection.

XX Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 17; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-229;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACACATTTGAGAGTATTTCATCCAGTGGCTACTGTGTTACTT 60  
 Db 1 atgagaatttcgaaacacatttgagaagtatttcctccatccagtgctactgtgttactt 60

QY 61 CTAAACAGTCATTTCTAACTGAAGCTGGCATTCATGCTTCTTCAATTTGGGCTGTTTCAGT 120  
 Db 61 ctaaacagtcattttctaaactgaagctggcattcattcttcattttgggcgtttcagt 120

QY 121 GCAGGGCTTCCTAAACACAGCCCACTGGCTGAATGTAATGAAGTATTGAAAAAATT 180  
 Db 121 gcagggcttcctaaacacagcccaactggctgaatgtaatgaagtatttggaaataatt 180

QY 181 GAAGATCTTATTCAATCTATGATATTTGATGCTACTTTATATACGGAAGTATGATGTTTCAAC 240  
 Db 181 gaagatcttattcaatctatgatatgttgatgctactttatatacaggaaagtatgattttcaac 240

QY 241 CCAGTTCGAAGTACAGCAATGAAGTGTCTTCTTGGAGTTTACAAGTATTATTTCACTT 300  
 Db 241 ccagttcgaagtacagcaatgaagtgtcttcttggagttttacaagtattatcttcaact 300

QY 301 GAGTCGGAGATGCAAGTATTTCATGATACAGTAAATCTGATCATCTAGCAACAC 360  
 Db 301 gagtcggagatgcaagtatttcgatgatacagtagaataatctgatcatctagcaaacac 360

QY 361 AGTTTGTCTTCTTAATGGGAATTAACAGATCTGGATCCAAAGATGTGAGGAACCTGGAG 420  
 Db 361 agtttgtcttcttaatgggaatttaacagatctggatccaaagtgtgaggaaactggag 420

QY 421 GAAAAAATATTAAAGAAATTTTGACAGATTTTGTACATATTGTCATATTTGTCATCAAC 480  
 Db 421 gaaaaaataattaaagaatttttgacagattttgtacatatgttccaaatgttcatcaac 480

QY 481 ACTTCTTGA 489  
 Db 481 acttcttga 489

RESULT 4  
 ID AAT42243  
 XX AAT42243 standard; DNA; 489 BP.  
 AC AAT42243;  
 XX  
 DT 05-FEB-1997 (first entry)  
 XX Human epithelium-derived T cell factor gene.  
 DE  
 XX Epithelium-derived T-cell factor; simian; human; culture; proliferation;  
 KW epithelial cell; differentiation; T-lymphocyte; African green monkey;  
 KW primer; PCR; polymerase chain reaction; amplification; probe; ss.  
 XX

OS Homo sapiens.

XX Key Location/Qualifiers  
 FH sig\_peptide 1..144  
 FT /\*tag= a  
 FT mat\_peptide 145..486  
 FT /\*tag= b

XX US5552303-A.  
 XX 03-SEP-1996.  
 XX 08-MAR-1993; 93US-0031399.  
 XX 08-MAR-1993; 93US-0031399.  
 XX (IMNV ) IMMUNEX CORP.  
 XX Anderson D, Eisenman J, Fung V, Grabstein K, Rauch C;  
 PI WPI; 1996-412063/41.  
 DR P-PSDB; AAW07255.  
 XX New isolated simian and human epithelium-derived T-cell factors -  
 PT which stimulate the proliferation and/or differentiation of  
 PT T-lymphocytes and T-cell lines  
 XX Claim 21; Column 23-24; 22pp; English.

CC This is the nucleotide sequence encoding a human epithelium-derived  
 CC T-cell factor (ETF). The gene was obtained using a 1.37 kb fragment of  
 CC the corresp. African green monkey gene (AAT42242) as a probe to screen a  
 CC cDNA library constructed from RNA derived from the IMJH cell line.  
 CC This cell line is derived by stable transformation of a human bone  
 CC marrow stromal cell culture with pSV3neo. From a pool of about 1000 cDNA  
 CC clones, one clone 141.hETF contained this sequence. ETF is a protein of  
 CC 15-17 kD which is expressed by epithelial cells and stimulates  
 CC proliferation and/or differentiation of precursor and/or mature T cells.  
 CC The protein is therefore useful for promoting long term in vivo culture  
 CC of T-lymphocytes and T-cell lines.

XX Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 17; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-229;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACACATTTGAGAGTATTTCATCCAGTGGCTACTGTGTTACTT 60  
 Db 1 atgagaatttcgaaacacatttgagaagtatttcctccatccagtgctactgtgttactt 60

QY 61 CTAAACAGTCATTTCTAACTGAAGCTGGCATTCATGCTTCTTCAATTTGGGCTGTTTCAGT 120  
 Db 61 ctaaacagtcattttctaaactgaagctggcattcattcttcattttgggcgtttcagt 120

QY 121 GCAGGGCTTCCTAAACACAGCCCACTGGCTGAATGTAATGAAGTATTGAAAAAATT 180  
 Db 121 gcagggcttcctaaacacagcccaactggctgaatgtaatgaagtatttggaaataatt 180

QY 181 GAAGATCTTATTCAATCTATGATATTTGATGCTACTTTATATACGGAAGTATGATGTTTCAAC 240  
 Db 181 gaagatcttattcaatctatgatatgttgatgctactttatatacaggaaagtatgattttcaac 240

QY 241 CCAGTTCGAAGTACAGCAATGAAGTGTCTTCTTGGAGTTTACAAGTATTATTTCACTT 300  
 Db 241 ccagttcgaagtacagcaatgaagtgtcttcttggagttttacaagtattatcttcaact 300

QY 301 GAGTCGGAGATGCAAGTATTTCATGATACAGTAAATCTGATCATCTAGCAACAC 360  
 Db 301 gagtcggagatgcaagtatttcgatgatacagtagaataatctgatcatctagcaaacac 360

QY 361 AGTTTGTCTTCTTAATGGGAATTAACAGATCTGGATCCAAAGATGTGAGGAACCTGGAG 420  
 Db 361 agtttgtcttcttaatgggaatttaacagatctggatccaaagtgtgaggaaactggag 420

QY 421 GAAAAAATATTAAAGAAATTTTGACAGATTTTGTACATATTGTCATATTTGTCATCAAC 480  
 Db 421 gaaaaaataattaaagaatttttgacagattttgtacatatgttccaaatgttcatcaac 480

QY 481 ACTTCTTGA 489  
 Db 481 acttcttga 489

Db	361	 agttctcctaattggaatgcaacagaatctggatgcaaagaatgaggaaactggag
Qy	421	GAAGAAATATTAAAGAATTTTTCGACAGATTTTGACATATTGTCCAATGTTCAACAAC
Db	421	gaaaaaatattaagaatttttcgcagagtgttgcatatatgtccaaatgttcatcaac
Qy	481	ACTCTCTTGA 489 
Db	481	actcttga 489
RESULT	5.	
ID	AAT36635	
XX	AAT36635 standard; cDNA; 489 BP.	
XX	AAT36635;	
DT	17-NOV-1996 (first entry)	
DE	Human interleukin-15 cDNA.	
KW	Interleukin-15; antagonist; mutein; graft versus host disease; allotraft; T-cell growth factor; ss.	
OS	Homo sapiens.	
PN	WO9626274-A1.	
PD	29-AUG-1996.	
PF	21-FEB-1996; 96WO-US02520.	
PR	22-FEB-1995; 95US-0392317.	
PA	(IMMV ) IMMUNEX CORP.	
PI	Grabstein KH, Paxton RJ, Pettit DK;	
DR	WPI; 1996-402367/40.	
DR	P-PADB; AAR98527.	
PT	Antagonists of interleukin-15 - are used to treat patients having symptoms of graft-versus-host disease and for prolonging allo:graft survival	
PS	Disclosure; Page 25; 32pp; English.	
CC	A cDNA clone (AAT36635) codes for human interleukin-15 (IL-15) (AAR98527), a T-cell growth factor. Muteins of human IL-15 or simian IL-15 (see also AAR98526) are useful as antagonists of IL-15 and can be prepd. by PCR-mediated mutagenesis of the encoding sequences. Preferred muteins have amino acid substitutions at Asp56 and/or Gln156 of the IL-15 protein that prevent signal transduction. They are useful for treating graft-versus-host disease and for prolonging allograft survival.	
SQ	Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;	

Db	121	gcagggtcttctctaaacagagcccaactgggtgaatgtaataagtgatttgaataaatt	180		
Qy	181	GAAGATCTTATTCAATCTATGTCATATTTGATGCTACTTTTATATACGGAAGTGTGTTCAAC	240		
Db	181	gaagatcttattcaatctatgcataatgatgctactttatacagaaagtgttcaac	240		
Qy	241	CCCAGTTCGAAGTAAACAGCAATGAAGTCTTCTCTTGGAGTTACAAGTTATTTTCACTT	300		
Db	241	cccagttgcaagtaacagcaatgaagtgtcttctcttgagggttaacaagttattcactt	300		
Qy	301	GAGTCCGAGATGCAAGTATTTCATGATACAGTAGAAAACTGATCATCTCTAGCAACAAC	360		
Db	301	gagtcggagatgcaagtattcatgatacagtagaaaaatctgatcatctctagcaacaac	360		
Qy	361	AGTTTGTCTTCTTAATGGGAATCTAACAGAACTCTGGATGCAAGAAGTGTGAGGAACGTGGAG	420		
Db	361	agtttgtcttctctaaatgggaatgtaacagaatctggatgcaagaatgtgaggaaactggag	420		
Qy	421	GAAGAAAATATTAAAGAAATTTTGGCAGAGCTTTGTGACATATTGTCCAAATGTTTCATCAAC	480		
Db	421	gaaaaaataattaaagaatttttgcagagttttgtacatatgtccaaatgttcatcaac	480		
Qy	481	ACTTCTTTGA 489			
Db	481	actcttga 489			
RESULT 6					
AAT58404					
ID	AAT58404 standard; cDNA; 489 BP.				
XX					
AC	AAT58404;				
XX					
DT	18-MAR-1997 (first entry)				
XX					
DE	Interleukin-15 coding sequence.				
XX					
KW	IL-15; interleukin-15; T-cell growth factor; proliferation; stimulate;				
KW	muscle growth; differentiation; hypertrophy; treat; atrophy; wasting;				
KW	skeletal; cardiac; muscle; congestive heart failure; diabetes-associated;				
KW	glucose-intolerance; dyslipidaemia; rhabdomyosarcoma; dystrophy; ss.				
XX					
OS	Homo sapiens.				
XX					
FH	Key	Location/Qualifiers			
FT	CDS	1..489			
FT		/*tag= a			
FT		/product= IL-15			
XX					
PN	W09637223-A1.				
XX					
PD	28-NOV-1996.				
XX					
PF	07-MAY-1996;	96WO-US06423.			
XX					
PR	24-MAY-1995;	95US-0535733.			
XX					
PA	(IMMV ) IMMUNEX CORP.				
XX					
PI	Grabstein KH, Quinn LS, Troutt AB;				
XX					
DR	WPI; 1997-020939/02.				
DR	P-PSDB; AAW01658.				
XX					
PT	Muscle trophic compsn. contg. interleukin 15 - for treating, e.g.				
PT	congestive heart failure, muscle wasting etc.				
XX					
PS	Disclosure; Page 12; 22pp; English.				
XX					
CC	This sequence encodes human interleukin-15 (IL-15) (see AAW01658), a				
CC	known T-cell growth factor that can support proliferation of an				
CC	IL-2-dependent cell line, CTL-2. Compsns. contg. IL-15 to stimulate				

CC muscle growth, differentiation or hypertrophy are claimed. The  
CC stimulation of muscle growth is useful for treating atrophy, or wasting,  
CC in particular, skeletal and cardiac muscle atrophy. The compsns. further  
CC comprises a steroid, growth hormone and insulin-like growth factor.  
CC Congestive heart failure, muscle wasting and diabetes-associated  
CC glucose-intolerance or dyslipidaemia, rhabdomyosarcoma and muscular  
CC dystrophy can all be treated by such compsns..  
xx  
SQ Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

```
Query Match 100.0%; Score 489; DB 18; Length 489;
Best Local Similarity 100.0%; Pred. No. 2.4e-229;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	ATGAGAAATTTGAAACACCAATTTGAGAAGATTTTCCATCCAGTGTACTTGTGTTTCACTT	60
Db	1	atgagaatttcgaaccacatttgagaagtatttccatccagtgctactcttggtttcaact	60
Qy	61	CTAAACAGTCATTTTCTTAACTGAAGCTGGCATTTCATGCTTTCATTTTGGCTGTTTCAGT	120
Db	61	ctaaacagtcattttcttaactgaagctggcattcagtcttcatttctggcctgtttccagt	120
Qy	121	GCAGGGCTTCCCTAAACAGAAAGCCAACCTGGGTGAATGTATAAGTGATTGTGAAAAAATTT	180
Db	121	gcagggtctctctaaacacagaagcccaactgggtgaaigtataagtgtatttgaaaaaatt	180
Qy	- 181	GAAGATCTTATTCAAATCTATGTCATATTGATGCTPACTTTATATACGGAAGTGTGTTTCA	240
Db	181	gaagatcttattcgaattctatgcatatgcatctgcatcttatatacaggaagtgatgtctac	240
Qy	241	CCCAGTTGCAAGTAAACAGCAATGAAGTGCTTTCTCTGGAGTTACAAGTTATTTTCACTT	300
Db	241	cccagttgcaagtaacagcaatggaagtgccttctctggagttacaagttatttccaact	300
Qy	301	GAGTCGGGAGATCCAAGTATTCATGATACAGTAGAAATCTGATCATCTCTACCAACAAC	360
Db	301	gagtcgggagatgcaagtgatctcatgatacagtagaaaaactgatactcctagacaacac	360
Qy	361	AGTTTGCTTCTTAATGGGAATGTAACAGAAATCTGGATGCAAAAGATGTGAGGAATGGGAG	420
Db	361	agtttgcttctctaattgggaatgtaacagaaactcggatgcaagaagtgtgagaaactggag	420
Qy	421	GAATAAAATTAAGAAGTTTTTGCAGAGCTTTTGTCATATTGTCCAAATGTTTCATCAAC	480
Db	421	gaataaaattataagaatttttgcagagcttttgcagagcttttgcagagcttttgcagagct	480
Qy	481	ACTTCTTGA	489
Db	481	actctcttga	489

RESULT 7  
AAV23554  
ID AAV23554 standard; cDNA; 489 BP.

AC AAV23554;

DT 13-JUL-1998 (first entry)

Human interleukin-15 coding sequence.

Human; interleukin-15; IL-15; T cell; B cell; proliferation; vaccine; cytokine; growth factor; ss.

OS Homo sapiens.

AA	Key	Location/Qualifiers
FH	CDS	1..489
FT		/*tag= a
FT		

PN US5747024-A.

QY 481 ACTTCTTGA 489

PD	05-MAY-1998.	
XX		
PF	19-JUN-1995; 95US-0504042.	
XX		
XX	19-JUL-1995; 95US-0504042.	
PR	08-MAR-1993; 93US-0031399.	
PR	22-APR-1994; 94US-0233606.	
PR	22-FEB-1995; 95US-0393305.	
XX		
XX	(IMMV ) IMMUNEX CORP.	
PA		
XX		
PI	Grabstein KH, Widmer MB;	
XX		
DR	WPI; 1998-285678/25.	
DR	P-PSDB; AAW53878.	
XX		
PT	Use of Interleukin-15 - to enhance immunogenicity of a vaccine	
XX		
PS	Disclosure; Column 5-6; 5pp; English.	
XX		
CC	This sequence encodes human Interleukin-15 (IL-15), which can be used in	
CC	the vaccine of the invention. The vaccine composition comprises an	
CC	immunogenic amount of a vaccine antigen (Ag) and an	
CC	immunogenicity-augmenting amount of IL-15. The composition is useful for	
CC	enhancing the immunogenicity of a vaccine. It causes proliferation and differentiation	
CC	of these cells and augments T cell mediated immune responses. The vaccine	
CC	composition can sufficiently elicit an immune response without being	
CC	deleterious to the recipient, especially when using pathogenically	
CC	deficient antigens. Some vaccines do not elicit a strong immune response	
CC	and cannot provide sufficient protection on further exposure to the	
CC	antigen.	
XX		
SQ	Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other:	

[illegible]

```

Db 481 actcttga 489
|||||
RESULT 8
AAV02873
ID AAV02873 standard; DNA; 489 BP.
XX
AC AAV02873;
XX
DT 08-MAY-1998 (first entry)
XX
DE Simian epithelium derived T-cell factor DNA.
XX
KW Epithelium derived T-cell factor; ETF; simian; gastrointestinal disease;
KW B-cell stimulation; epithelium; villi; CD4+; CD8+; T-cell stimulation;
KW treatment; prevention; ss.
XX
OS Simian.
XX
FH Key Location/Qualifiers
FT CDS 1..489
FT /tag= a
FT sig_peptide 1..48
FT /tag= b
FT mat_peptide 49..486
FT /tag= c
FT /product= ETF
FT /note= "Epithelium-derived T-cell factor"
XX
XX US5707616-A.
XX
XX 13-JAN-1998.
XX
XX 04-OCT-1996; 96US-0726817.
XX
XX 22-FEB-1995; 95US-0393305.
XX 08-MAR-1993; 93US-0031399.
XX 22-APR-1994; 94US-0233606.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Anderson DM, Eisenman JR, Fung V, Grabstein KH;
XX Rauch C;
XX
XX WPI; 1998-100295/09.
XX P-PSDB; AAW39185.
XX
XX Treatment or prevention of gastrointestinal diseases - by
XX administering epithelium-derived T-cell factor polypeptide
XX
XX Claim 1C; Column 35-36; 34pp; English.
XX
XX This sequence encodes a simian epithelium-derived T-cell factor (ETF)
XX which is used in a method for treating or preventing gastrointestinal
XX disease. These polypeptides have particular application in the treatment
XX of gastrointestinal disorders associated with disruption of the
XX gastrointestinal epithelium or villi such as chemotherapy- and
XX radiation-therapy induced enteritis (gut toxicity), mucositis, peptic
XX ulcer disease, gastroenteritis and colitis, villus atrophic disorders,
XX malignancy and inflammatory bowel disease. ETF polypeptides may also be
XX useful in the treatment of human immunodeficiency virus (HIV) and
XX HIV-associated disease due to their ability to stimulate CD4+ and CD8+
XX cells. Biologically active ETF may be used to treat a variety of other
XX diseases or conditions where T-cell or B cell stimulation is desired.
XX
XX Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;
XX
Query Match 100.0%; Score 489; DB 19; Length 489;
Best Local Similarity 100.0%; Pred. No. 2.4e-229;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 ATGAGAAATTCGAAACACATTTGAGAAGTATTTCATCCAGTGTCTACTTGTCTTACTT 60
Db 1 atgagaatttcgaaacacacatttgagaagcatttcctcatccagtgctacttggttactt 60
QY 61 CTAAACAGTCATTTTCTAACTGAAGCTGGCATTCATGTCTTTCATTTTGGGCTGTTTCAGT 120
Db 61 ctaaacagtcattttcttaactgaagctgagctgcatcttcatttttgggctgtttcagt 120
QY 121 GCAGGGCTTCCTAAACAGACAGACCCCACTGGGTGAATGTAAATAGTGATTTGAAAAAAT 180
Db 121 gcagggcttccttaaacagagagcccaactgggtgaatgttaagtatttgaaaaaatt 180
QY 181 GAAGATCTTATTCAATCTATGATATTTGATGCTACTTTATATACGGAAGTGTGTTTAC 240
Db 181 gaagatcttattcaatctatgctactatgctactcttatatacaggaagtgatgttcac 240
QY 241 CCCAGTTCGAAAGTAACAGCAATGAAGTCTTCTCTTGGAGTTACAAGTTATTTTTCAC 300
Db 241 cccagttgcaaaagtaacagcaatgaagtgtcttctcttggagttacaagttatttcactt 300
QY 301 GAGTCCGGAGATGCAAGTATTTCATGATACAGTAGAATAATCTGATCATCTCTAGCAACA 360
Db 301 gagtccggagatgcaagtatttcattcatatcacagttagaataatctgatcatctctagca 360
QY 361 AGTTTGTCTTCTTAATGGGAATCTAACAGAAATCTGGATGCAAGAATGTGAGGAAC 420
Db 361 agtttgtcttcttaattgggaatgcaacagaatctgagtgcaagaaagtggaggaact 420
QY 421 GAAAAAATATTAAAGAAATTTTTCGACAGAGTTTGTACATATTGTCCTCAAAATGTTTCA 480
Db 421 gaaaaaataattaaagaatttttcgagagttttgtacatatgttccaaatgttccaaat 480
QY 481 ACTTCTTGA 489
Db 481 actcttga 489
XX
RESULT 9
AAV29479
ID AAV29479 standard; DNA; 489 BP.
XX
XX AAX29479;
XX
XX 10-JUN-1999 (first entry)
XX
XX Simian epithelium-derived T-cell factor (ETF) encoding DNA.
XX
XX Epithelium-derived T-cell factor; ETF; immunoassay; enteritis; ulcer;
XX T cell proliferation; gastrointestinal disease; mucositis; colitis;
XX gastroenteritis; villus atrophy; malignancy; inflammatory bowel disease;
XX human immune deficiency virus; tumour; simian; ss.
XX
XX Mammalia.
XX
XX US5892001-A.
XX
XX 06-APR-1999.
XX
XX 04-OCT-1996; 96US-0725969.
XX
XX 22-FEB-1995; 95US-0393305.
XX 08-MAR-1993; 93US-0031399.
XX 22-APR-1994; 94US-0233606.
XX 04-OCT-1996; 96US-0725969.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Anderson DM, Eisenman JR, Fung V, Grabstein KH;
XX Rauch C;
XX
XX WPI; 1999-253930/21.
XX P-PSDB; AAY03756, AAY03757.
XX

```

PT Antibodies specific for epithelium-derived T-cell growth factor  
PS Claim 1; Columns 35-36; 34pp; English.  
XX  
CC The invention relates to an isolated antibody that binds specifically to  
CC a simian or human epithelium-derived T-cell factor (ETF) polypeptide. The  
CC antibodies are used, optionally when immobilized or labeled, to detect  
CC and quantify ETF in standard immunoassays. They may also be used as  
CC diagnostic and therapeutic agents, e.g. when conjugated to toxins (or  
CC their precursors) or radionuclides. ETF induces proliferation and/or  
CC differentiation of T cells (or their precursors), e.g. for use in  
CC establishing long term in vitro cultures; and is also used to treat  
CC gastrointestinal disease (e.g. enteritis or mucositis induced by  
CC chemotherapy or radiation, peptide ulcer, gastroenteritis, colitis,  
CC villus atrophy, malignancy and inflammatory bowel disease), to treat  
CC human immune deficiency virus infection or associated disease, or  
CC generally in any situation requiring stimulation of T or B cell  
CC proliferation, secretion of immunoglobulins or certain cytokines,  
CC increased anti-infectious disease immunity, induction of T-cell lytic  
CC activity or increased destruction of tumour or virus-infected cells. The  
CC present sequence represents a DNA encoding a simian ETF precursor  
CC polypeptide sequence.  
XX  
SQ Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 20; Length 489;  
Best Local Similarity 100.0%; Pred. No. 2.4e-229;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAATTCGAAACACCATTTGAGAAGTATTTCCTCCAGTGTCTACTGTGTTACTT 60  
Db 1 atgagaatttcgaaacacacatttgagaagatttcctccagtgctactgtgttactt 60

Qy 61 CTAAACAGTCATTTCTTAACCTGCACTGGCATTCATGCTTCATTTTGGGCTGTTTCAGT 120  
Db 61 ctaaacagtcattttcttaactgaagctggcattccttcatttgggctgtttcagt 120

Qy 121 CGAGGGCTTCCTAAACAGAACCCAACTGGGTGAATGTAATGAAGTATTGAAAAAATT 180  
Db 121 cgagggttcctaaacagaaagccaaactgggtgaatgtaataagtgattgaaaaaatt 180

Qy 181 GAAGATCTTATTCATCTATGATGCTACTTTATATACGGAAGTATGTTTCAC 240  
Db 181 gaagatcttattcaatctatgcattatgctactttatatacggaaagtatgttcac 240

Qy 241 CCCAGTTCGAAAGTAAACAGCAATGAAGTGCCTTCTCTTGGAGTTACAAGTTATTCAC 300  
Db 241 cccagttcgaaagttaaacagcaatgaagtgccttctcttggagttacaagttattcac 300

Qy 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAGAAAAATCTGATCATCTAGCAACAAC 360  
Db 301 gagtcggagatgcaagtattcatgatacagtagaaaaatctgatacctcagcaacaac 360

Qy 361 AGTTTGTCTTAAATGGAATGTAACAGAATCTGGATGCAAGAATGTGAGGAATCGGAG 420  
Db 361 agtttgtctctaaatgggaaatgaacagaatctggatgcaagaatgtgaggaactggag 420

Qy 421 GAAAAAATATTAAAGATTTTTCAGAGATTTTGTACATATTTGTCCAAATGTTTCATCAAC 480  
Db 421 gaaaaaataattaaagaatttttcagagatTTTGTACATATTTGTCCAAATGTTTCATCAAC 480

Qy 481 ACTTCTTGA 489  
Db 481 acttcttga 489

RESULT 10  
ID AAZ90032  
XX AAZ90032 standard; cDNA; 489 BP.  
AC AAZ90032;  
XX

DT 09-MAY-2000 (first entry)  
XX Human interleukin-15 (IL-15) nucleotide sequence.  
DE  
XX  
KW Interleukin-15; IL-15; antagonist; Irritable bowel disease; IBD;  
KW celiac disease; treatment; human; ss.  
OS Homo sapiens.  
XX  
PN WO200002582-A2.  
XX  
PD 20-JAN-2000.  
XX  
PF 09-JUL-1999; 99WO-GB02201.  
XX  
PR 10-JUL-1998; 98GB-0014892.  
XX  
PA (KENN-) KENNEDY INST RHEUMATOLOGY MATHILDA & TER.  
PI Londei M, Quarantino S, Maiuri L;  
XX  
DR WPI; 2000-171080/15.  
DR P-FSDB; AAY78595.  
XX  
PT Use of antagonists of interleukin-15 for treating an inflammatory bowel  
PT disease, particularly celiac disease -  
XX  
PS Disclosure; Page 70; 70pp; English.  
XX  
CC This sequence represents the human Interleukin 15 (IL-15) nucleotide  
CC sequence. The IL-15 nucleotide sequence and the protein encoded by it can  
CC be used to determine and create antagonists of IL-15. An antagonist of  
CC IL-15 can be used for treating an inflammatory bowel disease (IBD). The  
CC invention relates to the treatment of celiac disease using IL-15  
CC antagonists. The antagonists are preferably muteins of IL-15, antibodies  
CC against IL-15 or IL-15 molecules bound to chemical groups that interfere  
CC with the ability of IL-15 to effect a signal transduction through either  
CC the alpha or the gamma subunit of the IL-15 receptor complex. The IL-15  
CC antagonists of the invention can be used to treat irritable bow disease  
CC especially celiac disease.  
XX  
SQ Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 21; Length 489;  
Best Local Similarity 100.0%; Pred. No. 2.4e-229;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAATTCGAAACACCATTTGAGAAGTATTTCCTCCAGTGTCTACTGTGTTACTT 60  
Db 1 atgagaatttcgaaacacacatttgagaagatttcctccagtgctactgtgttactt 60

Qy 61 CTAAACAGTCATTTCTTAACCTGCACTGGCATTCATGCTTCATTTTGGGCTGTTTCAGT 120  
Db 61 ctaaacagtcattttcttaactgaagctggcattccttcatttgggctgtttcagt 120

Qy 121 CGAGGGCTTCCTAAACAGAACCCAACTGGGTGAATGTAATGAAGTATTGAAAAAATT 180  
Db 121 cgagggttcctaaacagaaagccaaactgggtgaatgtaataagtgattgaaaaaatt 180

Qy 181 GAAGATCTTATTCATCTATGATGCTACTTTATATACGGAAGTATGTTTCAC 240  
Db 181 gaagatcttattcaatctatgcattatgctactttatatacggaaagtatgttcac 240

Qy 241 CCCAGTTCGAAAGTAAACAGCAATGAAGTGCCTTCTCTTGGAGTTACAAGTTATTCAC 300  
Db 241 cccagttcgaaagttaaacagcaatgaagtgccttctcttggagttacaagttattcac 300

Qy 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAGAAAAATCTGATCATCTAGCAACAAC 360  
Db 301 gagtcggagatgcaagtattcatgatacagtagaaaaatctgatacctcagcaacaac 360

Qy 361 AGTTTGTCTTAAATGGAATGTAACAGAATCTGGATGCAAGAATGTGAGGAATCGGAG 420  
Db 361 agtttgtctctaaatgggaaatgaacagaatctggatgcaagaatgtgaggaactggag 420

Qy 421 GAAAAAATATTAAAGATTTTTCAGAGATTTTGTACATATTTGTCCAAATGTTTCATCAAC 480  
Db 421 gaaaaaataattaaagaatttttcagagatTTTGTACATATTTGTCCAAATGTTTCATCAAC 480

Qy 481 ACTTCTTGA 489  
Db 481 acttcttga 489

RESULT 10  
ID AAZ90032  
XX AAZ90032 standard; cDNA; 489 BP.  
AC AAZ90032;  
XX

Db 361 agttgtctctaaagggaatgaacagactggtgataaagaatgaggaaactggag 420  
QY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATGTCCAAATGTTCAAC 480  
Db 421 gaaaaaataataagaattttgcagagttttgtacattgttccaaatgttcaac 480  
QY 481 ACTTCTTGA 489  
Db 481 acttcttga 489

## RESULT 11

AAZ38244  
ID AAZ38244 standard; cDNA: 489 BP.  
XX  
AC AAZ38244;  
XX  
DT 09-FEB-2000 (first entry)  
XX  
DE Simian epithelium-derived T-cell factor (ETF) cDNA.  
XX  
KW ETF: epithelium-derived T-cell factor; T-cell; T-lymphocyte;  
KW proliferation; differentiation; growth factor; precursor; mature; CD4+;  
KW CD8+; gastrointestinal; epithelium; cell culture; treatment; HIV;  
KW gastrointestinal disease; gastroenteritis; colitis;  
KW inflammatory bowel disease; villus atrophic disorder; enteritis;  
KW chemotherapy; radiotherapy; gut toxicity; cancer; side effect;  
KW tolerated dose; ss.  
XX  
OS Mammalia.  
XX  
FH Key  
FT CDS 1..489  
FT Location/Qualifiers  
FT CDS 1..489  
FT /tag= a  
FT /product= "Simian ETF precursor protein (AAV52308)"  
FT 1..144  
FT sig\_peptide  
FT /tag= b  
FT mat\_peptide 145..489  
FT /tag= c  
FT /product= "Mature simian ETF (AAV52309)"  
XX  
US5985262-A.  
XX  
PD 16-NOV-1999.  
XX  
PF 03-FEB-1997; 97US-0794524.  
XX  
PR 22-FEB-1995; 95US-0393305.  
PR 04-OCT-1996; 96US-0726817.  
PR 08-MAR-1993; 93US-0031399.  
PR 22-APR-1994; 94US-0233606.  
XX  
PA (IMV ) IMMUNEX CORP.  
XX  
PI Rauch C, Fung V, Eisenman JR, Grabstein KH, Anderson DM;  
XX  
XX WPI; 2000-022267/02.  
DR P-PSDB; AAY52308, AAY52309.  
XX  
XX Stimulation of T-cells in human immunodeficiency virus infected  
PT patients -  
XX  
XX Claim 1; Columns 35-36; 33pp; English.

XX  
XX This sequence represents simian epithelium-derived T-cell factor (ETF)  
XX cDNA. ETF is a previously unidentified T-cell growth factor which  
XX stimulates precursor or mature CD4+ and CD8+ T-lymphocytes to proliferate  
XX and differentiate. It also promotes proliferation of the gastrointestinal  
XX epithelium. The protein can be used to promote long-term in vitro culture  
XX of T-lymphocytes and T-cell lines. ETF can be used for treating HIV  
XX infection, HIV-associated diseases, and other diseases or conditions  
XX where stimulation of T-cell proliferation would be desirable e.g., it

CC could be used to augment the destruction of tumour cells or virally-  
CC infected cells. ETF may also be used to treat or prevent gastrointestinal  
CC disease, including chemotherapy and radiotherapy associated enteritis,  
CC gastroenteritis, colitis, inflammatory bowel disease and villus atrophic  
CC disorders. Chemotherapy and radiotherapy associated enteritis (gut  
CC toxicity) results in bleeding and sepsis due to gastrointestinal flora  
CC entering the blood, and thus can limit the dosage of therapeutic agent  
CC administered to a cancer patient. ETF may therefore be used to increase  
CC the tolerated doses radiotherapy and chemotherapy.  
XX  
SQ Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 21; Length 489;  
Best Local Similarity 100.0%; Pred. No. 2.4e-229;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGAGAAATTCGAAACACACATTTGAGAGTATTTCATCCAGTGTCTACTGTGTACTT 60  
Db 1 atgagaatttcgaaaccacattttgagaagtatttccatccagtgctactgtgttactt 60  
QY 61 CTAACAGTCATTTCTACTGAAAGCTGGCATTTCATGCTTTCATTTGGGCTGTTCAGT 120  
Db 61 ctaaacagtcattttctactgaagctggcatttcattcttcatatttgggctgttca 120  
QY 121 GCAGGGCTTCCCTAAACAGAGCCCAACTGGGTGAATGTAATAGTCATTTGAAAAAATT 180  
Db 121 gcaggggcttccctaaacagagcccaactgggtgaatgtaatagtcattttgaaaaaatt 180  
QY 181 GAAGATCTTATTCAATCTATGCTATGATGCTACTTTATATACGAAAGTGTGTTCAAC 240  
Db 181 gaagatcttattcaatctatgctatgctactttatatacagaaagtgttcaac 240  
QY 241 CCCAGTTGCAAGTAACAGCAATGAAGTGTCTTCTCTGGAGTTCACAGTTATTTCACTT 300  
Db 241 cccagttgcaagtaacagcaatgaagtgtcttctctggagtgttacaagtattttcaact 300  
QY 301 GAGTCCGGAGATGCAAGTATTTCATGATACAGTAGAAATCTCATCTCCTAGCAACAAC 360  
Db 301 gagtccggagatgcaagtatttcattcatgacagtagaaaaactgatcatctagcaacaac 360  
QY 361 AGTTTGTCTTCTAATGGGAATGAACAGAACTGGATGCAAGAATGTGAGGAACCTGGAG 420  
Db 361 agtttgtcttctaaatgggaatgtaacagaactctggatgcaagaatgtgagaactggag 420  
QY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGTCCAAATGTTCAAC 480  
Db 421 gaaaaaataataagaattttgcagagattttgcagagattttgtacattgttccaaatgttcaac 480  
QY 481 ACTTCTTGA 489  
Db 481 acttcttga 489

## RESULT 12

AAZ14465  
ID AAD14465 standard; DNA: 489 BP.

XX  
AC AAD14465;

XX  
DT 15-NOV-2001 (first entry)

XX  
DE Human interleukin 15 (IL-15) DNA coding sequence.

XX  
KW Human; interleukin 15; IL-15; gene therapy; chromosome 4q31; infection;  
KW drug screening; anthropological lineage; paternity testing; HIV;  
KW Human Immunodeficiency Virus; forensic application; T-cell leukaemia; ds.  
OS Homo sapiens.

XX  
FH Key  
FT CDS 1..489  
FT Location/Qualifiers  
FT /tag= a

FT XX /product= "Human IL-15 protein"

PN WO200158914-A2.

XX 16-AUG-2001.

PD 08-FEB-2001; 2001WO-US04130.

XX 08-FEB-2000; 2000US-0181059.

XX (GENA-) GENAISSANCE PHARM INC.

PA Anastasio AE, Chew A, Denton RR, Nandabalan K, Stephens JC;

PI WPI: 2001-522460/57.

DR P-PSDB; AAE08576.

DR Novel polynucleotides comprising one of 11, P51-PS11, single nucleotide

PT polymorphisms in human interleukin-15 gene, and useful for treating

PT disorders affected by expression of function of interleukin-15 isogene

PT

XX Disclosure; Fig 2; 78pp; English.

PS

XX The present sequence is human interleukin-15 (IL-15) DNA coding sequence

CC located on chromosome 4q31. The polymorphic variants of IL-15 genes are

CC useful for studying the expression and function of IL-15 and expressing

CC IL-15 protein for use in screening for candidate drugs to treat diseases

CC related to IL-15 activity. Genotyping or haplotyping an individual at the

CC novel IL-15 polymorphic sites are useful for studying population

CC diversity, anthropological lineage, the significance of diversity and

CC lineage of the phenotypic level, paternity testing, forensic applications

CC and for identifying associations between IL-15 genetic variation and a

CC trait such as level of drug response or susceptibility to disease

CC Identifying an association between a genotype or haplotype and a trait,

CC is useful for developing diagnostic tests and therapeutic treatments for

CC infections, human immunodeficiency virus and T-cell leukaemia. The

CC identification of an association between a clinical response and a

CC genotype or haplotype (or haplotype pair) for the IL-15 gene may be the

CC basis for designing a diagnostic method to determine those individuals

CC who will or will not respond to the treatment, or alternatively, will

CC respond at a lower level, and thus may require more treatment, i.e. a

CC greater dose of a drug. The genotyping or haplotyping methods are also

CC useful for developing drugs targeting IL-15. The genotyping and

CC haplotyping methods are also useful in designing clinical trials. IL-15

CC DNA is useful for therapeutic purposes for treating disorders affected

CC by expression of function of novel IL-15 isogene and also in gene

CC therapy. Expression of an IL-15 isogene may be turned off by transforming

CC a targetted organ, tissue or cell population of an expression vector

CC that expresses high levels of untranslatable mRNA for the isogene.

XX

SQ Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 22; Length 489;

Best Local Similarity 100.0%; Pred. NO. 2.4e-229;

Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAACCCACATTGAGAGATATTCCATCCAGTCTACTTGTTACTT 60

Db 1 atgagatttcgaacccacattgagaagtattccatccagtgctacttggttactt 60

QY 61 CTAACAGTCAATTTCTAACTGAAGCTGGCATTCATGTCTTCATTTGGGCTGTTTCAGT 120

Db 61 ctaaacagtcatttcttaactgaagctggcattcatgcttcatttggcggtttcagt 120

QY 121 GCAGGGCTTCTAAACAGAGCCCACTGGGTGAATGTAATGATGTTGAAATAATT 180

Db 121 gcagggtctctaaacagagcccaactgggtgaatgtaataagtgatttgaaaaaatt 180

QY 181 GAAGATCTTATTCAATCTPATCATATTGCTACTCTTTATATACGGAAGTGATGTTTCCAC 240

Db 181 gaagatcttattcaatctatgcattgatctactttattatatacggaaagcgtggtccac 240

QY 241 CCCAGTTGCAAAAGTAACAGCAATGAAGTGCTTCTCTTTGGAGTTACAAGTTATTTCACCTT 300

Db 241 cccagttgcaaaagtaaacagcaatgaagtgcttctcttctcttgaggagttacaagttatttcaactt 300

QY 301 GAGTCCGGAGATGCAAGTATTTCATGATACAGTAGAATAATCTGATCATCTTAGCAAAACAAC 360

Db 301 gagtccggagatgcaagtatttcattgatcacagttagaataatctgattctctctagcaacaac 360

QY 361 AGTTTGCTCTTCTAATGCGAATGTACACAAATCTGGATGCAAAAGATGTGAGAACTGGAG 420

Db 361 agtttgctcttcttaataatggaatgtacagaatctggatgcaaaagatgtgaggaactggag 420

QY 421 GAAAAAATAATTAAAGAAATTTTGCAGAGTTTGTGACATATTGTCCAAATGTTTCATCAAC 480

Db 421 gaaaaaataattaaagaaatTTTGCAGAGTTTGTGACATATTGTCCAAATGTTTCATCAAC 480

QY 481 ACTTCTTTGA 489

Db 481 acttcttga 489

RESULT 13

AAF57017

ID AAF57017 standard; cDNA; 489 BP.

AC AAF57017;

XX 14-MAY-2001 (first entry)

DE Slmian ETF (sETF) polypeptide encoding cDNA.

XX Epithelium-derived T-cell factor; ETF; simian; human; enteritis;

KW gastrointestinal disease; mucositis; peptic ulcer; cytostatic;

KW villus atrophic disorder; inflammatory bowel disease; antinflammatory;

KW anti-HIV; antiviral; T-lymphocyte stimulator; ss.

OS Mammalia.

EH Key Location/Qualifiers

FT CDS 1..489

FT /\*tag= a

FT /product= "sETF"

FT sig\_peptide 1..144

FT /\*tag= b

FT mat\_peptide 145..486

FT /\*tag= c

FT /\*note= "specifically claimed (see AAB62013)"

XX US6184359-B1.

XX 06-FEB-2001.

XX 09-NOV-1998; 98US-0189193.

XX 22-FEB-1995; 95US-0393305.

XX 04-OCT-1996; 96US-0725969.

XX 08-MAR-1993; 93US-0031399.

XX 22-APR-1994; 94US-0233606.

XX (IMMV ) IMMUNEX CORP.

XX Grabstein KH, Anderson DM, Eisenman JR, Fung V, Rauch C;

PI WPI: 2001-217801/22.

DR P-PSDB; AAB62012, AAB62013.

XX New antibodies that specifically binds epithelium-derived T-cell factor

PT polypeptide useful for e.g. treating or preventing gastrointestinal

PT diseases, HIV and HIV-associated diseases, augmenting destruction of

PT tumour cells

XX Claim 1; Column 35-36; 35pp; English.

XX The invention relates to simian and human epithelium-derived T-cell  
 CC factor (ETF) polypeptides. Antibodies that specifically bind to the ETF  
 CC polypeptides are used for treating or preventing gastrointestinal  
 CC diseases, such as chemotherapy and radiation therapy-induced enteritis  
 CC and mucositis, peptic ulcer disease, villus atrophic disorders and  
 CC inflammatory bowel disease; for increasing tolerated doses for radiation  
 CC therapy and chemotherapy agents which are limited by gastrointestinal  
 CC toxicity; and for treating HIV and HIV-associated diseases. The  
 CC antibodies are further used to treat a variety of other diseases or  
 CC conditions where it is desired to stimulate proliferation of  
 CC T-lymphocytes and B lymphocytes, or the secretion of immunoglobulin B  
 CC lymphocytes, to augment anti-infectious disease immunity, to induce CTL,  
 CC LAK or NK lytic activity, or to augment the destruction of tumour cells  
 CC or cells infected with virus. The present sequence represents a cDNA  
 CC encoding the simian ETF (SETF) polypeptide.  
 XX  
 SQ Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 22; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-229;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACAAATTCGAACACCATTTGAGAGTATTTCCATCCAGTGTCTACTGTGTTACTT 60  
 Db 1 atgagaatttcgaaccacatttgagaagattttccatccagtgctactgtgtttactt 60

QY 61 CTAAACAGTCATTTCTTAACCTGAAGCTGGCATTCATCTTTCATTTTGGGCTGTTTCAGT 120  
 Db 61 ctaaacagtcattttctaacgaagctggcattcattcttcattttgggctgtttcagt 120

QY 121 GCAGGGCTTCCTTAAACAGACCCCAACTGGGTGAATGTAATGAAGTGTGAAAAAATTT 180  
 Db 121 gcagggtcttctaaacagagcccaactgggtgaatgtaataagtgattgaaaaaatt 180

QY 181 GAAGATCTTATTCATCTATGCATATTCATCTTATATACGGAAGTGTTCAC 240  
 Db 181 gaagatcttattcattcattcattgctattgctatttatacagggaagtgatttcac 240

QY 241 CCCAGTTCGCAAGTAAACAGCAATGAAGTGTCTTCTTTGGAGTTACAAGTTATTCAC 300  
 Db 241 cccagttgcaagtaaacagcaatgaagtgctttcttcttggagttacaaagtatttcactt 300

QY 301 GAGTCGGAGATGCAAGTATTCATGATACAGTAGAAAAATCTGATCATCTAGCAAAAC 360  
 Db 301 gagtcggagatgcaagtattcatgatacagtagaaaaatctgatcatcctagcaaaac 360

QY 361 AGTTTGTCTTCTAATGGAATGTACAGAACTCGATGCAAGAAATGTGAGAACTGGAG 420  
 Db 361 agtttgtcttctaatggaaatgtaacagaactctggatgcaagaagtgtgaggaactggag 420

QY 421 GAAAAAATATTAAGAAATTTTTCAGAGTTTGTACATATTTGTCCAATGTTTCATCAAC 480  
 Db 421 gaaaaaatattaaagaatttttcagagttttgtacatatgttgcataattgtccaaatgttcatcaac 480

QY 481 ACTTCTTGA 489  
 Db 481 acttcttga 489

RESULT 14  
 AAX56368  
 ID AAX56368 standard; DNA; 1202 BP.  
 AC AAX56368;  
 XX  
 XX 21-JUL-1999 (first entry)  
 DE Human IL-15 DNA.  
 XX  
 KW Human; interleukin 15; IL-15; ribozyme; enzymatic RNA; cleavage;  
 KW rheumatoid arthritis; inflammatory disorder; ds.

XX Homo sapiens.  
 OS  
 XX WO92323208-A2.  
 PN  
 XX 14-MAY-1999.  
 PD  
 XX 29-OCT-1998; 98WO-IB01837.  
 PF  
 XX 31-OCT-1997; 97US-0962503.  
 PR  
 XX (HISM ) HISAMITSU PHARM CO LTD.  
 PA  
 XX Hamanaka S, Nozawa I, Veerapaneni D;  
 PI  
 XX WPI; 1999-313334/26.  
 DR  
 XX  
 PT New ribozymes targeted to interleukin-15 mRNA  
 XX  
 PS Disclosure; Fig 8; 46pp; English.  
 CC The present sequence describes an isolated RNA molecule which  
 CC specifically cleaves mRNA encoding interleukin 15 (IL-15). The  
 CC enzymatic RNA molecules can bind to and cleave mRNA encoding IL-15.  
 CC They can be used for treating disorders associated with IL-15 such  
 CC as inflammatory disorders, e.g. rheumatoid arthritis by inhibiting  
 CC the synthesis of IL-15 in lymphocytes and preventing the recruitment  
 CC and activation of macrophages. They can also be used to develop  
 CC transgenic animals which can be used to identify the impact of  
 CC increased or decreased IL-15 levels on a particular pathway or  
 CC phenotype. The present sequence represents a human IL-15 DNA sequence.  
 XX  
 SQ Sequence 1202 BP; 355 A; 219 C; 249 G; 379 T; 0 other;

Query Match 100.0%; Score 489; DB 20; Length 1202;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-229;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACAAATTCGAACACCATTTGAGAGTATTTCCATCCAGTGTCTACTGTGTTACTT 60  
 Db 317 atgagaatttcgaaccacatttgagaagattttccatccagtgctactgtgtttactt 376

QY 61 CTAAACAGTCATTTCTTAACCTGAAGCTGGCATTCATCTTTCATTTTGGGCTGTTTCAGT 120  
 Db 377 ctaaacagtcattttctaacgaagctggcattcattcttcattttgggctgtttcagt 436

QY 121 GCAGGGCTTCCTTAAACAGACCCCAACTGGGTGAATGTAATGAAGTGTGAAAAAATTT 180  
 Db 437 gcagggtcttctaaacagagcccaactgggtgaatgtaataagtgattgaaaaaatt 496

QY 181 GAAGATCTTATTCATCTATGCATATTCATGCTACTTTATACGGAAGTGTTCAC 240  
 Db 497 gaagatcttattcattcattcattgctattgctatttatacagggaagtgatttcac 556

QY 241 CCCAGTTCGCAAGTAAACAGCAATGAAGTGTCTTCTTTGGAGTTACAAGTTATTCAC 300  
 Db 557 cccagttgcaagtaaacagcaatgaagtgctttcttcttggagttacaaagtatttcactt 616

QY 301 GAGTCGGAGATGCAAGTATTCATGATACAGTAGAAAAATCTGATCATCTAGCAAAAC 360  
 Db 617 gagtcggagatgcaagtattcatgatacagtagaaaaatctgatcatcctagcaaaac 676

QY 361 AGTTTGTCTTCTAATGGAATGTACAGAACTCGATGCAAGAAATGTGAGAACTGGAG 420  
 Db 677 agtttgtcttctaatggaaatgtaacagaactctggatgcaagaagtgtgaggaactggag 736

QY 421 GAAAAAATATTAAGAAATTTTTCAGAGTTTGTACATATTTGTCCAATGTTTCATCAAC 480  
 Db 737 gaaaaaatattaaagaatttttcagagttttgtacatatgttgcataattgtccaaatgttcatcaac 796

QY 481 ACTTCTTGA 489  
 Db 481 acttcttga 489

Db 797 actcttga 805

RESULT 15

AAF21342

XX AAF21342 standard; DNA; 1202 BP.

XX AAF21342;

XX 14-MAR-2001 (first entry)

XX Human low adenosine antisense oligonucleotide related sequence #2909.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;

XX human; airway disorder; bronchoconstriction; lung inflammation;

XX surfactant depletion; respiratory; bronchodilator; antiinflammatory;

XX immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;

XX respiratory obstruction; pulmonary obstruction; impeded respiration;

XX surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;

XX respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;

XX pulmonary hypertension; emphysema; pulmonary transplantation rejection;

XX chronic obstructive pulmonary disease; pulmonary infection; bronchitis;

XX cancer; ss.

OS Homo sapiens.

XX WO2000062736-A2.

PN 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US08020.

PF 06-APR-1999; 99US-0127958.

PR (UYEC-) UNIV EAST CAROLINA.

XX (NYCE/) NYCE J W.

PA Nyce JW;

PI WPI; 2000-679539/66.

XX Low adenosine (A) content antisense oligonucleotides which do not

XX trigger adenosine receptors during metabolism, useful e.g. for treating

XX cancers and respiratory obstructions -

XX Disclosure; Page 1344-1345; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense

XX oligonucleotides and compositions (I) comprising them. In the antisense

XX oligonucleotides the A is replaced by a 'Universal' or alternative base.

XX (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,

XX immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.

XX The antisense oligonucleotides and (I) can be used to down-regulate the

XX expression and or activity of target polypeptides associated with

XX lung/respiratory disorders and malignancies, such as stimulating and

XX activating peptide factors and transmitters, transcription factors,

XX immunoglobulins and antibodies, antibody receptors, cytokines and

XX chemokines, endogenously produced specific and non-specific enzymes,

XX binding proteins, adhesion molecules and their receptors, cytokine and

XX chemokine receptors, adenosine receptors, bradykinin receptors, central

XX nervous system (CNS) and peripheral nervous and non-nervous system

XX receptors, CNS and peripheral nervous and non-nervous system peptide

XX transmitters, defensins, growth factors, vasoactive peptides and

XX receptors, binding proteins and malignancy associated proteins. The

XX antisense oligonucleotides may be used in this way to treat disorders

XX including respiratory obstruction (especially pulmonary obstruction

XX and/or bronchoconstriction) and/or lung inflammation, allergy(ies)

XX and/or surfactant hypoproduction which are associated with a disease or

XX condition selected from pulmonary vasoconstriction, inflammation,

XX allergies, asthma, impeded respiration, respiratory distress syndrome

XX (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary

XX hypertension, emphysema, chronic obstructive pulmonary disease (COPD),

XX pulmonary transplantation rejection, pulmonary infections, bronchitis,

CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide

CC fragments and antisense oligonucleotides used in the exemplification of

CC the present invention.

XX Sequence 1202 BP; 355 A; 219 C; 249 G; 379 T; 0 other;

SQ

Query Match 100.0%; Score 489; DB 21; Length 1202;

Best Local Similarity 100.0%; Pred. No. 2.4e-229;

Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAAATTTGCAACACACATTTGAGAGATTTCCATCCAGTCTACTTGTGTTTACTT 60

Db 317 atgagaatttcgaacacacatttgagaagtatttccatccagtgctactgtgttactt 376

Qy 61 CTAACAGCTCAATTTTAACTGAGCTGGCATTCATGCTTTCATTTGGGCTGTTTCAGT 120

Db 377 cttaacagctcattcttaactgaagctggcattcatgtcttcatttgggctgttca 436

Qy 121 GCAGGGCTTCTAAACAGAACCAACGCGTGAATTAATTAAGTGAATTTGAAAAAAT 180

Db 437 gcagggtcttctaaacagagcccaactgggtgaatgaatgattgaaaaaatt 496

Qy 181 GAAGATCTTATTCATCTATTCATATTCATGCTCTCTTTATATACGGAAGTGTTCAC 240

Db 497 gaagatcttattcaatctatgcatattgctactcttatacaggaaagtgttccac 556

Qy 241 CCCAGTTCGCAAGTAACAGCAATGAAGTCTTCTCTGGAGTTACAAAGTTATTTCAC 300

Db 557 cccagttgcaagtaacagcaatgaagtgcttctctctctggggttacaagttatttca 616

Qy 301 GAGTCCGGAGATGCAAGTATTTCATGATACAGTAGAATAATCTGATCATCTAGCAACAC 360

Db 617 gagtccggagatgcaagtattcatgacagtagaataatctgacatctctagcaaacac 676

Qy 361 AGTTTGTCTTCTAATGGGAATGTAACAAATCTGATCAAGATGTCAGGAAGTGGAG 420

Db 677 agtttgtcttaattgggaatgtaacagaatctggatgcaagaatgtaggaactggag 736

Qy 421 GAAAAAATATTAAGAATTTTGCAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480

Db 737 gaaaaaataataagaattttgcagagttttgtacataattgtccaaatgttcatcaac 796

Qy 481 ACTTCTTGA 489

Db 797 actcttga 805

RESULT 16

AAA58044

ID AAA58044 standard; cDNA to mRNA; 1202 BP.

XX AAA58044;

AC AAA58044;

XX 10-OCT-2000 (first entry)

DT Human interleukin-15 (IL-15) cDNA copy of mRNA.

DE

XX Human interleukin-15; IL-15; antisense therapy; expression inhibition;

XX T-cell mediated immune response; autoimmune disorder;

XX inflammatory polyarthropathy; rheumatoid arthritis; transplant rejection;

XX graft versus host disease; lupus erythematosus; aschma;

XX inflammatory bowel disease; gene therapy; immunosuppressive;

XX antiinflammatory; ss.

XX Homo sapiens.

OS

XX Key Location/Qualifiers

XX 5'UTR 1..316

XX CDS 317..805

XX /\*tag= a

XX /\*tag= b

XX /\*product= "Human IL-15"





RESULT 19  
AAF211345  
ID AAF21345 standard; DNA; 17904 BP.  
XX  
AC AAF21345;  
XX  
DT 14-MAR-2001 (first entry)  
XX  
DE Human low adenosine antisenase oligonucleotide related sequence #2912.  
XX  
KW Low adenosine antisenase oligonucleotide; phosphorothioate; allergy;  
KW human; airway disorder; bronchoconstriction; lung inflammation;  
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
KW cancer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200062736-A2.  
XX  
PD 26-OCT-2000.  
XX  
PF 24-MAR-2000; 2000WO-US08020.  
XX  
PR 06-APR-1999; 99US-0127958.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PA (NYCE/) NYCE J W.  
XX  
PI Nyce JW;  
XX  
DR WPI; 2000-679539/66.  
XX  
PT Low adenosine (A) content antisenase oligonucleotides which do not  
PT trigger adenosine receptors during metabolism, useful e.g. for treating  
PT cancers and respiratory obstructions -  
XX  
PS Disclosure; Page 1349-1353; 1592pp; English.  
XX  
CC The present invention describes low adenosine (A) content antisenase  
CC oligonucleotides and compositions (I) comprising them. In the antisenase  
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.  
CC The antisenase oligonucleotides and (I) can be used to down-regulate the  
CC expression and or activity of target polypeptides associated with  
CC lung/respiratory disorders and malignancies, such as stimulating and  
CC activating peptide factors and transmitters, transcription factors,  
CC immunoglobulins and antibodies, antibody receptors, cytokines and  
CC chemokines, endogenously produced specific and non-specific enzymes,  
CC binding proteins, adhesion molecules and their receptors, cytokine and  
CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
CC nervous system (CNS) and peripheral nervous and non-nervous system  
CC transmitters, CNS and peripheral nervous and non-nervous system peptide  
CC transmitters, defensins, growth factors, vasoactive peptides and  
CC receptors, binding proteins and malignancy associated proteins. The  
CC antisenase oligonucleotides may be used in this way to treat disorders  
CC including respiratory obstruction (especially pulmonary obstruction  
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)  
CC and/or surfactant hypoproduction which are associated with a disease or  
CC condition selected from pulmonary vasoconstriction, inflammation,  
CC allergies, asthma, impeded respiration, respiratory distress syndrome  
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide

CC fragments and antisenase oligonucleotides used in the exemplification of  
CC the present invention.  
XX  
SQ Sequence 17904 BP; 6014 A; 2945 C; 3330 G; 5615 T; 0 other:  
  
Query Match 100.0%; Score 489; DB 21; Length 17904;  
Best Local Similarity 100.0%; Pred. No. 2.3e-229;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ATGAGAAATTCGAAACACATTTGAGAAATTTCCATCCAGTCTACTTGTGTTTACTT 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1565 atgagaatttcgaaacacatttgagaagatttccatccagtgctactgtgttactt 1624  
QY 61 CTAAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCATTTTGGGCTGTTTCA 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1625 ctaaacagtcattttctaaactgaagctggcatcattcttcttcttcttcttcttcttctt 1684  
QY 121 GCAGGGCTTCTTAAACAGAAAGCAACTGGTGGTGAATCTAATAAGTGAATTTGAAAAAAT 180  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1685 gcagggtcttctaaacagaaagcaactgggtgaatgaatgaatgaatgaatgaatgaatgaat 1744  
QY 181 GAAGATCTTATCAATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1745 gaagatcttattcaatctatgattgattgattgattgattgattgattgattgattgattgatt 1804  
QY 241 CCCAGTTGCAAGTAACAGCAATGAAGTCTTCTCTTGGAGTTACAGTTATTTTCACTT 300  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1805 cccagttgcaagtaacagcaatgaagtgcttcttcttcttcttcttcttcttcttcttcttctt 1864  
QY 301 GAGTCCGGAGATGCAAGTATTTCATGATACAGTAGAGAAATCTGATCATCTCTAGCAAAACA 360  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1865 gagtcggagagatgcaagtgatttcatgacagtagaagaatctgacatccctagcaaaacaac 1924  
QY 361 AGTTTGTCTTCTAATGGGAATGTAACAGAAATCTGGATGCAAGAAATGTGAGGAACCTGGAG 420  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1925 agttgtcttctaattgggaatgtaacagaatctggatgcaagaatgtgaggaactggag 1984  
QY 421 GAAAAAATATTAAAGAAATTTTTCGAGAGTTTGTACATATTTCCCAAAATGTTTCATCAAC 480  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1985 gaaaaaattattaaagaatttttgcagagtttgcagagtttgcagagtttgcagagtttgcagag 2044  
QY 481 ACTTCTTGA 489  
Db |||||||  
2045 acttcttga 2053  
  
RESULT 20  
AAF21227  
ID AAT97227 standard; DNA; 489 BP.  
XX  
AC AAT97227;  
XX  
DT 07-MAY-1998 (first entry)  
XX  
DE Wild-type Interleukin-15 (IL-15) encoding DNA.  
XX  
KW Interleukin-15; IL-15; mutant; human; treatment; autoimmune disease;  
KW psoriasis; multiple sclerosis; rheumatic arthritis; immune response;  
KW type 1 diabetes; AIDS; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..489  
FT /\*tag= a  
FT /product= "interleukin-15"  
FT sig\_peptide 1..144  
FT /\*tag= b  
FT mat\_peptide 145..486  
FT /\*tag= c  
FT misc\_feature 445..447  
FT /\*tag= d

```
FT /note= "the codon CAG encoding Gln can be substituted
FT 466..468
FT /*tag= e
FT /note= "the codon CAA encoding Gln can be substituted
FT by a codon encoding Asp"
XX
PN WO97411232-A1.
XX
XX 06-NOV-1997.
XX
XX 25-APR-1997; 97WO-US06931.
XX
XX 26-APR-1996; 96US-0016634.
XX
XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
XX Maslinski W, Strom T;
XX
XX WPI; 1997-549734/50.
XX
XX P-PSDB; AAW37369.
XX
XX Mutant interleukin 15 polypeptide(s) - used for treating auto-immune
XX diseases e.g psoriasis, multiple sclerosis etc.
XX
XX Disclosure; Pages 54-55; 86pp; English.
XX
XX This DNA encodes a wild-type interleukin-15 (IL-15) polypeptide. This
XX wild-type sequence can be mutated at codon positions 149 and 156 to
XX create a mutant IL-15 polypeptide. The mutant polypeptide is at least
XX 90% identical to wild-type IL-15 and is capable of inhibiting at least
XX one of the cellular events that normally occurs when wild-type IL-15
XX specifically binds to a cell surface receptor. The mutant IL-15 is used
XX for suppressing the immune response in a patient. It can be used for
XX treating autoimmune diseases such as rheumatic arthritis, type I diabetes
XX or a rheumatic disease selected from systemic lupus erythematosus (SLE),
XX Sjogren's syndrome, scleroderma, mixed connective tissue disease,
XX dermatomyositis, polymyositis, Reiter's syndrome and Behcet's disease.
XX It can also be used to treat Hashimoto's thyroiditis, Grave's disease,
XX multiple sclerosis, myasthenia gravis, encephalomyelitis, a variety of
XX pemphigus, psoriasis, inflammatory bowel disease, AIDS and vascular
XX injury. The mutant IL-15 can also be used for reducing the viability of
XX a cell that expresses a IL-15 receptor. It can also be used to diagnose
XX a disease treatable with an IL-15 antagonist.
XX
XX Sequence 489 BP; 159 A; 80 C; 95 G; 155 T; 0 other;
XX
SQ
Query Match 89.6%; Score 438; DB 18; Length 489;
Best Local Similarity 99.8%; Pred. No. 2.le-204;
Matches 488; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGAGAAATTCGAAACACATTTGAGAACTATTTCACCTCCAGTGCCTACTGTGTTTACTT 60
DB 1 atgagaatttcgaaccacatttgagaagcatttcctccatccagtcgacttggttacct 60
QY 61 CTAACAGCATTTTCTAACTGAAGTGGCATTCATGCTCTTCATTTGGGCTGTTTCAGT 120
DB 61 ctaaacagcattttctaaactgaagtcggcattcattcgtcttcattttggcggtttcagt 120
QY 121 GCAGGGCTTCCTAAACACAGCCCACTGGGTGAATGTAATAGTCATTGAAAAAATT 180
DB 121 gcagggttcctcaaaacagaaagccaaactgggtgaatgtaataagtgatttgaaaaaatt 180
QY 181 GAAGATCTTATCAATCTATGCATATTGCTACTTTATATACGAAAGTATGATGTTAC 240
DB 181 gaagatcttattcaactctatgcataattgattgctactttatatacggaaagtgtgtccac 240
QY 241 CCCAGTTGCAAGTAAACAGCAATGAAGTCTTTCTCTTGGAGTTACAAGTTATTTTCACTT 300
DB 241 cccagttgcaagtaaacagcaaatgaagtgtttctcttcttggagttacaagttatttcactt 300
QY 301 GAGTCGGGAGATGCAAGTATTTCATGTATACAGTAGAGAAAATCTGATCATCTCTAGCAACAC 360
```

```
DB 301 gagtcggagatgaagtagattatcatgatagatacagtagaaaaatctgatcatcctagcaaacac 360
QY 361 AGTTTCTCTCTTAATGGGAATGTAACAGAACTCTGGATGCAAAAGATGTGAGGAACCTGGAG 420
DB 361 agtttctctcttaacttaacgggaatgtaacagaatctggatgcaaaagaaagtgtgagaactggag 420
QY 421 GAAAAAATATTAAAGAATTTTTCAGAGTTCATATATTTGATATATTTCCAAAATGTTTCATCAAC 480
DB 421 gaaaaaaatattaaagaatttttgcagagttttgtacatatattgtccaaaatgttccaaatgttcalcaac 480
QY 481 ACTTCTTGA 489
DB 481 acttcttga 489
XX
XX RESULT 21
XX AAT97228
XX ID AAT97228 standard; DNA; 489 BP.
XX
XX AC AAT97228;
XX
XX DT 07-MAY-1998 (first entry)
XX
XX DE Mutant interleukin-15 (IL-15) encoding DNA.
XX
XX KW Interleukin-15; IL-15; mutant; human; treatment; autoimmune disease;
XX KW psoriasis; multiple sclerosis; rheumatic arthritis; immune response;
XX KW type 1 diabetes; AIDS; ss.
XX
XX OS Homo sapiens.
XX
XX FH Key
XX FT CDS
XX FT 1..489
XX FT /tag= a
XX FT /product= "mutant IL-15 polypeptide"
XX FT sig_peptide
XX FT 1..144
XX FT /tag= b
XX FT mat_peptide
XX FT 145..486
XX FT /tag= c
XX FT mutation
XX FT 445..447
XX FT /tag= d
XX FT /note= "wild-type codon CAG encoding Gln is mutated
XX FT by codon GAC encoding Asp"
XX FT mutation
XX FT 466..468
XX FT /tag= e
XX FT /note= "wild-type codon CAA encoding Gln is mutated
XX FT by codon GAC encoding Asp"
XX
XX PN WO97411232-A1.
XX
XX PD 06-NOV-1997.
XX
XX PF 25-APR-1997; 97WO-US06931.
XX
XX 26-APR-1996; 96US-0016634.
XX
XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
XX PI Maslinski W, Strom T;
XX
XX DR WPI; 1997-549734/50.
XX
XX DR P-PSDB; AAW37370.
XX
XX Mutant interleukin 15 polypeptide(s) - used for treating auto-immune
XX diseases e.g psoriasis, multiple sclerosis etc.
XX
XX Disclosure; Pages 56-57; 86pp; English.
XX
XX This DNA encodes a mutant interleukin-15 (IL-15) polypeptide. The
XX wild-type IL-15 sequence was mutated at codon positions 149 and 156 to
XX create this mutant IL-15 polypeptide. This mutant polypeptide is at least
```

CC 90% identical to wild-type IL-15 and is capable of inhibiting at least  
 CC one of the cellular events that normally occurs when wild-type IL-15  
 CC specifically binds to a cell surface receptor. The mutant IL-15 is used  
 CC for suppressing the immune response in a patient. It can be used for  
 CC treating autoimmune diseases such as rheumatic arthritis, type I diabetes  
 CC or a rheumatic disease selected from systemic lupus erythematosus (SLE),  
 CC Sjogren's syndrome, scleroderma, mixed connective tissue disease,  
 CC dermatomyositis, polymyositis, Reiter's syndrome and Behcet's disease.  
 CC It can also be used to treat Hashimoto's thyroiditis, Grave's disease,  
 CC multiple sclerosis, myasthenia gravis, encephalomyelitis, a variety of  
 CC pemphigus, psoriasis, inflammatory bowel disease, AIDS and vascular  
 CC injury. The mutant IL-15 can also be used for reducing the viability of  
 CC a cell that expresses a IL-15 receptor. It can also be used to diagnose  
 CC a disease treatable with an IL-15 antagonist.  
 XX  
 SQ

Sequence 489 BP; 158 A; 80 C; 96 G; 155 T; 0 other;

Query Match 80.4%; Score 393; DB 18; Length 489;  
 Best Local Similarity 99.8%; Pred. No. 2.2e-182;  
 Matches 443; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGAGATTTTCGAACACACATTTGAGAGATATTTCCATCCAGTGTACTTGTGTTACTT 60  
 Db 1 atggaatttcgaaccacacatttgagaagtatttccatccagtgctacttggtttactt 60  
 Qy 61 CTAACAGTCAATTTCTAACTGAAGTGGCATTTCATGCTTCTCATTTGGGCTGTTTCAGT 120  
 Db 61 cttaacagtcatttctcaacgaagctggcatttcattgcttcttcttgggctgttccagt 120  
 Qy 121 GCAGGGCTTCTTAAACAGAGCCCACTGGGTGAATGTAATGAATGATTTGAAAAAATTT 180  
 Db 121 gcagggcttcttaaacagagcccaactgggtgaatgtaataagtattgaaaaaatt 180  
 Qy 181 GAACATCTTATTCATCTATGTCATATTCATGCTACTTTATACGGAAGTGTGTTTCAC 240  
 Db 181 gaagattcttcaatctatgcatattgatgctactttatatacggaaagtgtgttccac 240  
 Qy 241 CCCAGTTGCAAGTAACAGCAATGAAGTGTCTTCTTGGAGTTACAGTATTTTCACTT 300  
 Db 241 cccagttgcaagtaacagcaatgaagtgtcttcttcttggagttacaagttatttccactt 300  
 Qy 301 GAGTCCGAGATGCAAGTATTCATGATACAGTAAATCTGATCCTCTAGCAAAACAC 360  
 Db 301 gagtccggagatgcaagtattcatgatacagtagaataatctgactctctagcaaaacac 360  
 Qy 361 AGTTTGTCTTCTAATGGAATGTAAAGATCTGGATGCAAGATGTGAGGAAGTGGAG 420  
 Db 361 agtttgtcttcttaatggaatgtaaagatctggatgcaagaagtgtgaggaactggag 420  
 Qy 421 GAAAAAATATTAAGAAATTTTGG 444  
 Db 421 gaaaaaatattaagaatttttg 444

RESULT 22  
 AAA35223  
 ID AAA35223 standard; DNA; 17844 BP.

AC AAA35223;

XX 28-JUL-2000 (first entry)

XX Human adenosine receptor related polynucleotide 2nd SEQ ID NO:97.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;  
 KW phosphorothioate; impaired respiration; inflammation; allergy;  
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
 KW antiallergic; antisthmatic; cytotatic; analgesic; impaired airway;  
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX OS

XX Homo sapiens.

XX WO200009525-A2.

XX 24-FEB-2000.

XX 03-AUG-1999; 99WO-US17712.

XX 03-AUG-1998; 98US-0095212.

XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW;

XX WPI; 2000-205971/18.

XX New antisense oligonucleotides useful for treating e.g. pulmonary  
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
 PT cancers -

XX Disclosure; Page 1264-1268; 1343pp; English.

XX The present invention describes a new composition comprising an  
 CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which  
 CC targets nucleic acids involved in bronchoconstriction, allergies, and/or  
 CC inflammation. The ON can have antiinflammatory, antiallergic,  
 CC antisthmatic, cytotatic and analgesic activities. The compositions are  
 CC useful for the treatment of diseases associated with inflammation,  
 CC impaired airways, including lung disease and diseases whose secondary  
 CC effects afflict the lungs of a subject. They can be used for treating  
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,  
 CC asthma, impaired respiration, respiratory distress syndrome, pain, cystic  
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
 CC carcinomas, and cancers which may metastasize to the lungs, including  
 CC breast and prostate cancer. The reduction of the adenosine content of  
 CC the ONs reduces side effects. The A-containing ONs break down with the  
 CC release of deoxyadenosine which activates adenosine receptors causing  
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
 CC nucleotide sequences given in the sequence listing from the present  
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last  
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences  
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680  
 CC (AAA32323 to AAA33992) are specifically claimed ONs from the present  
 CC invention. N.B. Sequences given in the disclosure of the present  
 CC invention do not match up with their corresponding SEQ ID NO: sequences  
 CC given in the sequence listing.

XX Sequence 17844 BP; 6000 A; 2932 C; 3322 G; 5590 T; 0 other;

Query Match 78.7%; Score 385; DB 21; Length 17844;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-178;  
 Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 TTGGGCTGTTTCAGTGCAGGGCTTCTTAAACACAGCAAGCCAACTGGGTGAATGTATATAG 164  
 Db 1609 ttgggctgtttcagtgcaaggcttcttcttaaacagagaagccaactgggtgaatgataag 1668

Qy 165 TGATTGAAAAAATTGAAGATCTTATTCAATCTATGATATTTGATGCTACTTTATATAC 224  
 Db 1669 tgattgaaaaaattggaagatcttattcaatctatgatactgagtcactttacatac 1728

Qy 225 GGAAGTATGTTTCAACCCAGTTCACAAAGTACACAGCAATGAAGTGTCTTCTCTGGAGTT 284  
 Db 1729 ggaaagtatgttcaacccagcttgcaagtaaacagcaatgaagtgtcttctctggagtt 1788

Qy 285 ACAAGTATTTCACCTTGATCGGAGATGCAAGTATTCATGATACAGTAGAAAACTGAT 344  
 Db 1789 acaagttatttcacttgatcggagatgcaagtagtattcatgatcatgacagtagaaatctgat 1848





Db 121 aagtgcttctctgaggtacaaagtatttctcaacttgatgctcgagatgcaagtattcat 180  
QY 325 GATACAGTAGAAATCTGATCATCTCTAGCAACACAGCTTGTCTCTAATGGGAATGTA 384  
Db 181 gatcacgtagaaaatctgatcatcctagcaacaacagtttctctcaatggggaatgta 240  
QY 385 ACAGAACTCTGGATGCAAAAGATGTGAGGAAGTGGAGGAAAAAATATTAAAGAAATTTTG 444  
Db 241 acagaatctggatgcaagaatgtgaggaactggaggaaaaataattaaagaattttg 300  
QY 445 CAGAGTTTGTACATATTGTCCAAATGTCATCAACACTTCTTGA 489  
Db 301 cagagttttgtacatatgtccaaatgttccatcaacacttttga 345

RESULT 26  
AAF57024  
ID AAF57024 standard; cDNA; 345 BP.  
XX  
AC AAF57024;  
DT 14-MAY-2001 (first entry)  
XX  
DE Simian ETF (SETF) mature polypeptide encoding cDNA.  
XX  
KW Epithelium-derived T-cell factor; ETF; simian; human; enteritis;  
KW gastrointestinal disease; mucositis; peptic ulcer; cytostatic;  
KW villus atrophic disorder; inflammatory bowel disease; antiinflammatory;  
KW anti-HIV; antiviral; T-lymphocyte stimulator; ss.  
XX  
OS Mammalia.

FH Key Location/Qualifiers  
FT CDS 1..345  
FT /\*tag= a  
FT /product= "mature SETF"  
XX  
PN US6184359-B1.  
XX  
PD 06-FEB-2001.  
XX  
PF 09-NOV-1998; 980US-0189193.  
XX  
PR 22-FEB-1995; 950US-0393305.  
PR 04-OCT-1996; 960US-0725969.  
PR 08-MAR-1993; 930US-0031399.  
PR 22-APR-1994; 940US-0233606.  
XX  
PA (IMMV ) IMMUNEX CORP.  
PI Grabstein KH, Anderson DM, Eisenman JR, Fung V, Rauch C;  
XX  
XX  
DR WPI: 2001-217801/22.  
DR P-PSDB; AAB62013.  
XX  
PT New antibodies that specifically binds epithelium-derived T-cell factor  
PT polypeptide useful for e.g. treating or preventing gastrointestinal  
PT diseases, HIV and HIV-associated diseases, augmenting destruction of  
PT tumour cells -  
XX  
PS Disclosure; Fig 1: 35pp; English.

CC The invention relates to simian and human epithelium-derived T-cell  
CC factor (ETF) polypeptides. Antibodies that specifically bind to the ETF  
CC polypeptides are used for treating or preventing gastrointestinal  
CC diseases, such as chemotherapy and radiation therapy-induced enteritis  
CC and mucositis, peptic ulcer disease, villus atrophic disorders and  
CC inflammatory bowel disease; for increasing tolerated doses for radiation  
CC therapy and chemotherapy agents which are limited by gastrointestinal  
CC toxicity; and for treating HIV and HIV-associated diseases. The  
CC antibodies are further used to treat a variety of other diseases or  
CC conditions where it is desired to stimulate proliferation of

CC T-lymphocytes and B lymphocytes, or the secretion of immunoglobulin B  
CC lymphocytes, to augment anti-infectious disease immunity, to induce CTL,  
CC LAK or NK lytic activity, or to augment the destruction of tumour cells  
CC or cells infected with virus. The present sequence represents a cDNA  
CC encoding the simian ETF (SETF) mature polypeptide.  
XX  
SQ Sequence 345 BP; 121 A; 49 C; 68 G; 107 T; 0 other;  
  
Query Match 70.6%; Score 345; DB 22; Length 345;  
Best Local Similarity 100.0%; Pred. No. 6.6e-159;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 145 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTTGAAGATCTTATTCAATCTATGCAT 204  
Db 1 aactgggtgaatgtaataagtatttgaaaaaaattgaagatcttattcaatctatgcatt 60  
QY 205 ATTGATGCTACTTTATATACGAAAGTGTATGTTTCAACCCAGTTGCANAGTAACAGCAATG 264  
Db 61 attgatgctactttatatacggaaagtgtgttccccccagttgcaaaagtaacagcaatg 120  
QY 265 AAGTGTCTTCTCTGAGTTACAAGTTATTTCACCTTGAGTCCGGAGATGCAAGTATTTCAT 324  
Db 121 aagtgtcttctctctgaggttacaagtatttccacttgatccggagatgcaagtattcat 180  
QY 325 GATACAGTAGAAAAATCTGATCATCTCTAGCAACACAGCTTGTCTCTAATGGGAATGTA 384  
Db 181 gatcacgtagaaaatctgatcatcctagcaacaacagtttctctcaatggggaatgta 240  
QY 385 ACAGAACTCTGGATGCAAAAGATGTGAGGAAGTGGAGGAAAAAATATTAAAGAAATTTTG 444  
Db 241 acagaatctggatgcaagaatgtgaggaactggaggaaaaataattaaagaattttg 300  
QY 445 CAGAGTTTGTACATATTGTCCAAATGTCATCAACACTTCTTGA 489  
Db 301 cagagttttgtacatatgtccaaatgttccatcaacacttttga 345

RESULT 27  
AAF21341  
ID AAF21341 standard; DNA; 1248 BP.  
XX  
AC AAF21341;  
XX  
DT 14-MAR-2001 (first entry)  
XX  
DE Human low adenosine antisense oligonucleotide related sequence #2908.  
XX  
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
KW human; airway disorder; bronchoconstriction; lung inflammation;  
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
KW cancer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200062736-A2.  
XX  
XX  
PD 26-OCT-2000.  
XX  
PF 24-MAR-2000; 2000WO-US08020.  
XX  
PR 06-APR-1999; 99US-0127958.  
XX  
XX (UYEC-) UNIV EAST CAROLINA.  
PA (NYCE/) NYCE J W.  
XX  
PI Nyce JW;

XX WPI; 2000-679539/66.

XX Low adenosine (A) content antisense oligonucleotides which do not

PT trigger adenosine receptors during metabolism, useful e.g. for treating

PT cancers and respiratory obstructions -

XX

PS Disclosure; Page 1344; 1592pp; English.

XX

XX The present invention describes low adenosine (A) content antisense

CC oligonucleotides and compositions (I) comprising them. In the antisense

CC oligonucleotides the A is replaced by a 'universal' or alternative base.

CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,

CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.

CC The antisense oligonucleotides and (I) can be used to down-regulate the

CC expression and or activity of target polypeptides associated with

CC lung/respiratory disorders and malignancies, such as stimulating and

CC activating peptide factors and transmitters, transcription factors,

CC immunoglobulins and antibodies, antibody receptors, cytokines and

CC chemokines, endogenously produced specific and non-specific enzymes,

CC binding proteins, adhesion molecules and their receptors, cytokine and

CC chemokine receptors, adenosine receptors, bradykinin receptors, central

CC nervous system (CNS) and peripheral nervous and non-nervous system

CC receptors, CNS and peripheral nervous and non-nervous system

CC transmitters, defensins, growth factors, vasoactive peptides and

CC receptors, binding proteins and malignancy associated proteins. The

CC antisense oligonucleotides may be used in this way to treat disorders

CC including respiratory obstruction (especially pulmonary obstruction

CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)

CC and/or surfactant hypoproduction which are associated with a disease or

CC condition selected from pulmonary vasoconstriction, inflammation,

CC allergies, asthma, impaired respiration, respiratory distress syndrome

CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary

CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),

CC pulmonary transplantation rejection, pulmonary infections, bronchitis,

CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide

CC fragments and antisense oligonucleotides used in the exemplification of

CC the present invention.

XX

SQ Sequence 1248 BP; 397 A; 209 C; 223 G; 419 T; 0 other;

RESULT 28

AAA35219

ID AAA35219 standard; DNA; 1248 BP.

XX

AC AAA35219;

XX

XX 28-JUL-2000 (first entry)

DT

XX Human adenosine receptor related polynucleotide 2nd SEQ ID NO:93.

DE

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;

CC phosphorothioate; impaired respiration; inflammation; allergy;

CC allergic disease; bronchoconstriction; inhibitor; antiinflammatory;

CC antiasthmatic; cytotstatic; analgesic; impaired airway;

CC lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;

CC respiratory distress syndrome; pain; cystic fibrosis; emphysema;

CC pulmonary hypertension; chronic obstructive pulmonary disease; COPD;

CC cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX

OS Homo sapiens.

XX

XX WO200009525-A2.

PN

XX 24-FEB-2000.

PD

XX 03-AUG-1999; 99WO-US17712.

PF

XX 03-AUG-1998; 98US-0095212.

PR

XX (UYEC-) UNIV EAST CAROLINA.

PA

XX Nyce JW;

PI

XX WPI; 2000-205971/18.

DR

XX New antisense oligonucleotides useful for treating e.g. pulmonary

PT vasoconstriction, inflammation, allergies, asthma, hypertension, or

PT bronchitis, emphysema, respiratory distress syndrome, ischemia or

PT cancers -

XX

PS Disclosure; Page 1260; 1343pp; English.

XX

XX The present invention describes a new composition comprising an

CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which

CC targets nucleic acids involved in bronchoconstriction, allergies, and/or

CC inflammation. The ON can have antiinflammatory, antiallergic,

CC antiasthmatic, cytostatic and analgesic activities. The compositions are

CC useful for the treatment of diseases associated with inflammation,

CC impaired airways, including lung disease and diseases whose secondary

CC effects afflict the lungs of a subject. They can be used for treating

CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,

CC asthma, impaired respiration, respiratory distress syndrome, pain, cystic

CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive

CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,

CC carcinomas, and cancers which may metastasize to the lungs, including

CC breast and prostate cancer. The reduction of the adenosine content of

CC the ONs reduces side effects. The A-containing ONs break down with the

CC release of deoxyadenosine which activates adenosine receptors causing

CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the

CC nucleotide sequences given in the sequence listing from the present

CC invention, which correspond to SEQ ID NO:1 to 185, and then the last

CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences

CC differ from the previously named sequences. SEQ ID NO:11 to 1680

CC (AAA32323 to AAA33992) are specifically claimed ONs from the present

CC invention. N.B. Sequences given in the disclosure of the present

CC invention do not match up with their corresponding SEQ ID NO: sequences

CC given in the sequence listing.

XX

SQ Sequence 1248 BP; 397 A; 209 C; 223 G; 419 T; 0 other;



```
XX PA (UYEC-) UNIV EAST CAROLINA.
XX PI (NYCE/) NYCE J W.
XX PI Nyce JW;
XX DR WPI; 2000-679539/66.
XX PT Low adenosine (A) content antisense oligonucleotides which do not
XX PT trigger adenosine receptors during metabolism, useful e.g. for treating
XX PT cancers and respiratory obstructions -
XX PS Disclosure; Page 1345-1348; 1592pp; English.
XX CC The present invention describes low adenosine (A) content antisense
XX CC oligonucleotides and compositions (I) comprising them. In the antisense
XX CC oligonucleotides the A is replaced by a 'universal' or alternative base.
XX CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
XX CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
XX CC The antisense oligonucleotides and (I) can be used to down-regulate the
XX CC expression and or activity of target polypeptides associated with
XX CC lung/respiratory disorders and malignancies, such as stimulating and
XX CC activating peptide factors and transmitters, transcription factors,
XX CC immunoglobulins and antibodies, antibody receptors, cytokines and
XX CC chemokines, endogenously produced specific and non-specific enzymes,
XX CC binding proteins, adhesion molecules and their receptors, cytokine and
XX CC chemokine receptors, adenosine receptors, bradykinin receptors, central
XX CC nervous system (CNS) and peripheral nervous and non-nervous system
XX CC receptors, CNS and peripheral nervous and non-nervous system peptide
XX CC transmitters, defensins, growth factors, vasoactive peptides and
XX CC receptors, binding proteins and malignancy associated proteins. The
XX CC antisense oligonucleotides may be used in this way to treat disorders
XX CC including respiratory obstruction (especially pulmonary obstruction
XX CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
XX CC and/or surfactant hypoproduction which are associated with a disease or
XX CC condition selected from pulmonary vasoconstriction, inflammation,
XX CC allergies, asthma, impeded respiration, respiratory distress syndrome
XX CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
XX CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
XX CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
XX CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
XX CC fragments and antisense oligonucleotides used in the exemplification of
XX CC the present invention.
XX SQ Sequence 14968 BP; 5108 A; 2436 C; 2758 G; 4666 T; 0 other;

Query Match      28.2%; Score 138; DB 21; Length 14968;
Best Local Similarity 100.0%; Pred. No. 1.1e-57;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 CCCAGTTGCAAGTAAACAGCAATGAAGTCTTCTTGTGGATTACAGTTATTTCACCTT 300
Db 10603 cccagttgcaagtaacagcaatgaagtcttcttctgtggattacaagttatttcactt 10662

QY 301 GAGTCCGAGATGCAAGTATTTCATGATACAGTAAATCTGATCCTCCTAGCAACAAC 360
Db 10663 gagtccggagatgcaagtatttcattcatgatacagtagaataatctgatcctcctagcaacaac 10722

QY 361 AGTTTGTCTTCTAATGG 378
Db 10723 agtttgtcttctaattggg 10740

RESULT 31
ID AAA35221
XX ID AAA35221 standard; DNA; 14968 BP.
XX AC AAA35221;
XX XX
XX DT 28-JUL-2000 (first entry)
XX XX
XX DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:95.
```

```
XX KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX OS Homo sapiens.
XX XX
XX PN WO200009525-A2.
XX PD 24-FEB-2000.
XX PF 03-AUG-1999; 99WO-US17712.
XX PR 03-AUG-1998; 98US-0095212.
XX PA (UYEC-) UNIV EAST CAROLINA.
XX PI Nyce JW;
XX DR WPI; 2000-205971/18.
XX CC New antisense oligonucleotides useful for treating e.g. pulmonary
XX CC vasoconstriction, inflammation, allergies, asthma, hypertension,
XX CC bronchitis, emphysema, respiratory distress syndrome, ischemia or
XX CC cancers -
XX PS Disclosure; Page 1260-1264; 1343pp; English.
XX CC The present invention describes a new composition comprising an
XX CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
XX CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
XX CC inflammation. The ON can have antiinflammatory, antiallergic,
XX CC antiasthmatic, cytostatic and analgesic activities. The compositions are
XX CC useful for the treatment of diseases associated with inflammation,
XX CC impaired airways, including lung disease and diseases whose secondary
XX CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
XX CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
XX CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
XX CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
XX CC carcinomas, and cancers which may metastasize to the lungs, including
XX CC breast and prostate cancer. The reduction of the adenosine content of
XX CC the ONs reduces side effects. The A-containing ONs break down with the
XX CC release of deoxyadenosine which activates adenosine receptors causing the
XX CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
XX CC nucleotide sequences given in the sequence listing from the present
XX CC invention, which correspond to SEQ ID NO:1 to 185, and then the last
XX CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
XX CC differ from the previously named sequences. SEQ ID NO:11 to 1680
XX CC (AAA32323 to AAA33992) are specifically claimed ONs from the present
XX CC invention. N.B. Sequences given in the disclosure of the present
XX CC invention do not match up with their corresponding SEQ ID NO: sequences
XX CC given in the sequence listing.
XX SQ Sequence 14968 BP; 5109 A; 2436 C; 2757 G; 4666 T; 0 other;
```

```
Query Match      28.2%; Score 138; DB 21; Length 14968;
Best Local Similarity 100.0%; Pred. No. 1.1e-57;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 CCCAGTTGCAAGTAAACAGCAATGAAGTCTTCTTGTGGATTACAGTTATTTCACCTT 300
Db 10603 cccagttgcaagtaacagcaatgaagtcttcttctgtggattacaagttatttcactt 10662

QY 301 GAGTCCGAGATGCAAGTATTTCATGATACAGTAAATCTGATCCTCCTAGCAACAAC 360
Db 10663 gagtccggagatgcaagtatttcattcatgatacagtagaataatctgatcctcctagcaacaac 10722
```

Qy 361 AGTTTGCTCTCTAATGGG 378  
|||||  
Db 10723 agttgtcttctaagg 10740

RESULT 32  
AAD14464  
ID AAD14464 standard; DNA; 14968 BP.  
AC AAD14464;  
XX  
DT 15-NOV-2001 (first entry)  
XX  
DE Human IL-15 gene allele.  
XX  
KW Human; interleukin 15; IL-15; gene therapy; chromosome 4q31; infection;  
KW drug screening; anthropological lineage; paternity testing; HIV;  
KW Human Immunodeficiency Virus; forensic application; T-cell leukaemia; ds.  
XX  
OS Homo sapiens.

XX FH Location/Qualifiers  
FH CDS 347..13604  
FT /tag= a  
FT /product= "Human IL-15 protein"  
FT intron 1..346  
FT /tag= b  
FT /cons\_splice= (5'site:NO, 3'site:NO)  
FT /number= 1  
FT exon 347..357  
FT /tag= c  
FT /number= 1  
FT intron 358..1350  
FT /tag= d  
FT /cons\_splice= (5'site:NO, 3'site:NO)  
FT /number= 2  
FT exon 1351..1448  
FT /tag= e  
FT /number= 2  
FT intron 1449..2806  
FT /tag= f  
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FT /number= 3  
FT exon 2807..2892  
FT /tag= g  
FT /number= 3  
FT intron 2893..8695  
FT /tag= h  
FT /number= 4  
FT exon 8696..8740  
FT /tag= i  
FT /number= 4  
FT intron 8741..10602  
FT /tag= j  
FT /number= 5  
FT exon 10603..10739  
FT /tag= k  
FT /number= 5  
FT intron 10740..13492  
FT /tag= l  
FT /number= 6  
FT /cons\_splice= (5'site:NO, 3'site:NO)  
FT /tag= m  
FT /number= 6  
FT intron 13605..14968  
FT /tag= n  
FT /number= 7  
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FT variation replace (191, C)

FT variation /tag= p  
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FT /tag= q  
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FT replace (333, T)  
FT /tag= s  
FT replace (367, A)  
FT /tag= t  
FT replace (431, T)  
FT /tag= u  
FT replace (504, C)  
FT /tag= v  
FT replace (1536, A)  
FT /tag= w  
FT replace (8866, A)  
FT /tag= x  
FT replace (10504, G)  
FT /tag= y  
XX WO200158914-A2.  
XX  
XX 16-AUG-2001.  
XX  
XX 08-FEB-2001; 2001WO-US04130.  
XX  
XX 08-FEB-2000; 2000US-0181059.  
XX  
XX (GENA-) GENAISSANCE PHARM INC.  
XX  
XX Anastasio AE, Chew A, Denton RR, Nandabalan K, Stephens JC;  
XX  
XX WPI: 2001-522460/57.  
XX P-PSDB: AAE08576.  
XX  
XX Novel polynucleotides comprising one of 11, PSL-PS11, single nucleotide  
XX polymorphisms in human interleukin-15 gene, and useful for treating  
XX disorders affected by expression of function of interleukin-15 isogene  
XX .  
XX  
XX Claim 19; Fig 1; 78pp; English.  
XX  
XX The present sequence is human interleukin-15 (IL-15) gene allele located  
XX on chromosome 4q31. The polymorphic variants of IL-15 genes are useful  
XX for studying the expression and function of IL-15 and expressing  
XX IL-15 protein for use in useful for screening for candidate drugs to  
XX treat diseases related to IL-15 activity. Genotyping or haplotyping an  
XX individual at the novel IL-15 polymorphic sites are useful for studying  
XX population diversity, anthropological lineage, the significance of  
XX diversity and lineage of the phenotypic level, paternity testing,  
XX forensic applications and for identifying associations between IL-15  
XX genetic variation and a trait such as level of drug response or  
XX susceptibility to disease. Identifying an association between a genotype  
XX or haplotype and a trait, is useful for developing diagnostic tests and  
XX therapeutic treatments for infections, human immunodeficiency virus and  
XX T-cell leukaemia. The identification of an association between a clinical  
XX response and a genotype or haplotype (or haplotype pair) for the IL-15  
XX gene may be the basis for designing a diagnostic method to determine  
XX those individuals who will or will not respond to the treatment, or  
XX alternatively, will respond at a lower level and thus may require more  
XX treatment, i.e. a greater dose of a drug. The genotyping or haplotyping  
XX methods are also useful for developing drugs targeting IL-15. The  
XX genotyping and haplotyping methods are also useful in designing clinical  
XX trials. IL-15 DNA is useful for therapeutic purposes for treating  
XX disorders affected by expression of function of novel IL-15 isogene and  
XX also in gene therapy. Expression of an IL-15 isogene may be turned off  
XX by transforming a targetted organ, tissue or cell population of an  
XX expression vector that expresses high levels of untranslatable mRNA for  
XX the isogene.  
XX  
XX Sequence 14968 BP; 5108 A; 2436 C; 2758 G; 4666 T; 0 other;  
XX SQ

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Query Match      28.2%; Score 138; DB 22; Length 14968;
Best Local Similarity 100.0%; Pred. No. 1.1e-57;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 CCCAGTTGCAAGTACAGCAATGAAGTCTTCTCTGGAGTTACAAGTTATTTCACCTT 300
    |||
Db 10603 cccagttgcaagtaacagcaatgaagtcttctctggagttacaagttatttcactt 10662
    |||

QY 301 GAGTCCGGAGATGCAAGTATTTCATGATACAGTAGAAAATCTGATCATCTTAGCAACAAC 360
    |||
Db 10663 gagtcggagaatcaagattatcatgatacagtagaataatctgatactcttagcaacaac 10722
    |||

QY 361 AGTTTGCTTCTTAATGGG 378
    |||
Db 10723 agttgtcttctaattg 10740

RESULT 34
AAT00524
ID AAT00524 standard; DNA; 14968 BP.
XX
AC AAD15838;
XX
DT 15-NOV-2001 (first entry)
XX
DE Human interleukin 15 (IL-15) gene.
XX
KW Human; interleukin 15; IL-15; gene therapy; chromosome 4q31; infection;
KW drug screening; anthropological lineage; paternity testing; HIV;
KW Human Immunodeficiency Virus; forensic application; T-cell leukaemia; ds.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_feature 101
    /*tag= a
    /note= "This degenerate base represents polymorphic site"
FT misc_feature 191
    /*tag= b
    /note= "This degenerate base represents polymorphic site"
FT misc_feature 192
    /*tag= c
    /note= "This degenerate base represents polymorphic site"
FT misc_feature 267
    /*tag= d
    /note= "This degenerate base represents polymorphic site"
FT misc_feature 333
    /*tag= e
    /note= "This degenerate base represents polymorphic site"
FT misc_feature 367
    /*tag= f
    /note= "This degenerate base represents polymorphic site"
FT misc_feature 431
    /*tag= g
    /note= "This degenerate base represents polymorphic site"
FT misc_feature 504
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FT misc_feature 1536
    /*tag= i
    /note= "This degenerate base represents polymorphic site"
FT misc_feature 8866
    /*tag= j
    /note= "This degenerate base represents polymorphic site"
FT misc_feature 10504
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    /note= "This degenerate base represents polymorphic site"
XX
PN WO200158914-A2.
XX
PD 16-AUG-2001.
XX
PF 08-FEB-2001; 2001WO-US04130.
```

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XX
PR 08-FEB-2000; 2000US-0181059.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Anastasio AE, Chew A, Denton RR, Nandabalan K, Stephens JC;
XX
DR WPI; 2001-522460/57.
XX
Novel polynucleotides comprising one of 11, PSI-PS11, single nucleotide
PT polymorphisms in human interleukin-15 gene, and useful for treating
PT disorders affected by expression of function of interleukin-15 isogene
PT
XX
PS Disclosure; Page 73-78; 78pp; English.
XX
CC The present sequence is human interleukin-15 (IL-15) gene located
CC on chromosome 4q31. The polymorphic variants of IL-15 genes are useful
CC for studying the expression and function of IL-15 and expressing
CC IL-15 protein for use in useful for screening for candidate drugs to
CC treat diseases related to IL-15 activity. Genotyping or haplotyping an
CC individual at the novel IL-15 polymorphic sites are useful for studying
CC population diversity, anthropological lineage, the significance of
CC diversity and lineage of the phenotypic level, paternity testing,
CC forensic applications and for identifying associations between IL-15
CC genetic variation and a trait such as level of drug response or
CC susceptibility to disease. Identifying an association between a genotype
CC or haplotype and a trait, is useful for developing diagnostic tests and
CC therapeutic treatments for infections, human immunodeficiency virus and
CC T-cell leukaemia. The identification of an association between a clinical
CC response and a genotype or haplotype (or haplotype pair) for the IL-15
CC gene may be the basis for designing a diagnostic method to determine
CC those individuals who will or will not respond to the treatment, or
CC alternatively, will respond at a lower level and thus may require more
CC treatment, i.e. a greater dose of a drug. The genotyping or haplotyping
CC methods are also useful for developing drugs targeting IL-15. The
CC genotyping and haplotyping methods are also useful in designing clinical
CC trials. IL-15 DNA is useful for therapeutic purposes for treating
CC disorders affected by expression of function of novel IL-15 isogene and
CC also in gene therapy. Expression of an IL-15 isogene may be turned off
CC by transforming a targetted organ, tissue or cell population of an
CC expression vector that expresses high levels of untranslatable mRNA for
CC the isogene.
XX
SQ Sequence 14968 BP; 5107 A; 2432 C; 2755 G; 4663 T; 11 other;

Query Match      28.2%; Score 138; DB 22; Length 14968;
Best Local Similarity 100.0%; Pred. No. 1.1e-57;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 CCCAGTTGCAAGTACAGCAATGAAGTCTTCTCTGGAGTTACAAGTTATTTCACCTT 300
    |||
Db 10603 cccagttgcaagtaacagcaatgaagtcttctctggagttacaagttatttcactt 10662
    |||

QY 301 GAGTCCGGAGATGCAAGTATTTCATGATACAGTAGAAAATCTGATCATCTTAGCAACAAC 360
    |||
Db 10663 gagtcggagaatcaagattatcatgatacagtagaataatctgatactcttagcaacaac 10722
    |||

QY 361 AGTTTGCTTCTTAATGGG 378
    |||
Db 10723 agttgtcttctaattg 10740

RESULT 34
AAT00524
ID AAT00524 standard; cDNA; 489 BP.
XX
AC AAT00524;
XX
DT 02-FEB-1996 (first entry)
XX
DE Simian interleukin-15 precursor.
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XX Interleukin-15; epithelium-derived T-cell factor; T lymphocyte; ss.  
KW Cebus apella.  
OS  
XX  
FH Key Location/Qualifiers  
FT CDS 1..489  
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FT /\*note= "claimed"  
FT misc\_feature 145..489  
FT /\*tag= b  
FT /\*note= "claimed"  
XX  
XX W09527722-A.  
XX  
XX 19-OCT-1995.  
XX  
XX 06-APR-1994; 94WO-US03793.  
XX  
XX 06-APR-1994; 94WO-US03793.  
XX  
XX (IMMV ) IMMUNEX CORP.  
XX  
XX Anderson DM, Eisenman JR, Fung V, Grabstein KH;  
XX Rauch C;  
XX  
XX WPI; 1995-373556/48.  
XX P-PSDB; AAR83436.  
XX  
XX Isolated DNA encoding polypeptide with mammalian IL-15 activity - which  
XX stimulates proliferation and differentiation of T cells, used for  
XX treating carcinoma(s), melanomas, etc. and viral infections  
XX  
XX Claim 28; Page 26; 48pp; English.  
XX  
XX A simian species of IL-15 (sIL-15) was purified and analysed by SDS-  
XX PAGE. Blosay of unstained gel slices indicated IL-15 activity was  
XX assoc. with proteins having mol. wts in the range of 15-17 kDa. The  
XX N-terminus of the 15-17 kDa was sequenced. The results indicated the  
XX identity of the first 33 AAs of AAR83309. Subsequent sequencing of a  
XX cDNA clone obtd. from a simian library provided a sequence encoding  
XX the polypeptide AAR83436. AAR83436 comprises a relatively short 48 AA  
XX leader sequence and a mature polypeptide AAR83309. The sequence of the  
XX N-terminal 31 AAs of AAR83309 was used to design synthetic PCR primers  
XX for the amplification of IL-15-specific DNA sequences. The first  
XX 6 AAs of the N-terminus were used to design one primer, a  
XX degenerate mixture coding for all possible codon usages - AAT00528.  
XX The AA sequences of the simian mature N-terminus 26-31 were used  
XX to design a second primer, a degenerate mixture coding for a  
XX complement of all possible codon usages of AAs 26-31, omitting  
XX posn. 3 of Val (AAT00529, AAT00530). Polyadenylated RNAs from CV-1/EBNA  
XX cells were used as templates. A 92 bp DNA fragment was used as a  
XX hybridisn. probe to screen a portion of a plasmid library contg.  
XX cDNA inserts prep. from CV-1/EBNA polyadenylated RNA. This  
XX resulted in the isolation of clone C85.sIL-15 that has an ORF  
XX given in AAT00524. AAR83309 is the active polypeptide & AAR83436 is  
XX the precursor polypeptide.  
XX  
XX Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other;

Query Match 21.9%; Score 107; DB 16; Length 489;  
Best Local Similarity 99.4%; Pred. No. 1.7e-42;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 67 AGTCATTTTCTAACTGAAGCTGCATTCATGCTTTCATTTTGGGCTGTTTCAGTCAGGG 126  
DB 67 agtcaattttctaactgaagctggcatcctcctcatttcttggcgtgtttccagcgcagg 126  
QY 127 CTTCCCTAAAACAGAACCAACTGGGTGAATGTAATAGTGATTGAAAAAATTGAAGAT 186  
DB 127 ctccctaaacagaaagcgaactgggtgaatgtaataagtgatttgaaaaaattgaagat 186

QY 187 CTTATTCAATCTATGCATATTGATGCTACTTATATAC 224  
DB 187 cttattcaatctatgcataattgatgctactattatatac 224  
RESULT 35  
AAQ84583  
ID AAQ84583 standard; cDNA; 489 BP.  
XX  
XX AAQ84583;  
XX  
XX 04-SEP-1995 (first entry)  
XX  
XX Simian IL-15 clone C85.sIL-15.  
XX  
XX Interleukin-15; IL-15; sIL-15; T-cell growth factor;  
XX African green monkey; CV-1; antitumor; virucide; ss.  
XX  
XX Cercopithecus aethiops.  
XX  
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XX CDS 1..489  
XX /\*tag= a  
XX /product= IL-15 precursor  
XX sig\_peptide 1..144  
XX /\*tag= b  
XX mat\_peptide 145..486  
XX /\*tag= c  
XX /product= mature IL-15  
XX  
XX ZA9402636-A.  
XX  
XX 28-DEC-1994.  
XX  
XX 18-APR-1994; 94ZA-0002636.  
XX  
XX 18-APR-1994; 94ZA-0002636.  
XX  
XX (IMMV ) IMMUNEX CORP.  
XX  
XX Anderson DM, Eisenman JR, Fung V, Grabstein KH;  
XX Rauch C;  
XX  
XX WPI; 1995-082473/11.  
XX P-PSDB; AAR66926.  
XX  
XX New purified interleukin-15 - which induces T cell proliferation  
XX and differentiation, used for the treatment of tumours and viral  
XX infection  
XX  
XX Disclosure; Page 26; 47pp; English.  
XX  
XX cDNA generated from PMA-stimulated CV-1/EBNA cells was amplified  
XX by PCR using primers based on the N-terminal sequence of simian  
XX interleukin-15 (sIL-15). A probe based on an isolated clone was used  
XX to screen a plasmid library containing cDNA inserts prepared from  
XX CV-1/EBNA poly-A RNA. Clone C85.sIL-15 was isolated that has the  
XX ORF given in AAQ84583.  
XX  
XX Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other;

Query Match 21.9%; Score 107; DB 16; Length 489;  
Best Local Similarity 99.4%; Pred. No. 1.7e-42;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 67 AGTCATTTTCTAACTGAAGCTGCATTCATGCTTTCATTTTGGGCTGTTTCAGTCAGGG 126  
DB 67 agtcaattttctaactgaagctggcatcctcctcatttcttggcgtgtttccagcgcagg 126  
QY 127 CTTCCCTAAAACAGAACCAACTGGGTGAATGTAATAGTGATTGAAAAAATTGAAGAT 186  
DB 127 ctccctaaacagaaagcgaactgggtgaatgtaataagtgatttgaaaaaattgaagat 186

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QY 187 CTTATTCAATCTATGATATGATGCTACTTTATATAC 224
|||||
Db 187 cttattcaatctatgcatattgatgctactttatatac 224

RESULT 36
AAT49456
ID AAT49456 standard; cDNA; 489 BP.
XX
AC AAT49456;
XX
DT 11-MAR-1997 (first entry)
XX
DE Human epithelium derived T cell factor cDNA.
XX
KW hETF; human IMTLH bone marrow stromal cell line; T-cell; B-cell;
KW lymphocyte; proliferation; differentiation; gastrointestinal;
KW HIV infection; human immunodeficiency virus; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..489
FT /tag= a
FT mat_peptide 145..486
FT /tag= b
FT /product= hETF
FT
XX
PN US5574138-A.
XX
PD 12-NOV-1996.
XX
PF 08-MAR-1993; 93US-0031399.
XX
PR 22-FEB-1995; 95US-0393305.
XX
PR 08-MAR-1993; 93US-0031399.
XX
PR 22-APR-1994; 94US-0233606.
XX
PA (IMMV ) IMMUNEX CORP.
XX
PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;
PI Rauch C;
XX
DR WPI: 1996-517923/51.
DR P-PSDB; AAW09100 AND AAW09101.
XX
PT New epithelium derived T cell factor - induces proliferation of T
PT and B cells, stimulates destruction of tumour and virus-infected
PT cells and protects against toxicity, partic. for treating intestinal
PT disease and HIV infection
XX
PS Claim 1; Fig 2; 35pp; English.
XX
CC Human ETF (epithelium derived T cell factor) cDNA was isolated by
CC screening a IMTLH cell cDNA library with a simian ETF probe. The
CC IMTLH cell line was derived from a stable transformation of a human
CC bone marrow stromal cell culture with pSV3Neo. Mature hETF induces
CC proliferation and/or differentiation of precursor or mature T cells
CC and is useful for promoting long-term in vitro culture of
CC T-lymphocytes and T-cell lines. It is used for treating
CC gastrointestinal diseases including peptic ulcer, colitis and
CC malignancy and for treating HIV infection.
XX
SQ Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other;

Query Match 21.9% Score 107; DB 17; Length 489;
Best Local Similarity 99.4%; Pred. No. 1.7e-42;
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTCCTCAAGCTGGCATTCATGCTCTTCATTTGGGCTGTTTCAGTGCAGG 126
|||||
Db 67 agtcattttcttaactgaagctggcattcattcttcttcttggctgttcagtcagg 126
QY 127 CTTCTTAAACAGACCACTGGGTGAATGTAATGAATGATTGAAAAAATTGAAGAT 186
|||||
Db 127 ctctcctaaacagacagccactgggtgaatgtaatgaatgattgaaaaaattgaagat 186
QY 187 CTTATTCAATCTATGATATGATGCTACTTTATATAC 224
|||||
Db 187 cttattcaatctatgcatattgatgctactttatatac 224

RESULT 37
AAT42242
ID AAT42242 standard; DNA; 489 BP.
XX
AC AAT42242;
XX
DT 05-FEB-1997 (first entry)
XX
DE Simian epithelium-derived T cell factor gene.
XX
KW Epithelium-derived T-cell factor; simian; human; culture; proliferation;
KW epithelial cell; differentiation; T-lymphocyte; African green monkey;
KW primer; PCR; polymerase chain reaction; amplification; probe; ss.
XX
OS Cercopithecus aethiops.
XX
FH Key Location/Qualifiers
FT sig_peptide 1..144
FT /tag= a
FT mat_peptide 145..486
FT /tag= b
XX
PN US5552303-A.
XX
PD 03-SEP-1996.
XX
PF 08-MAR-1993; 93US-0031399.
XX
PR 08-MAR-1993; 93US-0031399.
XX
PA (IMMV ) IMMUNEX CORP.
XX
PI Anderson D, Eisenman J, Fung V, Grabstein K, Rauch C;
PI
XX
DR WPI: 1996-412063/41.
DR P-PSDB; AAW07254.
XX
PT New isolated simian and human epithelium-derived T-cell factors -
PT which stimulate the proliferation and/or differentiation of
PT T-lymphocytes and T-cell lines
XX
PS Claim 21; Column 19-20; 22pp; English.
XX
CC This is the nucleotide sequence encoding a simian epithelium-derived
CC T-cell factor (ETF). The protein was purified from African green monkey
CC CV-1 kidney cells in culture by conventional chromatography: hydrophobic,
CC anion exchange and reverse phase HPLC, followed by separation by
CC SDS-PAGE. The proteins from the SDS-PAGE were transferred to a PVDF
CC membrane and the band corresp. to ETF was cut out for peptide sequencing.
CC Primers were synthesised based on this sequence and used to amplify a
CC 92 bp fragment from cDNA derived from CV-1/EBNA cells stimulated to
CC proliferate by phorbol 12-myristate 13-acetate. The 92 bp fragment was
CC labelled and used as a probe to isolate a clone C85.sETF which contained
CC this sequence. ETF is a protein of 15-17 kD which is expressed by
CC epithelial cells and stimulates proliferation and/or differentiation of
CC precursor and/or mature T cells. The protein is therefore useful for
CC promoting long term in vivo culture of T-lymphocytes and T-cell lines.
XX
SQ Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other;

Query Match 21.9% Score 107; DB 17; Length 489;
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Query Match 21.9%; Score 107; DB 19; Length 489;  
Best Local Similarity 99.4%; Pred. No. 1.7e-42;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTCTACTGAAGCTGCATTCATGCTTTCATTTTGGCGTGTTCAGTCAGGG 126  
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Db 67 agtcatttcttaactgaagctggcattcatgtcttcatttggcgctgttcagtcaggg 126  
|||||

QY 127 CTTCCTAAACAGAACCCAACTGGGTGAATGTAATGAAGTGAATTTGAAAAAATTGAAGAT 186  
|||  
Db 127 ctccctaaacagaaagcccaactg99ggaatgtaataagtgatttgaataaaattgaagat 186  
|||||

QY 187 CTATTTCAATCTATGCATATTGATGCTACTTTATATAC 224  
Db 187 cttattcaatctatgcattgctgctactttatatac 224

RESULT 40  
AAZ29480  
ID AAX29480 standard; DNA; 489 BP.  
AC AAX29480;  
DT 10-JUN-1999 (first entry)  
DE Human epithelium-derived T-cell factor (ETF) encoding DNA.  
KW Epithelium-derived T-cell factor; ETF; immunoassay; enteritis; ulcer;  
KW T cell proliferation; gastrointestinal disease; mucositis; colitis;  
KW gastroenteritis; villus atrophy; malignancy; inflammatory bowel disease;  
KW human immune deficiency virus; tumour; human; ss.  
OS Homo sapiens.  
PN US5892001-A.  
PX 06-APR-1999.  
XX 04-OCT-1996; 96US-0725969.  
XX 22-FEB-1995; 95US-0393305.  
PR 08-MAR-1993; 93US-0031399.  
PR 22-APR-1994; 94US-0233606.  
PR 04-OCT-1996; 96US-0725969.  
XX PA (IMMUNEX ) IMMUNEX CORP.  
XX Anderson DM, Eisenman JR, Fung V, Grabstein KH;  
PI Rauch C;  
XX WPI; 1999-253930/21.  
DR P-PSDB; AAY03758; AAY03759.  
XX Antibodies specific for epithelium-derived T-cell growth factor  
PT Claim 1; Columns 37-40; 34pp; English.  
PS The invention relates to an isolated antibody that binds specifically to  
CC a simian or human epithelium-derived T-cell factor (ETF) polypeptide. The  
CC antibodies are used, optionally when immobilized or labeled, to detect  
CC and quantify ETF in standard immunoassays. They may also be used as  
CC diagnostic and therapeutic agents, e.g. when conjugated to toxins (or  
CC their precursors) or radionuclides. ETF induces proliferation and/or  
CC differentiation of T cells (or their precursors), e.g. for use in  
CC establishing long term in vitro cultures; and is also used to treat  
CC gastrointestinal disease (e.g. enteritis or mucositis) induced by  
CC chemotherapy or radiation, peptide ulcer, gastroenteritis, colitis,  
CC villus atrophy, malignancy and inflammatory bowel disease), to treat  
CC human immune deficiency virus infection or associated disease, or  
CC generally in any situation requiring stimulation of T or B cell  
CC proliferation, secretion of immunoglobulins or certain cytokines,  
CC increased anti-infectious disease immunity, induction of T-cell lytic

CC activity or increased destruction of tumour or virus-infected cells. The  
CC present sequence represents a DNA encoding a human ETF precursor  
CC polypeptide sequence.  
XX Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other;  
SQ

Query Match 21.9%; Score 107; DB 20; Length 489;  
Best Local Similarity 99.4%; Pred. No. 1.7e-42;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTCTACTGAAGCTGCATTCATGCTTTCATTTTGGCGTGTTCAGTCAGGG 126  
|||||  
Db 67 agtcatttcttaactgaagctggcattcatgtcttcatttggcgctgttcagtcaggg 126  
|||||

QY 127 CTTCCTAAACAGAACCCAACTGGGTGAATGTAATGAAGTGAATTTGAAAAAATTGAAGAT 186  
|||  
Db 127 ctccctaaacagaaagcccaactg99ggaatgtaataagtgatttgaataaaattgaagat 186  
|||||

QY 187 CTATTTCAATCTATGCATATTGATGCTACTTTATATAC 224  
Db 187 cttattcaatctatgcattgctgctactttatatac 224

RESULT 41  
AAZ90031  
ID AAZ90031 standard; cDNA; 489 BP.  
AC AAZ90031;  
XX 09-MAY-2000 (first entry)  
DT 09-MAY-2000 (first entry)  
XX Simian interleukin-15 (IL-15) nucleotide sequence.  
DE Interleukin-15; IL-15; antagonist; irritable bowel disease; IBD;  
KW celiac disease; treatment; ss.  
XX Primate.  
XX WO200002582-A2.  
PN 20-JAN-2000.  
XX 09-JUL-1999; 99WO-GB02201.  
XX 10-JUL-1998; 98GB-0014892.  
XX (KENN-) KENNEDY INST RHEUMATOLOGY MATHILDA & TER.  
XX Londei M, Quarantino S, Maiuri L;  
PI WPI; 2000-171080/15.  
DR P-PSDB; AAY78594.  
XX Use of antagonists of interleukin-15 for treating an inflammatory bowel  
PT disease, particularly celiac disease  
PS Disclosure; Page 70; 70pp; English.  
XX This sequence represents the simian interleukin 15 (IL-15) nucleotide  
CC sequence. The IL-15 nucleotide sequence and the protein encoded by it can  
CC be used to determine and create antagonists of IL-15. An antagonist of  
CC IL-15 can be used for treating an inflammatory bowel disease (IBD). The  
CC invention relates to the treatment of celiac disease using IL-15  
CC antagonists. The antagonists are preferably mutants of IL-15, antibodies  
CC against IL-15 or IL-15 molecules bound to chemical groups that interfere  
CC with the ability of IL-15 to effect a signal transduction through either  
CC the alpha or the gamma subunit of the IL-15 receptor complex. The IL-15  
CC antagonists of the invention can be used to treat irritable bow disease  
CC especially celiac disease.  
XX Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other;  
SQ

```
Query Match      21.9%; Score 107; DB 21; Length 489;
Best Local Similarity 99.4%; Pred. No. 1.7e-42;
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTCTAACTGAAGCTGGCATTCATCTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126
   |||||||
DB 67 agtcattttcactgaagctggcattcatctcttcattttgggctgtttcagtcgaggg 126
   |||||||

QY 127 CTTCTTAAACAGAGCCAACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGAT 186
   |||||||
DB 127 ctccctaaacagagccaaactgggtgaatgtaataagtgatttgaaaaaaattgaagat 186
   |||||||

QY 187 CTTATTCATCTATGCATATTGATGCTACTTTATATAC 224
   |||||||
DB 187 cttattcaatctatgcattgctgctactttatatac 224
   |||||||

RESULT 42
AAZ38245
ID AAZ38245 standard; cDNA: 489 BP.
XX
AC AAZ38245;
XX
DT 09-FEB-2000 (first entry)
XX
DE Human epithelium-derived T-cell factor (ETF) cDNA.
XX
KW ETF; epithelium-derived T-cell factor; T-cell; T-lymphocyte;
KW proliferation; differentiation; growth factor; precursor; mature; CD4+;
KW CD8+; gastrointestinal; epithelium; cell culture; treatment; HIV;
KW gastrointestinal disease; gastroenteritis; colitis;
KW inflammatory bowel disease; villus atrophic disorder; enteritis;
KW chemotherapy; radiotherapy; gut toxicity; cancer; side effect;
KW tolerated dose; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..489
FT /tag= a
FT /product= "Human ETF precursor protein (AAZ52310)"
FT sig_peptide 1..144
FT /tag= b
FT mat_peptide 145..489
FT /tag= c
FT /product= "Mature human ETF (AAZ52311)".
XX
XX US5985262-A.
XX
XX 16-NOV-1999.
XX
XX 03-FEB-1997; 97US-0794524.
XX
XX 22-FEB-1995; 95US-0393305.
XX 04-OCT-1996; 96US-0726817.
XX 08-MAR-1993; 93US-0031399.
XX 22-APR-1994; 94US-0233606.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Rauch C, Fung V, Eisenman JR, Grabstein KH, Anderson DM;
XX WPI: 2000-022267/02.
XX P-PSDB: AAY52310, AAY52311.
XX
XX Stimulation of T-cells in human immunodeficiency virus infected
XX patients -
XX
XX Claim 1; Columns 37-40; 33pp; English.
XX
XX This sequence represents human epithelium-derived T-cell factor (ETF)
XX cDNA. ETF is a previously unidentified T-cell growth factor which
```

```
CC stimulates precursor or mature CD4+ and CD8+ T-lymphocytes to proliferate
CC and differentiate. It also promotes proliferation of the gastrointestinal
CC epithelium. The protein can be used to promote long-term in vitro culture
CC of T-lymphocytes and T-cell lines. ETF can be used for treating HIV
CC infection, HIV-associated diseases, and other diseases or conditions
CC where stimulation of T-cell proliferation would be desirable e.g., it
CC could be used to augment the destruction of tumour cells or virally-
CC infected cells. ETF may also be used to treat or prevent gastrointestinal
CC disease, including chemotherapy and radiotherapy associated enteritis,
CC gastroenteritis, colitis, inflammatory bowel disease and villus atrophic
CC disorders. Chemotherapy and radiotherapy associated enteritis (gut
CC toxicity) results in bleeding and sepsis due to gastrointestinal flora
CC entering the blood, and thus can limit the dosage of therapeutic agent
CC administered to a cancer patient. ETF may therefore be used to increase
CC the tolerated doses radiotherapy and chemotherapy.
XX
XX Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other;
SQ

Query Match      21.9%; Score 107; DB 21; Length 489;
Best Local Similarity 99.4%; Pred. No. 1.7e-42;
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTTCTAACTGAAGCTGGCATTCATCTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126
   |||||||
DB 67 agtcattttcactgaagctggcattcatctcttcattttgggctgtttcagtcgaggg 126
   |||||||

QY 127 CTTCTTAAACAGAGCCAACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTGAAGAT 186
   |||||||
DB 127 ctccctaaacagagccaaactgggtgaatgtaataagtgatttgaaaaaaattgaagat 186
   |||||||

QY 187 CTTATTCATCTATGCATATTGATGCTACTTTATATAC 224
   |||||||
DB 187 cttattcaatctatgcattgctgctactttatatac 224
   |||||||

RESULT 43
AAF57018
ID AAF57018 standard; cDNA: 489 BP.
XX
AC AAF57018;
XX
DT 14-MAY-2001 (first entry)
XX
DE Human ETF (hETF) polypeptide encoding cDNA.
XX
KW Epithelium-derived T-cell factor; ETF; simian; human; enteritis;
KW gastrointestinal disease; mucositis; peptic ulcer; cytostatic;
KW villus atrophic disorder; inflammatory bowel disease; antiinflammatory;
KW anti-HIV; antiviral; T-lymphocyte stimulator; ss.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..489
FT /tag= a
FT /product= "hETF"
FT sig_peptide 1..144
FT /tag= b
FT mat_peptide 145..486
FT /tag= c
FT /note= "specifically claimed (see AAB62015)"
XX
XX US6184359-B1.
XX
XX 06-FEB-2001.
XX
XX 09-NOV-1998; 98US-0189193.
XX
XX 22-FEB-1995; 95US-0393305.
XX 04-OCT-1996; 96US-0725969.
XX 08-MAR-1993; 93US-0031399.
XX 22-APR-1994; 94US-0233606.
```

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XX PA (IMMV ) IMMUNEX CORP.
XX PI Grabstein KH, Anderson DM, Eisenman JR, Fung V, Rauch C;
XX PI WPI; 2001-217801/22.
XX DR P-PSDB; AAB62014, AAB62015.
XX DR
XX PT New antibodies that specifically binds epithelium-derived T-cell factor
XX PT polypeptide useful for e.g. treating or preventing gastrointestinal
XX PT diseases. HIV and HIV-associated diseases, augmenting destruction of
XX PT tumour cells
XX XX
XX PS Claim 1: Column39-40; 35pp; English.
XX PS
XX CC The invention relates to simian and human epithelium-derived T-cell
XX CC factor (ETF) polypeptides. Antibodies that specifically bind to the ETF
XX CC polypeptides are used for treating or preventing gastrointestinal
XX CC diseases, such as chemotherapy and radiation therapy-induced enteritis
XX CC and mucositis, peptic ulcer disease, villus atrophic disorders and
XX CC inflammatory bowel disease; for increasing tolerated doses for radiation
XX CC therapy and chemotherapy agents which are limited by gastrointestinal
XX CC toxicity; and for treating HIV and HIV-associated diseases. The
XX CC antibodies are further used to treat a variety of other diseases or
XX CC conditions where it is desired to stimulate proliferation of
XX CC T-lymphocytes and B lymphocytes, or the secretion of immunoglobulin B
XX CC lymphocytes, to augment anti-infectious disease immunity, to induce CTL,
XX CC LAK or NK lytic activity, or to augment the destruction of tumour cells
XX CC or cells infected with virus. The present sequence represents a cDNA
XX CC encoding the human ETF (hETF) polypeptide.
XX SQ Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other;

Query Match 21.9%; Score 107; DB 22; Length 489;
Best Local Similarity 99.4%; Pred. No. 1.7e-42;
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 67 AGTCATTCTTCTACTGAAGTCGCATCATGCTTCATTTGGCGTGTTCAGTCAGGG 126
Db |||||
QY 127 CTTCTTAAACAGAACCCAACTGGGCGAATGTAATAGTGATTTGAAAAAATTTGAAGAT 186
Db |||||
QY 187 CTATTTCAATCTATGATATTTGATGCTACTTTATATAC 224
Db |||||

RESULT 44
AAT00525
ID AAT00525 standard; cDNA; 345 BP.
XX AC AAT00525;
XX XX
XX DT 02-FEB-1996 (first entry)
XX XX
XX DE Simian interleukin-15 mature polypeptide.
XX XX
XX KW Interleukin-15; epithelium-derived T-cell factor; T lymphocyte; ss.
XX OS
XX SS Cebus apella.
XX FH Key Location/Qualifiers
XX FT 1..345
XX FT /*tag= a
XX FT /label= precursor nts 145-489
XX FT /note= "claimed"
XX PN W09527722-A.
XX XX
```

```
PD 19-OCT-1995.
XX XX
XX PF 06-APR-1994; 94WO-US03793.
XX XX
XX PR 06-APR-1994; 94WO-US03793.
XX XX
XX PA (IMMV ) IMMUNEX CORP.
XX XX
XX PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;
XX PI Rauch C;
XX XX
XX DR WPI; 1995-373556/48.
XX DR P-PSDB; AAR83309.
XX XX
XX PT Isolated DNA encoding polypeptide with mammalian IL-15 activity - which
XX PT stimulates proliferation and differentiation of T cells, used for
XX PT treating carcinoma(s), melanomas, etc. and viral infections
XX XX
XX PS Claim 2: Page 26; 48pp; English.
XX XX
XX CC A simian species of IL-15 (sIL-15) was purified and analysed by SDS-
XX CC PAGE. Bioassay of unstained gel slices indicated IL-15 activity was
XX CC assoc. with proteins having mol. wts in the range of 15-17 kDa. The
XX CC N-terminus of the 15-17 kDa was sequenced. The results indicated the
XX CC identity of the first 33 AAs of AAR83309. Subsequent sequencing of a
XX CC cDNA clone obtd. from a simian library provided a sequence encoding
XX CC the polypeptide AAR83436. AAR83436 comprises a relatively short 48 AA
XX CC leader sequence and a mature polypeptide AAR83309. The sequence of the
XX CC N-terminal 31 AAs of AAR83309 was used to design synthetic PCR primers
XX CC for the amplification of IL-15-specific DNA sequences. The first
XX CC 6 AAs of the N-terminus were used to design one primer, a
XX CC degenerate mixture coding for all possible codon usages - AAT00528.
XX CC The AA sequences of the simian mature N-terminus 26-31 were used
XX CC to design a second primer, a degenerate mixture coding for a
XX CC complement of all possible codon usages of AAs 26-31, omitting
XX CC posn. 3 of Val (AAT00529, AAT00530). Polyadenylated RNAs from CV-1/EBNA
XX CC cells were used as templates. A 92 bp DNA fragment was used as a
XX CC hybridisation probe to screen a portion of a plasmid library contg.
XX CC cDNA inserts prepd. from CV-1/EBNA polyadenylated RNA. This
XX CC resulted in the isolation of clone C85.sIL-15 that has an ORF
XX CC given in AAT00524. AAR83309 is the active polypeptide & AAR83436 is
XX CC the precursor polypeptide. AAT00525 encodes the active polypeptide.
XX SQ Sequence 345 BP; 124 A; 50 C; 64 G; 107 T; 0 other;

Query Match 16.4%; Score 80; DB 16; Length 345;
Best Local Similarity 100.0%; Pred. No. 2.8e-29;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 AACTGGGTGAATGTAATAGTGATTTGAAAAAATTTGAGATCTTATTCATCTATGCAT 204
Db |||||
QY 205 ATTGATGCTACTTTATATAC 224
Db |||||
Db 61 attgatgctactttatatac 80

RESULT 45
AAF57025
ID AAF57025 standard; cDNA; 345 BP.
XX AC AAF57025;
XX XX
XX DT 14-MAY-2001 (first entry)
XX XX
XX DE Human ETF (hETF) mature polypeptide encoding cDNA.
XX XX
XX KW Epithelium-derived T-cell factor; ETF; simian; human; enteritis;
XX KW gastrointestinal disease; mucositis; peptic ulcer; cytostatic;
XX KW villus atrophic disorder; inflammatory bowel disease; antiinflammatory;
XX KW anti-HIV; antiviral; T-lymphocyte stimulator; ss.
```

```
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT 1..345
XX FT /tag= a
XX FT /product= "mature hETF"
XX PN US6184359-B1.
XX PD 06-FEB-2001.
XX XX
XX XX 09-NOV-1998; 98US-0189193.
XX PF 22-FEB-1995; 95US-0393305.
XX PR 04-OCT-1996; 96US-0725969.
XX PR 08-MAR-1993; 93US-0031399.
XX PR 22-APR-1994; 94US-0233606.
XX XX
XX PA (IMV ) IMMUNEX CORP.
XX XX
XX PI Grabstein KH, Anderson DM, Eisenman JR, Fung V, Rauch C;
XX XX
XX DR WPI; 2001-217801/22.
XX DR P-PSDB; AAB62015.
XX XX
XX XX New antibodies that specifically binds epithelium-derived T-cell factor
XX PT polypeptide useful for e.g. treating or preventing gastrointestinal
XX PT diseases, HIV and HIV-associated diseases, augmenting destruction of
XX PT tumour cells -
XX XX
XX XX Disclosure; Fig 2; 35pp; English.
XX XX
XX CC The invention relates to simian and human epithelium-derived T-cell
XX CC factor (ETF) polypeptides. Antibodies that specifically bind to the ETF
XX CC polypeptides are used for treating or preventing gastrointestinal
XX CC diseases, such as chemotherapy and radiation therapy-induced enteritis
XX CC and mucositis, peptic ulcer disease, villus atrophic disorders and
XX CC inflammatory bowel disease; for increasing tolerated doses for radiation
XX CC therapy and chemotherapy agents which are limited by gastrointestinal
XX CC toxicity; and for treating HIV and HIV-associated diseases. The
XX CC antibodies are further used to treat a variety of other diseases or
XX CC conditions where it is desired to stimulate proliferation of
XX CC T-lymphocytes and B lymphocytes, or the secretion of immunoglobulin B
XX CC lymphocytes, to augment anti-infectious disease immunity, to induce CTL,
XX CC LAK or NK lytic activity, or to augment the destruction of tumour cells
XX CC or cells infected with virus. The present sequence represents a cDNA
XX CC encoding the human ETF (hETF) mature polypeptide.
XX XX
XX XX Sequence 345 BP; 124 A; 50 C; 64 G; 107 T; 0 other;
XX XX

Query Match 16.4%; Score 80; DB 22; Length 345;
Best Local Similarity 100.0%; Pred. No. 2.8e-29;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 AACGTGGGTGAATGTAATGAAGTATTGAAAAAATGAAGATCTTATTCAATCTATGCAT 204
DB 1 aactgggtggaatgtaataagtgattgaaaaaaattgaagatcttattcaatctatgcac 60

QY 205 ATTGATGCTACTTTATATAC 224
DB 61 attgatgctactttatataac 80

RESULT 46
AAL25950/c
ID AAL25950 standard; cDNA; 384 BP.
XX XX
XX AC AAL25950;
XX XX
XX XX 07-DEC-2001 (first entry)
XX XX
XX PR 14-JAN-2000; 2000US-0176077.
```

```
DE XX Human breast cancer expressed polynucleotide 18407.
XX KW Human; breast cancer; cell marker; cytostatic; ss.
XX OS Homo sapiens.
XX PN WO200151628-A2.
XX XX
XX PD 19-JUL-2001.
XX XX
XX PF 10-JAN-2001; 2001WO-US00798.
XX XX
XX PR 14-JAN-2000; 2000US-0176077.
XX PR 14-MAR-2000; 2000US-0189167.
XX PR 24-MAR-2000; 2000US-0192099.
XX PR 29-MAR-2000; 2000US-0193480.
XX PR 15-MAY-2000; 2000US-0205230.
XX PR 09-JUN-2000; 2000US-0211315.
XX PR 25-JUL-2000; 2000US-0220534.
XX XX
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX XX
XX PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX XX
XX XX WPI; 2001-451856/48.
XX XX
XX PT New peptide useful as a marker for the diagnosis of breast cancer -
XX PS Claim 1; Page 3400; 3695pp; English.
XX XX
XX CC The invention relates to human breast cancer expressed polynucleotides
XX CC (AAL07544-AAL26789) and methods of assessing whether a patient is
XX CC afflicted with breast cancer by examining the correlation between the
XX CC expression of certain markers and the cancerous state of breast cells.
XX CC The polynucleotides and encoded polypeptides are potential markers for
XX CC detecting, diagnosing, monitoring, characterising, treating and
XX CC potentially preventing breast cancer. The polynucleotides and encoded
XX CC polypeptides are also useful for isolating compounds with cytostatic
XX CC activity.
XX XX
XX XX Sequence 384 BP; 126 A; 63 C; 67 G; 127 T; 1 other;
XX XX

Query Match 5.9%; Score 29; DB 22; Length 384;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 461 TTCTCCAAATGTTTCATCAACACTTCTTGA 489
DB 275 TTGTCCAAATGTTTCATCAACACTTCTTGA 247

RESULT 47
AAL19115/c
ID AAL19115 standard; cDNA; 474 BP.
XX XX
XX XX AAL19115;
XX XX
XX XX 07-DEC-2001 (first entry)
XX XX
XX DE Human breast cancer expressed polynucleotide 11572.
XX KW Human; breast cancer; cell marker; cytostatic; ss.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200151628-A2.
XX XX
XX PD 19-JUL-2001.
XX XX
XX PF 10-JAN-2001; 2001WO-US00798.
XX XX
XX XX 14-JAN-2000; 2000US-0176077.
```

PR 14-MAR-2000; 2000US-0189167.  
PR 24-MAR-2000; 2000US-0192099.  
PR 29-MAR-2000; 2000US-0193480.  
PR 15-MAY-2000; 2000US-0205230.  
PR 09-JUN-2000; 2000US-0211315.  
PR 25-JUL-2000; 2000US-0220534.  
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX Lillie J, Xu Y, Wang Y, Steinmann K;  
XX WPI; 2001-451856/48.  
XX New peptide useful as a marker for the diagnosis of breast cancer -  
XX Claim 1; Page 2067; 3695pp; English.  
XX The invention relates to human breast cancer expressed polynucleotides  
CC (AAL07544-RAL26789) and methods of assessing whether a patient is  
CC afflicted with breast cancer by examining the correlation between the  
CC expression of certain markers and the cancerous state of breast cells.  
CC The polynucleotides and encoded polypeptides are potential markers for  
CC detecting, diagnosing, monitoring, characterising, treating and  
CC potentially preventing breast cancer. The polynucleotides and encoded  
CC polypeptides are also useful for isolating compounds with cytostatic  
CC activity.  
XX Sequence 474 BP; 155 A; 76 C; 87 G; 155 T; 1 other;  
SQ

Query Match 5.9%; Score 29; DB 22; Length 474;  
Best Local Similarity 100.0%; Pred. No. 0.00025;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 461 TTGTCCAAATGTTTCATCAACACTTCTTGA 489  
DB 279 TTGTCCAAATGTTTCATCAACACTTCTTGA 251  
|||||

RESULT 48  
AAL08205/c  
ID AAL08205 standard; cDNA; 506 BP.  
XX AAL08205;  
XX 07-DEC-2001 (first entry)  
XX Human breast cancer expressed polynucleotide 662.  
XX Human; breast cancer; cell marker; cytostatic; ss.  
XX Homo sapiens.  
XX WO200151628-A2.  
XX 19-JUL-2001.  
XX 10-JAN-2001; 2001WO-US00798.  
XX 14-JAN-2000; 2000US-0176077.  
XX 14-MAR-2000; 2000US-0189167.  
PR 24-MAR-2000; 2000US-0192099.  
PR 29-MAR-2000; 2000US-0193480.  
PR 15-MAY-2000; 2000US-0205230.  
PR 09-JUN-2000; 2000US-0211315.  
PR 25-JUL-2000; 2000US-0220534.  
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX Lillie J, Xu Y, Wang Y, Steinmann K;  
XX WPI; 2001-451856/48.  
XX

PT New peptide useful as a marker for the diagnosis of breast cancer -  
XX Claim 1; Page 198; 3695pp; English.  
XX The invention relates to human breast cancer expressed polynucleotides  
CC (AAL07544-RAL26789) and methods of assessing whether a patient is  
CC afflicted with breast cancer by examining the correlation between the  
CC expression of certain markers and the cancerous state of breast cells.  
CC The polynucleotides and encoded polypeptides are potential markers for  
CC detecting, diagnosing, monitoring, characterising, treating and  
CC potentially preventing breast cancer. The polynucleotides and encoded  
CC polypeptides are also useful for isolating compounds with cytostatic  
CC activity.  
XX Sequence 506 BP; 155 A; 87 C; 106 G; 155 T; 3 other;  
SQ

Query Match 5.9%; Score 29; DB 22; Length 506;  
Best Local Similarity 100.0%; Pred. No. 0.00025;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 461 TTGTCCAAATGTTTCATCAACACTTCTTGA 489  
DB 315 TTGTCCAAATGTTTCATCAACACTTCTTGA 287  
|||||

RESULT 49  
AAZ88713/c  
ID AAZ88713 standard; cDNA; 27 BP.  
XX AAZ88713;  
XX 11-MAY-2000 (first entry)  
XX Human IL-15 targetted antisense oligonucleotide HCL-105.  
XX IL-15; interleukin 15; human; anti-IL15; anti-inflammatory; hepatotropic;  
KW anti-arthritis; neuroprotective; antiproliferative; antiulcer; antisense;  
KW gene therapy; macrophage; inflammatory disorder; bowel disease; primer;  
KW arthritis; cirrhosis; multiple sclerosis; chronic liver disease;  
KW ulcerative colitis; cell proliferative disorder; treatment; ss.  
XX Homo sapiens.  
XX WO200001851-A1.  
XX 13-JAN-2000.  
XX 07-JUL-1999; 99WO-US15499.  
XX 07-JUL-1998; 98US-0091873.  
XX (HISM ) HISAMITSU PHARM CO LTD.  
XX Veerapanane D, Hamaoka S, Hiroyuki K, Nozawa I;  
XX WPI; 2000-171026/15.  
XX Novel antisense oligonucleotides targeted to interleukin-15 used to  
XX treat inflammatory diseases and cell proliferative diseases such as  
XX inflammatory bowel disease and chronic liver disease -  
XX Claim 12; Fig 2; 52pp; English.  
XX This invention describes novel antisense oligonucleotides of 8-40  
XX nucleic acids, targeted to interleukin-15 (IL-15). The products of the  
XX invention have anti-IL15, anti-inflammatory, hepatotropic,  
XX anti-arthritis, neuroprotective, antiproliferative and antiulcer activity  
XX and can be used for gene therapy. The antisense oligonucleotides are used  
XX to inhibit interleukin-15 (IL-15) expression and production, and prevent  
XX the recruitment and activation of macrophages. They are used to treat  
XX diseases associated with an increased expression of IL-15. Such diseases  
XX include inflammatory disorders, such as inflammatory bowel disease,  
XX

CC arthritis, cirrhosis, multiple sclerosis, chronic liver disease,  
CC ulcerative colitis and cell proliferative disorders. The treatment may  
CC be in vivo or ex vivo. The antisense oligonucleotides of the invention  
CC are specific for interleukin-15 (IL-15), and can be delivered  
CC exogenously or can be expressed from DNA or RNA vectors. AA288709-288723  
CC represent the antisense ligonucleotides disclosed in the method of the  
CC invention.

XX SQ Sequence 27 BP; 4 A; 7 C; 7 G; 9 T; 0 other;  
SQ Sequence 27 BP; 4 A; 7 C; 7 G; 9 T; 0 other;

Query Match 5.5%; Score 27; DB 21; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.0024;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 GGGCTTCCTAAACAGACGACCAACTGG 150  
|||||  
Db 27 GGGCTTCCTAAACAGACGACCAACTGG 1

RESULT 50  
AA288711/c  
ID AA288711 standard; cDNA; 30 BP.  
XX AC  
XX AA288711;  
XX AC  
XX 11-MAY-2000 (first entry)  
XX DE Human IL-15 targetted antisense oligonucleotide HCL-103.  
XX IL-15; interleukin 15; human; anti-IL15; anti-inflammatory; hepatotropic;  
KW anti-arthritis; neuroprotective; antiproliferative; antiulcer; antisense;  
KW gene therapy; macrophage; inflammatory disorder; bowel disease; primer;  
KW arthritis; cirrhosis; multiple sclerosis; chronic liver disease;  
KW ulcerative colitis; cell proliferative disorder; treatment; ss.  
XX OS Homo sapiens.  
XX WO200001851-A1.  
XX PN 13-JAN-2000.  
XX PD 07-JUL-1999; 99WO-0515499.  
XX PF 07-JUL-1998; 98US-0091873.  
XX PR (HISM ) HISAMITSU PHARM CO LTD.  
XX PA Veerapanane D, Hamanaka S, Hiroyuki K, Nozawa I;  
XX WPI; 2000-171026/15.  
XX DR Novel antisense oligonucleotides targeted to interleukin-15 used to  
XX PT treat inflammatory diseases and cell proliferative diseases such as  
XX PT inflammatory bowel disease and chronic liver disease -  
XX PS Claim 12; Fig 2; 52pp; English.  
XX CC This invention describes novel antisense oligonucleotides of 8-40  
CC nucleic acids, targeted to interleukin-15 (IL-15). The products of the  
CC invention have anti-IL15, anti-inflammatory, hepatotropic,  
CC anti-arthritis, neuroprotective, antiproliferative and antiulcer activity  
CC and can be used for gene therapy. The antisense oligonucleotides are used  
CC to inhibit interleukin-15 (IL-15) expression and production, and prevent  
CC the recruitment and activation of macrophages. They are used to treat  
CC diseases associated with an increased expression of IL-15. Such diseases  
CC include inflammatory disorders, such as inflammatory bowel disease,  
CC arthritis, cirrhosis, multiple sclerosis, chronic liver disease,  
CC ulcerative colitis and cell proliferative disorders. The treatment may  
CC be in vivo or ex vivo. The antisense oligonucleotides of the invention  
CC are specific for interleukin-15 (IL-15), and can be delivered  
CC exogenously or can be expressed from DNA or RNA vectors. AA288709-288723  
CC represent the antisense ligonucleotides disclosed in the method of the

CC invention.  
XX SQ Sequence 30 BP; 8 A; 6 C; 4 G; 12 T; 0 other;  
SQ Sequence 30 BP; 8 A; 6 C; 4 G; 12 T; 0 other;

Query Match 5.5%; Score 27; DB 21; Length 30;  
Best Local Similarity 100.0%; Pred. No. 0.0024;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

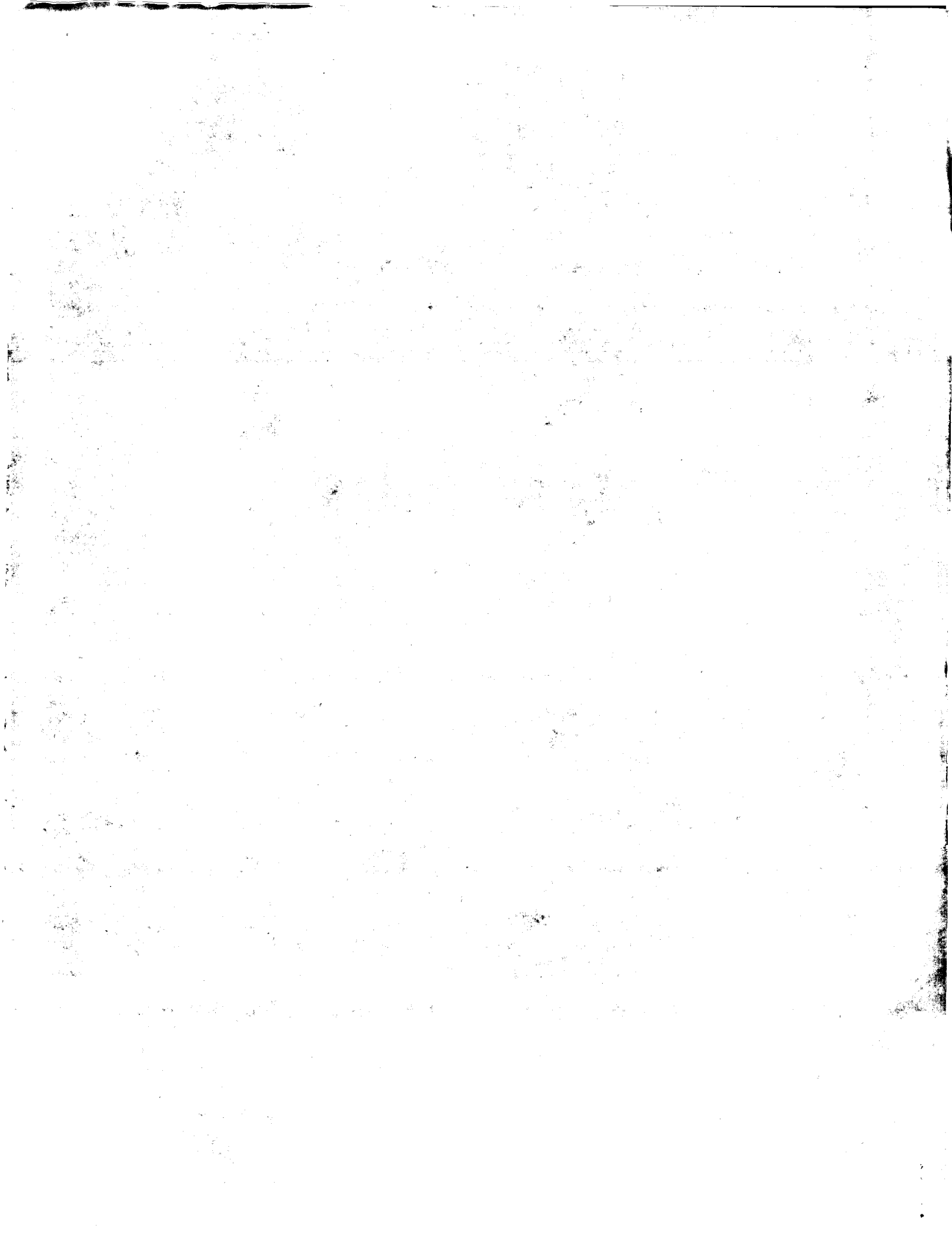
QY 1 ATGAGAATTCGAACACACATTGTGAGA 27  
|||||  
Db 27 ATGAGAATTCGAACACACATTGTGAGA 1

Search completed: August 6, 2002, 21:37:06  
Job time: 4655 sec

Fri Aug 9 11:13:32 2002

us-09-724-841-1.01112.rng

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 6, 2002, 20:07:30 ; Search time 1856.14 seconds  
(without alignments)  
5513.095 Million cell updates/sec

Title: US-09-724-841-1

Perfect score: 489

Sequence: 1 ATGAGATTTCGAACACCA.....TGTCATCAACACTTCTTGA 489

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 12

Total number of hits satisfying chosen parameters: 265713

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_mu.\*  
20: em\_om.\*  
21: em\_or.\*  
22: em\_ov.\*  
23: em\_pat.\*  
24: em\_ph.\*  
25: em\_pl.\*  
26: em\_ro.\*  
27: em\_sts.\*  
28: em\_un.\*  
29: em\_vi.\*  
30: em\_htg\_hum.\*  
31: em\_htg\_inv.\*  
32: em\_htg\_other.\*  
33: em\_htgo\_inv.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	489	100.0	489	6	AR070281	AR070281 Sequence
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5	489	100.0	489	6	AR122046	AR122046 Sequence
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7	489	100.0	489	6	AR125105	AR125105 Sequence
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9	489	100.0	489	6	AX320244	AX320244 Sequence
10	489	100.0	489	6	I25783	I25783 Sequence 4
11	489	100.0	489	6	I28849	I28849 Sequence 1
12	489	100.0	489	6	I62692	I62692 Sequence 1
13	489	100.0	489	6	I79219	I79219 Sequence 1
14	489	100.0	489	6	AR103280	AR103280 Sequence
15	489	100.0	489	6	AX024715	AX024715 Sequence
16	489	100.0	489	6	AX301227	AX301227 Sequence
17	489	100.0	489	6	HSU14407	U14407 Human inter
18	444	90.8	489	6	AX320242	AX320242 Sequence
19	438	89.6	489	6	AR094649	AR094649 Sequence
20	438	89.6	489	6	BD008811	BD008811 Antagonis
21	402	82.2	453	9	HSIL15MR	Z38000 H.sapiens m
22	393	80.4	489	6	AR094650	AR094650 Sequence
23	393	80.4	489	6	BD008812	BD008812 Antagonis
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25	380	77.7	643	9	HSIL15MR2	X94223 H.sapiens m
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29	345	70.6	345	6	I28856	I28856 Sequence 12
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31	329	67.3	1248	6	AR087004	AR087004 Sequence
32	329	67.3	1248	6	AF031167	AF031167 Homo sapi
33	142	29.0	492	9	AB000555	AB000555 Macaca fa
34	142	29.0	559	9	MMU19843	U19843 Macaca mula
35	138	28.2	14968	9	HSDNAIL15	X91233 H.sapiens I
36	138	28.2	178438	9	AC096774	AC096774 Homo sapi
37	107	21.9	489	6	AR004267	AR004267 Sequence
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41	107	21.9	489	6	AR122045	AR122045 Sequence
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44	107	21.9	489	6	AX006785	AX006785 Sequence
45	107	21.9	489	6	I25782	I25782 Sequence 1
46	107	21.9	489	6	I28850	I28850 Sequence 4
47	107	21.9	489	6	I79220	I79220 Sequence 4
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53	80	16.4	345	6	I79227	I79227 Sequence 13
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58	32	6.5	489	4	AF108148	AF108148 Felis cat
59	30	6.1	489	4	AF149700	AF149700 Ovis arie
60	30	6.1	1250	10	MMU14332	U14332 Mus musculu
61	28	5.7	441	10	AF015718	AF015718 Rattus no
62	28	5.7	489	10	AF015719	AF015719 Rattus no
63	28	5.7	1313	10	RNU69272	U69272 Rattus norv
64	23	4.7	30	6	AX353399	AX353399 Sequence
65	23	4.7	162922	2	AC011281	AC011281 Homo sapi
66	22	4.5	165509	2	AC009886	AC009886 Homo sapi
67	21	4.3	21	6	AR103271	AR103271 Sequence
68	21	4.3	21	6	AR103273	AR103273 Sequence
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77	21	4.3	69	6	AR024356	Antagonis	150	19	3.9	8964	6	AX349013	Sequence
78	21	4.3	69	6	AR122053	Sequence	c 151	19	3.9	11681	1	AE007746	Clostridi
79	21	4.3	69	6	AR122875	Sequence	c 152	19	3.9	12029	1	AE007746	Plasmodiu
80	21	4.3	69	6	AR125112	Sequence	c 153	19	3.9	19131	6	AX251474	Sequence
81	21	4.3	1736	3	PIA222862	Pichia an	c 154	19	3.9	39882	2	AL356289	Human DNA
82	21	4.3	38199	3	AC009745	Drosophill	c 155	19	3.9	52891	2	AC107919	Homo sapi
83	21	4.3	40018	2	AC018103	Drosophill	c 156	19	3.9	55307	2	AC014684	Drosophill
84	21	4.3	44006	2	AC010215	Drosophill	c 157	19	3.9	58407	1	MI12CG	Methanococc
85	21	4.3	44264	3	CEC47D12	Caenorhabdi	c 158	19	3.9	63646	9	HSJ256K2A	Human DNA
86	21	4.3	453000	2	AC027515	Homo sapi	c 159	19	3.9	68465	9	AL162384	Human DNA
87	21	4.3	160939	2	AC012423	Homo sapi	c 160	19	3.9	68702	9	AL445193	Human DNA
88	21	4.3	165639	3	AC099623	Mus muscu	c 161	19	3.9	68702	9	AL445193	Human DNA
89	21	4.3	175179	3	AC009254	Drosophill	c 162	19	3.9	69269	2	AC101436	Mus muscu
90	21	4.3	177129	2	AC037481	Homo sapi	c 163	19	3.9	69269	2	AC101436	Mus muscu
91	21	4.3	179947	2	AC009786	Homo sapi	c 164	19	3.9	68743	9	AL139349	Human DNA
92	21	4.3	201627	2	AC017068	Homo sapi	c 165	19	3.9	88013	9	AC091372	Human DNA
93	21	4.3	221234	2	AC026261	Homo sapi	c 166	19	3.9	88013	9	AC091372	Human DNA
94	21	4.3	311800	3	AE003781	Drosophill	c 167	19	3.9	90605	2	AC026450	Human DNA
95	20	4.1	20	6	A89381	Sequence 15	c 168	19	3.9	94973	9	AL645819	Human DNA
96	20	4.1	20	6	AX024721	Sequence	c 169	19	3.9	98085	2	AL139427	Homo sapi
97	20	4.1	20	6	AX024722	Sequence	c 170	19	3.9	102223	2	AL139427	Homo sapi
98	20	4.1	20	6	AX024723	Sequence	c 171	19	3.9	103419	2	AL139427	Homo sapi
99	20	4.1	20	6	AX024724	Sequence	c 172	19	3.9	107331	2	AL139427	Homo sapi
100	20	4.1	20	6	AX024725	Sequence	c 173	19	3.9	110000	10	AE008683-2	Rattus no
101	20	4.1	230	9	HSCORS04	Human 3-hyd	c 174	19	3.9	119555	2	AL353790	Human DNA
102	20	4.1	1542	9	HSU12789	Human clone	c 175	19	3.9	121450	2	AL355541	Human DNA
103	20	4.1	2058	6	AX337379	Sequence	c 176	19	3.9	123855	10	MM303011	Mus muscu
104	20	4.1	2058	6	HSU36784	H. sapiens m	c 177	19	3.9	125184	9	AL357141	Human DNA
105	20	4.1	3484	3	MSU36784	Metridium s	c 178	19	3.9	131732	10	AF259071	Mus muscu
106	20	4.1	17443	3	MSAF000203	Metridium	c 179	19	3.9	133571	2	AC094717	Rattus no
107	20	4.1	31570	8	AF288091	Thraustoc	c 180	19	3.9	133709	2	AC094717	Rattus no
108	20	4.1	54585	2	AC100191	Mus muscu	c 181	19	3.9	139255	9	AC092326	Homo sapi
109	20	4.1	62222	2	AC110500	Mus muscu	c 182	19	3.9	139255	9	AC092326	Homo sapi
110	20	4.1	65882	9	AL589734	Human DNA	c 183	19	3.9	142434	2	AL351264	Human DNA
111	20	4.1	69200	2	AC034294	Homo sapi	c 184	19	3.9	142434	2	AL351264	Human DNA
112	20	4.1	71165	2	AC099819	Homo sapi	c 185	19	3.9	145226	2	AP004284	Homo sapi
113	20	4.1	90693	9	AC005592	Homo sapi	c 186	19	3.9	148109	2	AC018918	Homo sapi
114	20	4.1	91025	2	AP0059270	Human DNA	c 187	19	3.9	150288	2	AC015572	Homo sapi
115	20	4.1	101458	2	AP000680	Human sapi	c 188	19	3.9	150288	2	AC015572	Homo sapi
116	20	4.1	105118	9	AC019127	Homo sapi	c 189	19	3.9	150391	2	AC011764	Drosophill
117	20	4.1	112424	9	HS1013A10	Human DNA	c 190	19	3.9	150965	2	AC011764	Drosophill
118	20	4.1	137495	2	AC104998	Homo sapi	c 191	19	3.9	153210	2	AC010373	Homo sapi
119	20	4.1	152287	2	AC067795	Homo sapi	c 192	19	3.9	153693	9	AL355338	Human DNA
120	20	4.1	152966	9	AL359713	Human DNA	c 193	19	3.9	153693	9	AL355338	Human DNA
121	20	4.1	155711	3	VIV1D10	Plasmodiu	c 194	19	3.9	153762	2	AC051650	Homo sapi
122	20	4.1	160972	30	AC021417	Homo sapi	c 195	19	3.9	154236	2	AC051650	Homo sapi
123	20	4.1	161218	2	AC011171	Homo sapi	c 196	19	3.9	154313	9	AL590011	Human DNA
124	20	4.1	162547	2	AC022172	Homo sapi	c 197	19	3.9	154979	9	AL590011	Human DNA
125	20	4.1	163342	2	AC105313	Homo sapi	c 198	19	3.9	155825	2	AC023503	Homo sapi
126	20	4.1	163807	2	AC018934	Homo sapi	c 199	19	3.9	157399	2	AP003167	Homo sapi
127	20	4.1	163807	2	AC018934	Homo sapi	c 200	19	3.9	157800	2	AL357074	Homo sapi
128	20	4.1	164868	9	AC016045	Homo sapi	c 201	19	3.9	159430	2	AL137024	Human DNA
129	20	4.1	168018	2	AL592186	Homo sapi	c 202	19	3.9	159790	2	AC013613	Homo sapi
130	20	4.1	173512	2	AC068565	Homo sapi	c 203	19	3.9	161100	2	AC023569	Homo sapi
131	20	4.1	174422	2	AC098206	Rattus no	c 204	19	3.9	161812	9	HS197017	Human DNA
132	20	4.1	176704	2	AC013703	Homo sapi	c 205	19	3.9	162345	3	AC006415	Drosophill
133	20	4.1	182087	2	AC055790	Homo sapi	c 206	19	3.9	164481	2	AC034152	Homo sapi
134	20	4.1	187960	9	AP000866	Homo sapi	c 207	19	3.9	164637	2	AC073513	Homo sapi
135	20	4.1	191734	2	AC016560	Homo sapi	c 208	19	3.9	165901	10	MM437P9	Mus muscu
136	20	4.1	193029	2	AL355594	Homo sapi	c 209	19	3.9	166384	2	AC074113	Homo sapi
137	20	4.1	208035	2	AC006520	Mus muscu	c 210	19	3.9	167001	9	AC005747	Homo sapi
138	20	4.1	213447	2	AL354875	Homo sapi	c 211	19	3.9	167806	2	AC092572	Homo sapi
139	20	4.1	214484	9	AP001830	Homo sapi	c 212	19	3.9	167949	9	AC087821	Homo sapi
140	20	4.1	316704	9	AF2392583	Sequence	c 213	19	3.9	168155	9	AP004580	Homo sapi
141	19	3.9	19	6	AR129564	Sequence	c 214	19	3.9	168703	2	AC021588	Homo sapi
142	19	3.9	25	6	AR094646	Sequence	c 215	19	3.9	168714	2	AC106619	Rattus no
143	19	3.9	25	6	AX320246	Sequence	c 216	19	3.9	168838	2	AC024929	Homo sapi
144	19	3.9	25	6	BD008808	Antagonis	c 217	19	3.9	170099	2	AC092459	Homo sapi
145	19	3.9	2354	9	AF134202	Homo sapi	c 218	19	3.9	170156	9	AP003174	Homo sapi
146	19	3.9	3080	8	KLMBP1	X74159 K.lactis MB	c 219	19	3.9	170208	2	AC106695	Rattus no

c 220	19	3.9	172378	2	AC021696	AC021696 Homo sapi	293	18	3.7	39	6	AR125110	AR125110 Sequence
221	19	3.9	173705	2	AC012256	Homo sapi	c 294	18	3.7	45	6	AR024355	Sequence
222	19	3.9	175040	2	AC072023	Homo sapi	c 295	18	3.7	45	6	AR122052	Sequence
223	19	3.9	175578	2	AC087435	Homo sapi	c 296	18	3.7	45	6	AR122874	Sequence
224	19	3.9	176617	2	AC022232	Mus muscu	c 297	18	3.7	45	6	AR122511	Sequence
225	19	3.9	178101	2	AC024437	Homo sapi	c 298	18	3.7	51	6	AX199645	Sequence
226	19	3.9	178127	2	AC079076	Homo sapi	c 299	18	3.7	211	11	HS067XA9	Sequence
227	19	3.9	178793	2	AC097015	Homo sapi	c 300	18	3.7	871	10	AB04431S04	Sequence
228	19	3.9	179589	2	AC018860	Homo sapi	c 301	18	3.7	967	3	PF058K	Mus muscu
229	19	3.9	181459	2	AC053477	Homo sapi	c 302	18	3.7	1465	10	MMDR1A03	Mus muscu
230	19	3.9	185065	9	AC026472	Homo sapi	c 303	18	3.7	1826	9	AK054588	Homo sapi
c 231	19	3.9	185074	2	AC093526	Homo sapi	c 304	18	3.7	1852	9	BC021164	Homo sapi
c 232	19	3.9	185764	2	AC025289	Homo sapi	c 305	18	3.7	2319	5	XL060094	Xenopus lae
c 233	19	3.9	186141	9	AC004988	Homo sapi	c 306	18	3.7	2535	5	XL060093	Xenopus lae
c 234	19	3.9	186695	3	AC013351	Drosophi	c 307	18	3.7	2795	8	NSRUBSSU	Nicotiana s
c 235	19	3.9	187375	9	AC019292	Homo sapi	c 308	18	3.7	2975	10	MUSHSP86A	Mouse heat
c 236	19	3.9	187780	9	AC108716	Homo sapi	c 309	18	3.7	3149	3	AF019981	Dictyoste
c 237	19	3.9	187947	9	CNS05TF6	Human chr	c 310	18	3.7	3950	9	HSASTRA2	Human alpha
c 238	19	3.9	188782	9	AC023150	Homo sapi	c 311	18	3.7	4318	9	HSU97058	Human Hud g
c 239	19	3.9	190000	2	AC006425	Homo sapi	c 312	18	3.7	5200	1	EHNTPOP	E.hirae ntp
240	19	3.9	191080	2	AC106521	Rattus no	c 313	18	3.7	5965	4	AB059398	Bos tauru
241	19	3.9	191300	2	AC103899	Bos tauru	c 314	18	3.7	7845	3	AB023655	Dictyoste
c 242	19	3.9	192632	2	AC069381	Homo sapi	c 315	18	3.7	9985	1	AE007685	Clostridi
243	19	3.9	193306	2	AC025512	Homo sapi	c 316	18	3.7	11288	1	ENENMP	Enterococu
244	19	3.9	193852	2	AC016544	Homo sapi	c 317	18	3.7	14399	8	SPAC1F12	S.pombe chr
245	19	3.9	194508	2	AC087473	Human chr	c 318	18	3.7	17433	6	AX323781	Sequence
246	19	3.9	194587	9	CNS05TCS	Human chr	c 319	18	3.7	19185	2	AC020287	Drosophi
247	19	3.9	197817	9	AC015716	Homo sapi	c 320	18	3.7	20727	2	AC014780	Drosophi
248	19	3.9	198927	2	AC026863	Homo sapi	c 321	18	3.7	23180	2	AC107244	Rattus no
c 249	19	3.9	199524	2	AC107938	Homo sapi	c 322	18	3.7	24947	2	AC107509	Rattus no
c 250	19	3.9	200000	2	AC007117	Homo sapi	c 323	18	3.7	25987	3	CEE01G66	Rattus no
c 251	19	3.9	200633	2	AC104248	Homo sapi	c 324	18	3.7	26474	3	CELF38H12	Caenorhabd
c 252	19	3.9	202333	2	AC080144	Mus muscu	c 325	18	3.7	26547	3	U70844	Caenorhabd
253	19	3.9	202768	2	AC092345	Mus muscu	c 326	18	3.7	27079	2	AL512627	Human DNA
c 254	19	3.9	202773	2	AC069476	Homo sapi	c 327	18	3.7	35710	2	AC100510	Mus muscu
c 255	19	3.9	203523	9	AC068127	Homo sapi	c 328	18	3.7	38569	9	AC005491	Homo sapi
256	19	3.9	203720	9	AC093861	Homo sapi	c 329	18	3.7	38623	9	AF035396	Homo sapi
c 257	19	3.9	206631	9	AC003798	Homo sapi	c 330	18	3.7	39011	2	AC036140	Homo sapi
c 258	19	3.9	206633	2	AC020574	Homo sapi	c 331	18	3.7	40372	9	AC011521	Homo sapi
c 259	19	3.9	206773	9	AP003173	Homo sapi	c 332	18	3.7	42054	3	U97193	Homo sapi
260	19	3.9	207160	2	AC016464	Mus muscu	c 333	18	3.7	42313	3	U13645	Caenorhabd
261	19	3.9	207309	2	AC099792	Homo sapi	c 334	18	3.7	42701	5	AL591589	Caenorhabd
262	19	3.9	211173	2	AL646097	Mus muscu	c 335	18	3.7	42861	3	CEF52B11	Zebrafish
263	19	3.9	212134	2	AC024037	Homo sapi	c 336	18	3.7	42931	9	AC109695	Caenorhabd
264	19	3.9	213854	2	AL663047	Homo sapi	c 337	18	3.7	43310	9	AC011519	Rattus no
c 265	19	3.9	213854	9	AC090420	Mus muscu	c 338	18	3.7	43887	8	YSCD9740	Saccharomyc
c 266	19	3.9	216706	2	AL669976	Mus muscu	c 339	18	3.7	49480	9	AL450269	Human DNA
267	19	3.9	220683	2	AC015577	Homo sapi	c 340	18	3.7	50497	2	AC106668	Rattus no
c 268	19	3.9	229665	3	AL162398	Homo sapi	c 341	18	3.7	50824	2	AC109190	Mus muscu
269	19	3.9	298283	3	AE003782	Drosophi	c 342	18	3.7	53789	2	AC103646	Mus muscu
c 270	19	3.9	318221	2	PFMAL13P3	Plasmodiu	c 343	18	3.7	56749	2	AC102668	Mus muscu
c 271	18	3.7	18	6	A89379	Sequence 15	c 344	18	3.7	57991	9	AF013593	Homo sapi
c 272	18	3.7	18	6	A89382	Sequence 15	c 345	18	3.7	58155	2	AC010094	Mus muscu
c 273	18	3.7	18	6	A89383	Sequence 15	c 346	18	3.7	58643	2	AC087193	Homo sapi
c 274	18	3.7	18	6	A89382	Sequence 15	c 347	18	3.7	61564	2	AC105005	Homo sapi
c 275	18	3.7	18	6	A89383	Sequence 15	c 348	18	3.7	62263	9	AL583843	Human DNA
c 276	18	3.7	18	6	AR087028	Sequence	c 349	18	3.7	62587	2	AC087732	Homo sapi
c 277	18	3.7	18	6	AR087029	Sequence	c 350	18	3.7	62747	2	AC087475	Homo sapi
c 278	18	3.7	18	6	AR087030	Sequence	c 351	18	3.7	62918	2	AC087475	Homo sapi
c 279	18	3.7	18	6	AR087031	Sequence	c 352	18	3.7	64044	8	SCE9163	Saccharomyc
c 280	18	3.7	18	6	AR087032	Sequence	c 353	18	3.7	64679	2	AC068348	Homo sapi
c 281	18	3.7	18	6	AR087033	Sequence	c 354	18	3.7	66814	2	AC106011	Homo sapi
c 282	18	3.7	18	6	AR087040	Sequence	c 355	18	3.7	67158	2	AC044837	Homo sapi
c 283	18	3.7	18	6	AR087041	Sequence	c 356	18	3.7	67310	2	AC110142	Rattus no
c 284	18	3.7	18	6	AR087042	Sequence	c 357	18	3.7	67884	2	AC090561	Homo sapi
c 285	18	3.7	18	6	AR087043	Sequence	c 358	18	3.7	68234	9	AC022410	Homo sapi
c 286	18	3.7	18	6	AR087044	Sequence	c 359	18	3.7	68446	2	AC110592	Homo sapi
c 287	18	3.7	18	6	AR087045	Sequence	c 360	18	3.7	69345	2	AC105016	Homo sapi
c 288	18	3.7	26	6	AR094647	Sequence	c 361	18	3.7	69867	9	HSJ757N13	Human DNA
c 289	18	3.7	26	6	AX320247	Sequence	c 362	18	3.7	70564	2	AC024426	Homo sapi
c 290	18	3.7	26	6	BD008809	Antagonis	c 363	18	3.7	70802	2	AC024426	Homo sapi
c 291	18	3.7	39	6	AR024354	Sequence	c 364	18	3.7				
292	18	3.7	39	6	AR122051	Sequence	c 365	18	3.7				
	18	3.7	39	6	AR122873	Sequence							

c 366	18	3.7	71319	2	AC009670	AC009670 Homo sapi	c 439	18	3.7	137571	2	AC079539	AC079539 Mus muscu
367	18	3.7	71522	8	AB006703	AB006703 Arabidops	440	18	3.7	138373	2	AC011380	AC011380 Homo sapi
368	18	3.7	71664	9	AC003692	AC003692 Human Chr	441	18	3.7	139260	2	AC066587	AC066587 Homo sapi
369	18	3.7	73334	6	AX347027	AX347027 Sequence	442	18	3.7	141833	9	AL442063	AL442063 Human DNA
370	18	3.7	73334	6	AX356494	AX356494 Sequence	443	18	3.7	142085	9	AL359707	AL359707 Human DNA
c 371	18	3.7	73862	2	AC010613	AC010613 Rattus no	c 444	18	3.7	142190	2	AC021415	AC021415 Homo sapi
c 372	18	3.7	74586	2	AC060793	AC060793 Homo sapi	c 445	18	3.7	142396	9	AL157407	AL157407 Human DNA
c 373	18	3.7	74982	9	AP000786	AP000786 Homo sapi	c 446	18	3.7	142549	2	AP004271	AP004271 Oryza sat
c 374	18	3.7	75440	9	AC060795	AC060795 Homo sapi	c 447	18	3.7	142629	2	AP002479	AP002479 Homo sapi
c 375	18	3.7	76564	2	AC010512	AC010512 Homo sapi	c 448	18	3.7	142640	2	AC006399	AC006399 Homo sapi
c 376	18	3.7	77034	2	AC068413	AC068413 Homo sapi	c 449	18	3.7	142990	2	AC104383	AC104383 Homo sapi
c 377	18	3.7	77839	2	AC010660	AC010660 Rattus no	c 450	18	3.7	144257	9	AP003112	AP003112 Homo sapi
c 378	18	3.7	78595	9	AC018668	AC018668 Homo sapi	c 451	18	3.7	144703	2	AC092995	AC092995 Homo sapi
379	18	3.7	79666	9	AL136969	AL136969 Human DNA	c 452	18	3.7	145384	2	AC026068	AC026068 Homo sapi
380	18	3.7	80770	8	AB005240	AB005240 Arabidops	c 453	18	3.7	145428	2	AC092272	AC092272 Homo sapi
381	18	3.7	81172	2	AC036240	AC036240 Homo sapi	c 454	18	3.7	145668	2	AC107467	AC107467 Rattus no
382	18	3.7	84300	9	HSJ104A17	HSJ104A17 Human DNA	c 455	18	3.7	146727	2	AC019317	AC019317 Homo sapi
383	18	3.7	84881	9	AL390726	AL390726 Human DNA	c 456	18	3.7	146836	9	AC024410	AC024410 Homo sapi
c 384	18	3.7	84952	2	AC015487	AC015487 Homo sapi	c 457	18	3.7	146903	2	AL137245	AL137245 Human DNA
c 385	18	3.7	85195	9	AL136093	AL136093 Human DNA	c 458	18	3.7	146994	9	AC020845	AC020845 Mus muscu
c 386	18	3.7	87871	8	ATT4C12	ATT4C12 Arabidops	c 459	18	3.7	147259	2	AC099487	AC099487 Homo sapi
387	18	3.7	91202	2	AC007609	AC007609 Homo sapi	c 460	18	3.7	147423	9	AC099487	AC099487 Homo sapi
388	18	3.7	94435	9	AC016140	AC016140 Homo sapi	c 461	18	3.7	147484	2	AL590088	AL590088 Homo sapi
389	18	3.7	95097	9	AC022202	AC022202 Homo sapi	c 462	18	3.7	148018	2	HSJ3613A2	HSJ3613A2 Human DNA
c 390	18	3.7	95554	2	AC093284	AC093284 Homo sapi	c 463	18	3.7	149002	2	AL445484	AL445484 Homo sapi
c 391	18	3.7	95554	2	AF068716	AF068716 Arabidops	c 464	18	3.7	149064	2	AC106432	AC106432 Rattus no
c 392	18	3.7	95589	2	AC093299	AC093299 Homo sapi	c 465	18	3.7	149307	2	AC10858	AC10858 Homo sapi
c 393	18	3.7	95899	2	AL591104	AL591104 Human DNA	c 466	18	3.7	150312	9	CNS01R1J	AL163613 Human chr
394	18	3.7	101946	2	AL365320	AL365320 Homo sapi	c 467	18	3.7	150519	2	AC097847	AC097847 Rattus no
395	18	3.7	102343	2	AC106551	AC106551 Rattus no	c 468	18	3.7	151171	2	AC020775	AC020775 Homo sapi
c 396	18	3.7	103370	9	AL161656	AL161656 Human DNA	c 469	18	3.7	151348	2	AC087713	AC087713 Homo sapi
c 397	18	3.7	103916	9	AC004225	AC004225 Homo sapi	c 470	18	3.7	151424	2	AL672073	AL672073 Mus muscu
c 398	18	3.7	107330	9	AC019178	AC019178 Homo sapi	c 471	18	3.7	151498	2	AC099331	AC099331 Homo sapi
399	18	3.7	107705	3	AC024826	AC024826 Caenorhab	c 472	18	3.7	151559	2	AC015863	AC015863 Homo sapi
c 400	18	3.7	107705	3	AC024826	AC024826 Caenorhab	c 473	18	3.7	151651	2	AC011633	AC011633 Homo sapi
401	18	3.7	108182	9	AC009308	AC009308 Homo sapi	c 474	18	3.7	151903	2	AC024349	AC024349 Homo sapi
402	18	3.7	108924	3	AC005889	AC005889 Drosophil	c 475	18	3.7	151951	2	AC084300	AC084300 Homo sapi
403	18	3.7	109333	2	AC105893	AC105893 Rattus no	c 476	18	3.7	151987	2	AP004339	AP004339 Oryza sat
404	18	3.7	110000	10	AE008686	AE008686 Mus muscu	c 477	18	3.7	152387	2	AC099672	AC099672 Homo sapi
405	18	3.7	110096	2	AC097150	AC097150 Rattus no	c 478	18	3.7	152387	2	AC025746	AC025746 Homo sapi
c 406	18	3.7	111414	2	AC020265	AC020265 Drosophil	c 479	18	3.7	152432	2	AC025746	AC025746 Homo sapi
407	18	3.7	112709	2	AP003758	AP003758 Oryza sat	c 480	18	3.7	152878	3	CEV18D10A	CEV18D10A
c 408	18	3.7	112944	9	AC025761	AC025761 Homo sapi	c 481	18	3.7	153046	2	AC095531	AC095531 Rattus no
c 409	18	3.7	113250	9	AC004900	AC004900 Homo sapi	c 482	18	3.7	153297	2	AC027558	AC027558 Homo sapi
410	18	3.7	113596	2	AC105357	AC105357 Homo sapi	c 483	18	3.7	153310	2	AC100724	AC100724 Mus muscu
411	18	3.7	113609	2	AC011368	AC011368 Homo sapi	c 484	18	3.7	153741	9	AL355350	AL355350 Human DNA
c 412	18	3.7	114519	9	AL157813	AL157813 Human DNA	c 485	18	3.7	153764	9	AL355350	AL355350 Human DNA
c 413	18	3.7	114791	9	HSJ850E9	HSJ850E9 Human DNA	c 486	18	3.7	153823	9	AC013551	AC013551 Homo sapi
c 414	18	3.7	117083	9	AC021264	AC021264 Homo sapi	c 487	18	3.7	153860	2	AC016301	AC016301 Homo sapi
c 415	18	3.7	117979	2	AC098538	AC098538 Rattus no	c 488	18	3.7	153873	2	AL139160	AL139160 Homo sapi
c 416	18	3.7	121157	2	AC094303	AC094303 Rattus no	c 489	18	3.7	154052	2	AC027099	AC027099 Homo sapi
417	18	3.7	121552	8	ATF128A	ATF128A Arabidops	c 490	18	3.7	154289	2	AC025577	AC025577 Homo sapi
c 418	18	3.7	122181	9	AF222866	AF222866 Homo sapi	c 491	18	3.7	154649	9	AC064854	AC064854 Homo sapi
c 419	18	3.7	122181	9	AC094197	AC094197 Rattus no	c 492	18	3.7	155022	2	AC108176	AC108176 Bos tauru
c 420	18	3.7	123241	2	AC022090	AC022090 Homo sapi	c 493	18	3.7	155297	2	AL162257	AL162257 Homo sapi
c 421	18	3.7	123331	9	AC005164	AC005164 Homo sapi	c 494	18	3.7	155349	2	AC022645	AC022645 Homo sapi
c 422	18	3.7	123837	9	AL645688	AL645688 Mus muscu	c 495	18	3.7	155380	2	AC022645	AC022645 Homo sapi
c 423	18	3.7	125837	9	AC016553	AC016553 Homo sapi	c 496	18	3.7	155380	2	AC022645	AC022645 Homo sapi
c 424	18	3.7	126301	9	HS708E5	HS708E5 Human DNA	c 497	18	3.7	155380	2	AC022645	AC022645 Homo sapi
c 425	18	3.7	126910	9	AC005856	AC005856 Homo sapi	c 498	18	3.7	155416	9	AL160286	AL160286 Human DNA
c 426	18	3.7	127174	2	AC094479	AC094479 Rattus no	c 499	18	3.7	155439	9	AC008626	AC008626 Homo sapi
c 427	18	3.7	128500	9	AC069426	AC069426 Homo sapi	c 500	18	3.7	155603	2	AC068517	AC068517 Homo sapi
c 428	18	3.7	128632	2	AC079622	AC079622 Homo sapi	c 501	18	3.7	155667	2	AC067911	AC067911 Homo sapi
c 429	18	3.7	129108	9	AC011482	AC011482 Homo sapi	c 502	18	3.7	155813	2	AC019350	AC019350 Homo sapi
c 430	18	3.7	129451	2	AC022411	AC022411 Homo sapi	c 503	18	3.7	155822	9	CNS01DUV	CNS01DUV Human chr
c 431	18	3.7	131570	2	AC026772	AC026772 Homo sapi	c 504	18	3.7	156184	2	AC041018	AC041018 Homo sapi
c 432	18	3.7	132114	9	AC026772	AC026772 Homo sapi	c 505	18	3.7	156335	2	AC008219	AC008219 Drosophil
c 433	18	3.7	134462	9	AC001231	AC001231 Genomic s	c 506	18	3.7	156385	2	AC012109	AC012109 Homo sapi
c 434	18	3.7	134924	2	AC104458	AC104458 Homo sapi	c 507	18	3.7	156623	2	AC095104	AC095104 Rattus no
c 435	18	3.7	134959	30	AL139218	AL139218 Human DNA	c 508	18	3.7	156750	2	AC006097	AC006097 Homo sapi
c 436	18	3.7	135439	2	AC080065	AC080065 Homo sapi	c 509	18	3.7	157750	2	AC011653	AC011653 Homo sapi
c 437	18	3.7	137152	2	AP004564	AP004564 Oryza sat	c 510	18	3.7	157832	2	AC011653	AC011653 Homo sapi
c 438	18	3.7	137454	2	AC069360	AC069360 Homo sapi	c 511	18	3.7	158151	9	CNS05TDT	CNS05TDT Human chr

c 512	18	3.7 158288	2	AC092770	AC092770 Homo sapi	585	18	3.7 170658	2	AC025838	AC025838 Homo sapi
c 513	18	3.7 158426	2	AC094845	AC094845 Rattus no	586	18	3.7 170761	9	CNS05TER	AL359240 Human chr
c 514	18	3.7 159612	30	AC069095	AC069095 Homo sapi	c 587	18	3.7 170846	9	AC068121	AC068121 Homo sapi
c 515	18	3.7 159759	2	AC096247	AC096247 Rattus no	c 588	18	3.7 170944	2	AC094217	AC094217 Rattus no
c 516	18	3.7 159769	9	AL353590	AL353590 Human DNA	c 589	18	3.7 170949	2	AL669850	AL669850 Mus muscu
c 517	18	3.7 159927	9	AC007131	AC007131 Homo sapi	c 590	18	3.7 170962	2	AL389927	AL389927 Homo sapi
c 518	18	3.7 160087	9	AC091352	AC091352 Rattus no	c 591	18	3.7 171069	2	AP003845	AP003845 Oryza sat
c 519	18	3.7 160237	2	AC016199	AC016199 Homo sapi	c 592	18	3.7 171697	2	AC093548	AC093548 Drosophil
c 520	18	3.7 160371	2	AL157876	AL157876 Homo sapi	c 593	18	3.7 171901	2	AC027240	AC027240 Homo sapi
c 521	18	3.7 160375	2	AL157876	AL157876 Homo sapi	c 594	18	3.7 171970	2	AP004764	AP004764 Oryza sat
c 522	18	3.7 160441	2	AL606724	AL606724 Mus muscu	c 595	18	3.7 172229	2	AC073300	AC073300 Homo sapi
c 523	18	3.7 160492	9	AP001884	AP001884 Homo sapi	c 596	18	3.7 172284	2	AC109482	AC109482 Homo sapi
c 524	18	3.7 160502	2	AC024039	AC024039 Homo sapi	c 597	18	3.7 172611	9	AC019129	AC019129 Homo sapi
c 525	18	3.7 160502	2	AC024039	AC024039 Homo sapi	c 598	18	3.7 172794	2	AC096201	AC096201 Rattus no
c 526	18	3.7 160701	2	AP004618	AP004618 Oryza sat	c 599	18	3.7 173508	9	AC096385	AC096385 Homo sapi
c 527	18	3.7 160708	2	AC068406	AC068406 Homo sapi	c 600	18	3.7 173644	8	AC093568	AC093568 Homo sapi
c 528	18	3.7 160815	2	AP001895	AP001895 Homo sapi	c 601	18	3.7 174631	2	AC069059	AC069059 Homo sapi
c 529	18	3.7 161422	2	AC108686	AC108686 Homo sapi	c 602	18	3.7 174642	2	AC091769	AC091769 Homo sapi
c 530	18	3.7 161549	9	AC073174	AC073174 Homo sapi	c 603	18	3.7 174963	2	AC022145	AC022145 Homo sapi
c 531	18	3.7 161757	2	AC044901	AC044901 Homo sapi	c 604	18	3.7 175160	9	CNS01DS9	AL121694 Human chr
c 532	18	3.7 161855	2	AC067769	AC067769 Homo sapi	c 605	18	3.7 175588	9	AC027119	AC027119 Homo sapi
c 533	18	3.7 161855	2	AC067769	AC067769 Homo sapi	c 606	18	3.7 175594	9	AL162503	AL162503 Human DNA
c 534	18	3.7 161871	10	AC005938	AC005938 Mus muscu	c 607	18	3.7 175750	2	AC026297	AC026297 Homo sapi
c 535	18	3.7 162023	9	AC084033	AC084033 Homo sapi	c 608	18	3.7 176034	9	CNS01DX5	AL139023 Human chr
c 536	18	3.7 162167	2	AC109638	AC109638 Homo sapi	c 609	18	3.7 176292	9	AP002407	AP002407 Homo sapi
c 537	18	3.7 162809	2	AC011379	AC011379 Homo sapi	c 610	18	3.7 176405	2	AC027399	AC027399 Homo sapi
c 538	18	3.7 163031	9	AC024947	AC024947 Homo sapi	c 611	18	3.7 176476	2	AC096094	AC096094 Rattus no
c 539	18	3.7 163102	9	AC093749	AC093749 Homo sapi	c 612	18	3.7 176689	9	AL162414	AL162414 Human DNA
c 540	18	3.7 163228	9	AC090939	AC090939 Homo sapi	c 613	18	3.7 177019	9	AC022833	AC022833 Homo sapi
c 541	18	3.7 163372	2	AC087744	AC087744 Homo sapi	c 614	18	3.7 177037	9	AL163542	AL163542 Human DNA
c 542	18	3.7 163673	2	AC027598	AC027598 Homo sapi	c 615	18	3.7 177051	2	AC011142	AC011142 Homo sapi
c 543	18	3.7 163712	2	AC009568	AC009568 Homo sapi	c 616	18	3.7 177112	9	AC002452	AC002452 Human BAC
c 544	18	3.7 163772	2	AC079985	AC079985 Homo sapi	c 617	18	3.7 177300	9	AC096741	AC096741 Homo sapi
c 545	18	3.7 163861	9	AL356772	AL356772 Human DNA	c 618	18	3.7 177312	9	AC079801	AC079801 Homo sapi
c 546	18	3.7 163889	2	AC004958	AC004958 Homo sapi	c 619	18	3.7 177987	9	AC107052	AC107052 Homo sapi
c 547	18	3.7 164308	2	AC011280	AC011280 Homo sapi	c 620	18	3.7 178188	2	AC087341	AC087341 Homo sapi
c 548	18	3.7 164364	2	AC098932	AC098932 Homo sapi	c 621	18	3.7 178640	2	AC069170	AC069170 Homo sapi
c 549	18	3.7 165105	2	AC024240	AC024240 Homo sapi	c 622	18	3.7 178984	2	AC084023	AC084023 Oryza sat
c 550	18	3.7 165110	9	AC068087	AC068087 Homo sapi	c 623	18	3.7 179002	2	AC068931	AC068931 Homo sapi
c 551	18	3.7 165199	9	AC003973	AC003973 Homo sapi	c 624	18	3.7 179209	2	AC091549	AC091549 Homo sapi
c 552	18	3.7 165199	9	AC003973	AC003973 Homo sapi	c 625	18	3.7 179258	2	AC103562	AC103562 Homo sapi
c 553	18	3.7 165208	2	AC098770	AC098770 Rattus no	c 626	18	3.7 179401	2	AC083805	AC083805 Homo sapi
c 554	18	3.7 165262	2	AP003181	AP003181 Homo sapi	c 627	18	3.7 179465	2	AC027024	AC027024 Homo sapi
c 555	18	3.7 165496	2	AC097242	AC097242 Homo sapi	c 628	18	3.7 179525	2	AC094760	AC094760 Rattus no
c 556	18	3.7 165904	2	AL158148	AL158148 Homo sapi	c 629	18	3.7 179528	9	AC026189	AC026189 Homo sapi
c 557	18	3.7 165933	2	AC109797	AC109797 Bos tauru	c 630	18	3.7 179669	2	AC109463	AC109463 Homo sapi
c 558	18	3.7 166163	2	AL627325	AL627325 Danio rer	c 631	18	3.7 179691	2	AL591644	AL591644 Homo sapi
c 559	18	3.7 166307	2	OSJN01012	OSJN01012 Oryza sat	c 632	18	3.7 179775	2	AC103452	AC103452 Rattus no
c 560	18	3.7 166357	9	AC026307	AC026307 Homo sapi	c 633	18	3.7 180189	9	AL365510	AL365510 Human DNA
c 561	18	3.7 166504	9	AC008275	AC008275 Homo sapi	c 634	18	3.7 180401	9	AC007489	AC007489 Homo sapi
c 562	18	3.7 166508	2	AL513343	AL513343 Homo sapi	c 635	18	3.7 180510	9	AC022415	AC022415 Homo sapi
c 563	18	3.7 166567	2	AC097102	AC097102 Homo sapi	c 636	18	3.7 180630	3	AC007975	AC007975 Drosophil
c 564	18	3.7 166715	9	HS30801	293403 Human genom	c 637	18	3.7 180713	2	AC106818	AC106818 Homo sapi
c 565	18	3.7 166772	2	CNS01RHA	AC098691 Homo sapi	c 638	18	3.7 181570	9	AC068738	AC068738 Homo sapi
c 566	18	3.7 167108	9	CNS01RHA	AL161666 Human chr	c 639	18	3.7 181745	9	AC008179	AC008179 Homo sapi
c 567	18	3.7 167174	9	AC013492	AC013492 Homo sapi	c 640	18	3.7 181904	2	AC027623	AC027623 Homo sapi
c 568	18	3.7 167437	2	AC033068	AC033068 Homo sapi	c 641	18	3.7 181997	2	AC055849	AC055849 Homo sapi
c 569	18	3.7 167462	2	AC103496	AC103496 Rattus no	c 642	18	3.7 182026	2	AC011313	AC011313 Homo sapi
c 570	18	3.7 167623	2	AC073450	AC073450 Homo sapi	c 643	18	3.7 182026	2	AC012569	AC012569 Homo sapi
c 571	18	3.7 167887	2	AC032606	AC032606 Homo sapi	c 644	18	3.7 182260	9	AC068700	AC068700 Homo sapi
c 572	18	3.7 168387	2	AC106308	AC106308 Rattus no	c 645	18	3.7 183290	9	AL161646	AL161646 Human DNA
c 573	18	3.7 169072	2	AC069525	AC069525 Homo sapi	c 646	18	3.7 183833	9	AL161646	AL161646 Human DNA
c 574	18	3.7 169075	2	AC093276	AC093276 Homo sapi	c 647	18	3.7 184023	2	AC018947	AC018947 Homo sapi
c 575	18	3.7 169273	2	AC078905	AC078905 Homo sapi	c 648	18	3.7 184327	2	AC069392	AC069392 Homo sapi
c 576	18	3.7 169566	2	AC073579	AC073579 Homo sapi	c 649	18	3.7 185087	2	AL627386	AL627386 Mus muscu
c 577	18	3.7 169730	3	AC010006	AC010006 Drosophil	c 650	18	3.7 185281	2	AC011214	AC011214 Homo sapi
c 578	18	3.7 169825	9	AC012652	AC012652 Homo sapi	c 651	18	3.7 185636	2	AC027109	AC027109 Homo sapi
c 579	18	3.7 169825	9	AC012652	AC012652 Homo sapi	c 652	18	3.7 185721	2	AC019108	AC019108 Homo sapi
c 580	18	3.7 169857	3	AC094703	AC094703 Rattus no	c 653	18	3.7 185921	2	AC023039	AC023039 Homo sapi
c 581	18	3.7 170057	3	AC009197	AC009197 Drosophil	c 654	18	3.7 185921	2	AC023039	AC023039 Homo sapi
c 582	18	3.7 170131	2	AC084379	AC084379 Homo sapi	c 655	18	3.7 186072	2	AC022372	AC022372 Homo sapi
c 583	18	3.7 170202	2	AL161934	AL161934 Homo sapi	c 656	18	3.7 186072	2	AC022372	AC022372 Homo sapi
c 584	18	3.7 170222	2	AL161934	AL161934 Homo sapi	c 657	18	3.7 186117	2	AC072046	AC072046 Homo sapi
	18	3.7 170460	3	AC010012	AC010012 Drosophil		18	3.7 186164	2	AC106411	AC106411 Rattus no

658	18	3.7	186159	2	AC093708	AC093708 Pan trogl	731	18	3.7	211999	2	AC087039	Mus muscu
659	18	3.7	186531	9	AC024606	AC024606 Homo sapi	732	18	3.7	212172	9	AC073531	Homo sapi
660	18	3.7	186660	2	AC026107	AC026107 Homo sapi	733	18	3.7	213379	2	AC094767	Rattus no
661	18	3.7	186865	2	AC095269	AC095269 Rattus no	734	18	3.7	213870	2	AC105204	Homo sapi
662	18	3.7	186881	2	AL646048	AL646048 Mus muscu	735	18	3.7	214765	2	AC106552	Rattus no
663	18	3.7	187266	2	AC073984	AC073984 Homo sapi	736	18	3.7	217532	2	AL645543	Mus muscu
664	18	3.7	187418	2	AC090580	AC090580 Homo sapi	737	18	3.7	218214	2	AL591417	Mus muscu
665	18	3.7	188205	9	AC003986	AC003986 Homo sapi	738	18	3.7	218774	2	AC079182	Mus muscu
666	18	3.7	188349	9	AL390197	AL390197 Human DNA	739	18	3.7	219635	2	AL390207	Homo sapi
667	18	3.7	188629	9	AC084365	AC084365 Homo sapi	740	18	3.7	223135	2	AL662802	Mus muscu
668	18	3.7	189006	2	AC103467	AC103467 Rattus no	741	18	3.7	223847	2	AL662802	Mus muscu
669	18	3.7	189621	2	AL589681	AL589681 Mus muscu	742	18	3.7	225054	3	AC108896	Bos tauru
670	18	3.7	189791	2	AC041047	AC041047 Homo sapi	743	18	3.7	225879	3	AE003776	Drosophill
671	18	3.7	189981	9	AC011629	AC011629 Homo sapi	744	18	3.7	235659	2	AC098876	Mus muscu
672	18	3.7	191161	9	AC018822	AC018822 Homo sapi	745	18	3.7	237530	2	AC022780	Mus muscu
673	18	3.7	191161	9	AC018503	AC018503 Homo sapi	746	18	3.7	238741	2	AC068894	Homo sapi
674	18	3.7	191284	2	AC109362	AC109362 Homo sapi	747	18	3.7	240065	2	AC093481	Mus muscu
675	18	3.7	191373	10	AP001295	AP001295 Mus muscu	748	18	3.7	244530	2	AC097044	Rattus no
676	18	3.7	191502	2	AC098735	AC098735 Mus muscu	749	18	3.7	245530	2	AC097044	Rattus no
677	18	3.7	191549	9	AC010582	AC010582 Homo sapi	750	18	3.7	247071	2	AC078805	Homo sapi
678	18	3.7	191962	2	AC048342	AC048342 Homo sapi	751	18	3.7	252022	9	AC002366	Human xp2
679	18	3.7	192027	2	AC067715	AC067715 Mus muscu	752	18	3.7	267547	3	AE003623	Drosophill
680	18	3.7	192296	9	AC009654	AC009654 Homo sapi	753	18	3.7	275272	2	AC097195	Rattus no
681	18	3.7	192780	2	AL162723	AL162723 Human DNA	754	18	3.7	284207	2	AC103329	Rattus no
682	18	3.7	192994	2	AC011978	AC011978 Homo sapi	755	18	3.7	285431	2	PFMAL13P4	AL049181 Plasmodiu
683	18	3.7	193212	9	AC007405	AC007405 Homo sapi	756	18	3.7	298908	2	AC019010	Homo sapi
684	18	3.7	193309	2	AL6772051	AL6772051 Mus muscu	757	18	3.7	299300	2	AC006882	Caenorhab
685	18	3.7	193587	2	AC009268	AC009268 Homo sapi	758	18	3.7	299300	2	AC006881	Caenorhab
686	18	3.7	193632	9	AC093649	AC093649 Homo sapi	759	18	3.7	303396	2	AC092975	Homo sapi
687	18	3.7	193713	2	AC093658	AC093658 Homo sapi	760	18	3.7	308600	2	AC033053	Homo sapi
688	18	3.7	194034	9	AL592148	AL592148 Human DNA	761	18	3.7	309838	3	AE003474	AE003474 Drosophill
689	18	3.7	194332	2	AC095507	AC095507 Rattus no	762	18	3.7	314150	1	CJ11168X1	AL139074 Campyloba
690	18	3.7	194575	2	AC023140	AC023140 Homo sapi	763	18	3.7	328215	2	AC107462	Homo sapi
691	18	3.7	194622	2	AC098597	AC098597 Homo sapi	764	18	3.7	331909	2	AC060230	Homo sapi
692	18	3.7	194733	2	AC025744	AC025744 Homo sapi	765	18	3.7	349980	6	AX282123	Sequence
693	18	3.7	194777	9	CSN06C81	CSN06C81 Mus muscu	766	18	3.7	349980	6	AX282715	Sequence
694	18	3.7	195007	9	AC099557	AC099557 Homo sapi	767	18	3.5	349980	6	A89380	Sequence 15
695	18	3.7	196355	9	AC099557	AC099557 Homo sapi	768	17	3.5	17	6	A89380	Sequence 15
696	18	3.7	196431	2	CSN01D05	CSN01D05 Homo sapi	769	17	3.5	144	11	AX199646	Sequence
697	18	3.7	196550	9	AC020734	AC020734 Homo sapi	770	17	3.5	144	11	G44141	G44141 WIAT-3781-S
698	18	3.7	196946	2	AL645470	AL645470 Mus muscu	771	17	3.5	280	3	DPVPA37M1	X92832 D.pini sate
699	18	3.7	197650	2	AL391243	AL391243 Homo sapi	772	17	3.5	311	9	AF047279	Homo sapi
700	18	3.7	197828	2	AC034169	AC034169 Homo sapi	773	17	3.5	311	9	AF052775	Homo sapi
701	18	3.7	197850	2	AC048348	AC048348 Homo sapi	774	17	3.5	311	9	AF052776	Homo sapi
702	18	3.7	198088	2	AC078957	AC078957 Homo sapi	775	17	3.5	313	1	AF052778	Homo sapi
703	18	3.7	198233	9	AL669895	AL669895 Mus muscu	776	17	3.5	392	6	U93694	Borrelia bu
704	18	3.7	198431	9	AC109994	AC109994 Homo sapi	777	17	3.5	406	10	PHDLTRC	AX310126 Sequence
705	18	3.7	198480	2	AC025077	AC025077 Homo sapi	778	17	3.5	437	6	AX340651	Sequence
706	18	3.7	198726	2	AC018986	AC018986 Homo sapi	779	17	3.5	457	3	DMU24572	U24572 Drosophila
707	18	3.7	199420	9	CSN01D0V	CSN01D0V Human chr	780	17	3.5	464	6	E64398	E64398 Peptide hav
708	18	3.7	199812	9	AC023480	AC023480 Homo sapi	781	17	3.5	464	6	E64398	E64398 Peptide hav
709	18	3.7	200439	2	AC079007	AC079007 Homo sapi	782	17	3.5	470	11	HS65516S	AB015335 Homo sapi
710	18	3.7	200839	2	AC067865	AC067865 Homo sapi	783	17	3.5	500	11	G33279	AX10747 Sequence
711	18	3.7	201132	2	AC099614	AC099614 Mus muscu	784	17	3.5	500	11	G33279	G33279 human SFS S
712	18	3.7	201176	2	AC092058	AC092058 Homo sapi	785	17	3.5	653	9	AF330205	AF330205 Homo sapi
713	18	3.7	201502	9	AC013738	AC013738 Homo sapi	786	17	3.5	668	8	AF157179	AF157179 Chaetocla
714	18	3.7	202375	2	AC109798	AC109798 Bos tauru	787	17	3.5	700	9	HSXNP21	U97092 Homo sapien
715	18	3.7	203020	2	AC092832	AC092832 Homo sapi	788	17	3.5	717	14	CA1279178	AB079255 Coxsackie
716	18	3.7	204310	2	AC017094	AC017094 Homo sapi	789	17	3.5	758	8	AB079255	AB079255 Coxsackie
717	18	3.7	205332	10	AL596265	AL596265 Mouse DNA	790	17	3.5	758	8	AB079255	AB079255 Coxsackie
718	18	3.7	205987	2	AC087488	AC087488 Homo sapi	791	17	3.5	774	14	CA1279177	AB040439 Medicago
719	18	3.7	205987	2	AL512273	AL512273 Homo sapi	792	17	3.5	815	8	AB040439	AB040439 Homo sapi
720	18	3.7	207263	2	AC100750	AC100750 Mus muscu	793	17	3.5	843	9	AF213434	AF213434 Homo sapi
721	18	3.7	208410	2	AL670360	AL670360 Mus muscu	794	17	3.5	845	6	I07694	I07694 Sequence 17
722	18	3.7	208506	2	AP003530	AP003530 Homo sapi	795	17	3.5	895	1	RP282357	Z82357 R.prowazeki
723	18	3.7	209287	9	AC012077	AC012077 Homo sapi	796	17	3.5	933	10	AY073111	AY073111 Mus muscu
724	18	3.7	209925	9	AF002223	AF002223 Human gen	797	17	3.5	937	14	S77150	S77150 [3' LTR] [d
725	18	3.7	210115	9	AL442127	AL442127 Human DNA	798	17	3.5	962	1	BBU04282	U04282 Borrelia bu
726	18	3.7	211230	2	AC012540	AC012540 Mus muscu	800	17	3.5	964	5	AF265379	AF265379 Ophlocara
727	18	3.7	211301	2	AC100752	AC100752 Mus muscu	801	17	3.5	1011	6	AX224521	AX224521 Sequence
728	18	3.7	211305	2	AC099975	AC099975 Homo sapi	802	17	3.5				
729	18	3.7	211458	2	AC095183	AC095183 Rattus no	803	17	3.5				
730	18	3.7	211610	2	AL591165	AL591165 Mus muscu	803	17	3.5				

804	17	3.5	1011	6	I26671	I26671 Sequence 3	c 877	17	3.5	4680	1	VEIMCDA	I22208 Veillonella
c 805	17	3.5	1027	1	PMDFRVI	Z86002 P.mirabilis	c 878	17	3.5	4680	1	VPMCOADCA	Z24754 V.parvula m
806	17	3.5	1055	2	AC006711	AC006711 Caenorhab	c 879	17	3.5	4967	6	AX285153	AX285153 Sequence
807	17	3.5	1056	8	XL066288	U66288 Xenopus lae	880	17	3.5	5019	6	AX106914	AX106914 Sequence
c 808	17	3.5	1099	8	GSU30348	U30348 Gracilariop	c 881	17	3.5	5034	9	AB051469	AB051469 Homo sapi
c 809	17	3.5	1126	8	AF036339	AF036339 Euphorbia	882	17	3.5	5170	3	AF042826	AF042826 Toxoplas
c 810	17	3.5	1150	4	BTAL8308	Y18308 Bos taurus	883	17	3.5	5649	3	AF317883	AF317883 Synechoco
c 811	17	3.5	1214	1	AF378156	AF378156 Mycoplas	c 884	17	3.5	5800	9	AB051474	AB051474 Homo sapi
c 812	17	3.5	1237	3	NFU43127	U43127 Naegleria f	885	17	3.5	6248	9	D86984	D86984 Human mRNA
c 813	17	3.5	1448	6	I20877	I20877 Sequence 1	886	17	3.5	6446	6	AX251082	AX251082 Sequence
c 814	17	3.5	1565	14	AF251407	AF251407 Influenza	c 887	17	3.5	6556	3	AF080447	AF080447 Plasmodiu
c 815	17	3.5	1565	14	AF251423	AF251423 Influenza	c 888	17	3.5	6558	5	AB046524	AB046524 Gallus ga
816	17	3.5	1565	14	FLANJ8	M76606 Influenza A	c 889	17	3.5	6536	6	AX345693	AX345693 Sequence
817	17	3.5	1565	14	FLANPAG	M63754 Influenza A	c 890	17	3.5	6639	10	RNO297736	RNO297736
818	17	3.5	1565	14	FLANPAP	M63762 Influenza A	c 891	17	3.5	6730	2	AC020058	AC020058
819	17	3.5	1565	14	FLASHR2NP	M22570 Influenza A	c 892	17	3.5	6751	3	CELMYOD	CELMYOD
820	17	3.5	1565	14	FLASRWI67	M76607 Influenza A	c 893	17	3.5	6886	9	BSA271220	BSA271220
c 821	17	3.5	1629	9	BC020762	BC020762 Homo sapi	c 894	17	3.5	6897	3	DMRT412G	DMRT412G
c 822	17	3.5	1722	9	HSMB000473	AL050177 Homo sapi	895	17	3.5	6900	1	AF288402	AF288402
c 823	17	3.5	1763	3	AF140021	AF140021 Heliothis	896	17	3.5	7814	1	HSU28154	HSU28154
c 824	17	3.5	1763	3	HVU23506	U23506 Heliothis v	897	17	3.5	8389	4	BTATJ5638	BTATJ5638
c 825	17	3.5	1776	6	I20878	I20878 Sequence 3	c 898	17	3.5	8890	9	BSA297549	BSA297549
826	17	3.5	1807	8	AF2471134	AF2471134 Limnanthe	c 899	17	3.5	9021	9	AC025816	AC025816
c 827	17	3.5	1812	9	AF02416511	BC016511 Homo sapi	c 900	17	3.5	9133	8	EGRCPPSAAB	EGRCPPSAAB
c 828	17	3.5	1843	9	AK024886	AK024886 Homo sapi	c 901	17	3.5	9393	2	AC012703	AC012703
c 829	17	3.5	1877	8	SCYNL092W	Z71368 S.cerevisia	902	17	3.5	9331	1	AE001299	AE001299
830	17	3.5	1883	9	HUMFBRB	J00129 Human fibri	c 903	17	3.5	10050	1	AF154675	AF154675
831	17	3.5	1958	9	AK027797	AK027797 Homo sapi	c 904	17	3.5	10223	1	AE003948	AE003948
c 832	17	3.5	2013	8	GMLBC3N	X15061 Glycine max	905	17	3.5	10879	1	AF099088	AF099088
c 833	17	3.5	2036	8	SCYGL250W	Z72772 S.cerevisia	906	17	3.5	10901	2	AC020044	AC020044
c 834	17	3.5	2174	1	AF378153	AF378153 Mycoplas	907	17	3.5	10994	5	GGA308518	GGA308518
c 835	17	3.5	2174	1	AF378154	AF378154 Mycoplas	908	17	3.5	11010	1	AE006246	AE006246
c 836	17	3.5	2174	1	AF378155	AF378155 Mycoplas	909	17	3.5	11130	1	AF312861	AF312861
c 837	17	3.5	2174	1	AF378158	AF378158 Mycoplas	c 910	17	3.5	11321	1	AE002671	AE002671
c 838	17	3.5	2174	1	AF378159	AF378159 Mycoplas	911	17	3.5	11632	1	AE002254	AE002254
c 839	17	3.5	2210	9	AB056838	AB056838 Macaca fa	c 912	17	3.5	11656	1	AE004228	AE004228
c 840	17	3.5	2245	1	AB045340	AB045340 Staphyloc	913	17	3.5	12580	1	AE000910	AE000910
c 841	17	3.5	2263	1	AB038464	AB038464 Enterococ	c 914	17	3.5	12663	1	AE001130	AE001130
c 842	17	3.5	2274	10	MMU3066625	AJ336625 Mus muscu	c 915	17	3.5	13086	2	AC014193	AC014193
c 843	17	3.5	2296	6	AX336447	AX336447 Sequence	c 916	17	3.5	13299	1	U32702	U32702
c 844	17	3.5	2296	6	HSRNLALAGA	X86401 H.sapiens m	c 917	17	3.5	13458	1	AE007614	AE007614
c 845	17	3.5	2319	3	AY069171	AY069171 Drosophi	c 918	17	3.5	13865	3	DMU23836	DMU23836
c 846	17	3.5	2330	9	S68805	S68805 L-arginine:	c 919	17	3.5	14261	8	SCTRNAORE	SCTRNAORE
c 847	17	3.5	2351	9	BC004141	BC004141 Homo sapi	c 920	17	3.5	14368	9	AL391602	AL391602
c 848	17	3.5	2371	9	HSMDINT	Y13187 Homo sapien	c 921	17	3.5	14947	2	AC014403	AC014403
c 849	17	3.5	2431	3	AY069133	AY069133 Drosophi	c 922	17	3.5	15909	3	AB048355	AB048355
c 850	17	3.5	2439	1	AF162991	AF162991 Mycoplas	c 923	17	3.5	16157	1	AE001670	AE001670
c 851	17	3.5	2454	9	AF284766	AF284766 Homo sapi	c 924	17	3.5	16435	1	AE001125	AE001125
c 852	17	3.5	2472	10	AF052042	AF052042 Rattus no	c 925	17	3.5	16648	9	BSA278717	BSA278717
c 853	17	3.5	2583	3	U91833	U91833 Caenorhabdi	c 926	17	3.5	16754	4	AF217811	AF217811
c 854	17	3.5	2583	10	AB015723	AB015723 Rattus no	c 927	17	3.5	17286	2	AC109930	AC109930
c 855	17	3.5	2654	3	DIDG17A	M18106 Dictyosteli	c 928	17	3.5	17822	3	AE002754	AE002754
c 856	17	3.5	2654	9	HSP113122	AJ001697 Homo sapi	c 929	17	3.5	18722	4	BTAT37934	BTAT37934
c 857	17	3.5	2664	2	AC014518	AC014518 Drosophi	c 930	17	3.5	19507	2	AC110133	AC110133
c 858	17	3.5	2776	1	AF378157	AF378157 Mycoplas	c 931	17	3.5	19510	3	CEF32H5	CEF32H5
c 859	17	3.5	2821	9	AK022715	AK022715 Homo sapi	c 932	17	3.5	21668	2	AC107478	AC107478
c 860	17	3.5	2825	9	AK000757	AK000757 Homo sapi	c 933	17	3.5	21698	3	AF026204	AF026204
c 861	17	3.5	2831	9	AK000757	AK001698 Homo sapi	c 934	17	3.5	22004	2	AC017362	AC017362
c 862	17	3.5	2831	9	HSP113161	AX106916 Sequence	c 935	17	3.5	22973	3	AF023458	AF023458
c 863	17	3.5	2979	6	SCYGL249W	W72771 S.cerevisia	c 936	17	3.5	23055	2	AC102486	AC102486
c 864	17	3.5	3017	8	SCYGL249W	W72771 S.cerevisia	c 937	17	3.5	23135	3	AC024766	AC024766
c 865	17	3.5	3024	2	AC012773	L01498 Drosophila	c 938	17	3.5	23797	8	AP004258	AP004258
c 866	17	3.5	3066	3	DROHSC3A	AJ001696 Homo sapi	c 939	17	3.5	24130	2	AC018303	AC018303
c 867	17	3.5	3143	8	HSP113711	AJ001696 Homo sapi	c 940	17	3.5	24177	1	AE000785	AE000785
c 868	17	3.5	3350	8	OSGOS9G	X51909 O.sativa (	c 941	17	3.5	24629	3	CER07D5	CER07D5
c 869	17	3.5	3365	9	AK056457	AK056457 Homo sapi	c 942	17	3.5	25065	9	CAE074098	CAE074098
c 870	17	3.5	3644	9	AF284765	AF284765 Homo sapi	c 943	17	3.5	25347	3	CEC18D4	CEC18D4
c 871	17	3.5	3656	9	HSL81728	L81728 Homo sapien	c 944	17	3.5	25426	3	CELY39A3A	CELY39A3A
c 872	17	3.5	3780	3	AF238312	AF238312 Dictyoste	c 945	17	3.5	25482	2	AC106366	AC106366
c 873	17	3.5	3876	5	S80986	S80986 svp[40]-svp	c 946	17	3.5	25520	3	AF099918	AF099918
c 874	17	3.5	3879	3	AF080446	AF080446 Plasmodiu	c 947	17	3.5	26853	2	AC108942	AC108942
c 875	17	3.5	3942	3	PBE298080	AJ298080 Plasmodiu	c 948	17	3.5	27368	1	CER008D7	CER008D7
c 876	17	3.5	4411	8	SCSLNI	AF212167 Limulus p	c 949	17	3.5	28601	1	AE000784	AE000784
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BASE COUNT		159 a	79 c	95 g	156 t
ORIGIN					
Query Match 100.0%; Score 489; DB 6; Length 489;					
Best Local Similarity 100.0%; Pred. No. 2.6e-236;					
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	ATGAGAATTTTCGAACACACATTTGAGAAGTATTTCCATCCAGTGGCTACTTCTGTTTACTT	60		
Db	1	ATGAGAATTTTCGAACACACATTTGAGAAGTATTTCCATCCAGTGGCTACTTCTGTTTACTT	60		
Qy	61	CTAAACAGTCAATTTCTTAACCTGAAGCTGGCAATTCATGCTTTCAATTTTGGGCTGTTTCACT	120		
Db	61	CTAAACAGTCAATTTCTTAACCTGAAGCTGGCAATTCATGCTTTCAATTTTGGGCTGTTTCACT	120		
Qy	121	GCAGGGCTTCTTAAACAGAGCCAACTGGGTGAATGTAAATAGTGAATTAAGTGAATTTGAAAAAAT	180		
Db	121	GCAGGGCTTCTTAAACAGAGCCAACTGGGTGAATGTAAATAGTGAATTAAGTGAATTTGAAAAAAT	180		
Qy	181	GAAGATCTTATTTCAATCTATGTCATATTTGATGCTACTTTTATATACGGAAGTGTATTTTCAAC	240		
Db	181	GAAGATCTTATTTCAATCTATGTCATATTTGATGCTACTTTTATATACGGAAGTGTATTTTCAAC	240		
Qy	241	CCAGTTCGAAAAGTAAACAGCAATGAAGTCTCTTTGGAGTTTACAAGTTATTTTCACTT	300		
Db	241	CCAGTTCGAAAAGTAAACAGCAATGAAGTCTCTTTGGAGTTTACAAGTTATTTTCACTT	300		
Qy	301	GAGTCGGAGATGCAAGTATTTTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATG	360		
Db	301	GAGTCGGAGATGCAAGTATTTTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATG	360		
Qy	361	AGTTTGTCTTCTTAATGGGAATGTAACAGCAATCTGGATCGCAAGAAATGTGAGGAATGGAG	420		
Db	361	AGTTTGTCTTCTTAATGGGAATGTAACAGCAATCTGGATCGCAAGAAATGTGAGGAATGGAG	420		
Qy	421	GAAGAAATATTAAGAAATTTTTCGAGAGTATTTGTCATATTTGTCATATTTGTCATATTTGTCAT	480		
Db	421	GAAGAAATATTAAGAAATTTTTCGAGAGTATTTGTCATATTTGTCATATTTGTCATATTTGTCAT	480		
Qy	481	ACTTCTTGA 489			
Db	481	ACTTCTTGA 489			
RESULT 2					
LOCUS AR024349					
DEFINITION Sequence 2 from patent US 5795966.					
ACCESSION AR024349					
VERSION AR024349.1 GI:3977643					
KEYWORDS					
SOURCE Unknown.					
ORGANISM Unknown.					
REFERENCE 1 (bases 1 to 489)					
AUTHORS Grabstein, K.H., Pettit, D.K. and Paxton, R.J.					
TITLE Antagonists of interleukin-15					
JOURNAL Patent: US 5795966-A 2 18-AUG-1998;					
FEATURES					
Location/Qualifiers					
source 1. 489					
/organism="unknown"					
BASE COUNT 159 a 79 c 95 g 156 t					
ORIGIN					
Query Match 100.0%; Score 489; DB 6; Length 489;					
Best Local Similarity 100.0%; Pred. No. 2.6e-236;					
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	ATGAGAATTTTCGAACACACATTTGAGAAGTATTTCCATCCAGTGGCTACTTCTGTTTACTT	60		
Db	1	ATGAGAATTTTCGAACACACATTTGAGAAGTATTTCCATCCAGTGGCTACTTCTGTTTACTT	60		

BASE COUNT		159 a	79 c	95 g	156 t
ORIGIN					
Query Match 100.0%; Score 489; DB 6; Length 489;					
Best Local Similarity 100.0%; Pred. No. 2.6e-236;					
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	ATGAGAATTTTCGAACACACATTTGAGAAGTATTTCCATCCAGTGGCTACTTCTGTTTACTT	60		
Db	1	ATGAGAATTTTCGAACACACATTTGAGAAGTATTTCCATCCAGTGGCTACTTCTGTTTACTT	60		

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QY 61 CTAACAGTCATTTCTAACTGAAGCTGGCATTCTATGCTCTTCATTTTGGGCTGTTTCAGT 120
DB 61 CTAACAGTCATTTCTAACTGAAGCTGGCATTCTATGCTCTTCATTTTGGGCTGTTTCAGT 120
QY 121 GCAGGGCTTCTAAACAGAGCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAAATT 180
DB 121 GCAGGGCTTCTAAACAGAGCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAAATT 180
QY 181 GAAGATCTTATTCATCTATGCATATTGATGCTACTTTATATACGGAAGTGATGTTTCAC 240
DB 181 GAAGATCTTATTCATCTATGCATATTGATGCTACTTTATATACGGAAGTGATGTTTCAC 240
QY 241 CCCAGTTGCAAAAGTAACAGCAATGAAGTGCTTCTCTGGAGTTACAAAGTTATTTCACTT 300
DB 241 CCCAGTTGCAAAAGTAACAGCAATGAAGTGCTTCTCTGGAGTTACAAAGTTATTTCACTT 300
QY 301 GAGTCCCGAGATGCAAGTATTCATGATACAGTAGAGAAATCTGATCATCTCTAGCAAAAC 360
DB 301 GAGTCCCGAGATGCAAGTATTCATGATACAGTAGAGAAATCTGATCATCTCTAGCAAAAC 360
QY 361 AGTTTGCTTCTTAATGGGAATGTAACAGAATCTGGATGCAAGAATCTGAGGAACCTGGAG 420
DB 361 AGTTTGCTTCTTAATGGGAATGTAACAGAATCTGGATGCAAGAATCTGAGGAACCTGGAG 420
QY 421 GAAAAAATATTAAGAATTTTTCAGAGATTTTGTACATATTGTCCAAATGTTTCATCAAC 480
DB 421 GAAAAAATATTAAGAATTTTTCAGAGATTTTGTACATATTGTCCAAATGTTTCATCAAC 480
QY 481 ACTTCTTGA 489
DB 481 ACTTCTTGA 489

RESULT 3
AR070281
LOCUS AR070281 489 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 1 from patent US 5892001.
ACCESSION AR070281
VERSION AR070281.1 GI:7221169
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 489)
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE Epithelium-derived T-cell factor antibodies
JOURNAL Patent: US 5892001-A 1 06-APR-1999;
FEATURES
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BASE COUNT 159 a 79 c 95 g 156 t
ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 2.6e-236;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACCAACATTTGAGAAGTATTTCCATCCAGTGCCTCATTTTGGGCTGTTTCAGT 120
DB 1 ATGAGAAATTCGAAACCAACATTTGAGAAGTATTTCCATCCAGTGCCTCATTTTGGGCTGTTTCAGT 120
QY 61 CTAACAGTCATTTCTAACTGAAGCTGGCATTCTATGCTCTTCATTTTGGGCTGTTTCAGT 180
DB 61 CTAACAGTCATTTCTAACTGAAGCTGGCATTCTATGCTCTTCATTTTGGGCTGTTTCAGT 180
QY 121 GCAGGGCTTCTAAACAGAGCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAAATT 180
DB 121 GCAGGGCTTCTAAACAGAGCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAAATT 180
QY 181 GAAGATCTTATTCATCTATGCATATTGATGCTACTTTATATACGGAAGTGATGTTTCAC 240
DB 181 GAAGATCTTATTCATCTATGCATATTGATGCTACTTTATATACGGAAGTGATGTTTCAC 240
QY 241 CCCAGTTGCAAAAGTAACAGCAATGAAGTGCTTCTCTGGAGTTACAAAGTTATTTCACTT 300
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QY 301 GAGTCCCGAGATGCAAGTATTCATGATACAGTAGAGAAATCTGATCATCTCTAGCAAAAC 360
DB 301 GAGTCCCGAGATGCAAGTATTCATGATACAGTAGAGAAATCTGATCATCTCTAGCAAAAC 360
QY 361 AGTTTGCTTCTTAATGGGAATGTAACAGAATCTGGATGCAAGAATCTGAGGAACCTGGAG 420
DB 361 AGTTTGCTTCTTAATGGGAATGTAACAGAATCTGGATGCAAGAATCTGAGGAACCTGGAG 420
QY 421 GAAAAAATATTAAGAATTTTTCAGAGATTTTGTACATATTGTCCAAATGTTTCATCAAC 480
DB 421 GAAAAAATATTAAGAATTTTTCAGAGATTTTGTACATATTGTCCAAATGTTTCATCAAC 480
QY 481 ACTTCTTGA 489
DB 481 ACTTCTTGA 489

RESULT 4
AR085740
LOCUS AR085740 489 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1 from patent US 5985262.
ACCESSION AR085740
VERSION AR085740.1 GI:10012506
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 489)
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE Method of treatment with epithelium derived T-cell factor
JOURNAL Patent: US 5985262-A 1 16-NOV-1999;
FEATURES
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BASE COUNT 159 a 79 c 95 g 156 t
ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 2.6e-236;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACCAACATTTGAGAAGTATTTCCATCCAGTGCCTCATTTTGGGCTGTTTCAGT 60
DB 1 ATGAGAAATTCGAAACCAACATTTGAGAAGTATTTCCATCCAGTGCCTCATTTTGGGCTGTTTCAGT 60
QY 61 CTAACAGTCATTTCTAACTGAAGCTGGCATTCTATGCTCTTCATTTTGGGCTGTTTCAGT 120
DB 61 CTAACAGTCATTTCTAACTGAAGCTGGCATTCTATGCTCTTCATTTTGGGCTGTTTCAGT 120
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DB 121 GCAGGGCTTCTAAACAGAGCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAAATT 180
QY 181 GAAGATCTTATTCATCTATGCATATTGATGCTACTTTATATACGGAAGTGATGTTTCAC 240
DB 181 GAAGATCTTATTCATCTATGCATATTGATGCTACTTTATATACGGAAGTGATGTTTCAC 240
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QY 301 GAGTCCCGAGATGCAAGTATTCATCATACAGTAGAGAAATCTGATCATCTCTAGCAAAAC 360
DB 301 GAGTCCCGAGATGCAAGTATTCATCATACAGTAGAGAAATCTGATCATCTCTAGCAAAAC 360
QY 361 AGTTTGCTTCTTAATGGGAATGTAACAGAATCTGGATGCAAGAATCTGAGGAACCTGGAG 420
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DB 181 GAAGATCTTATTCATCTATGCATATTGATGCTACTTTATATACGGAAGTGATGTTTCAC 240
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QY 301 GAGTCCCGAGATGCAAGTATTCATGATACAGTAGAGAAATCTGATCATCTCTAGCAAAAC 360
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QY 361 AGTTTGCTTCTTAATGGGAATGTAACAGAATCTGGATGCAAGAATCTGAGGAACCTGGAG 420
DB 361 AGTTTGCTTCTTAATGGGAATGTAACAGAATCTGGATGCAAGAATCTGAGGAACCTGGAG 420
QY 421 GAAAAAATATTAAGAATTTTTCAGAGATTTTGTACATATTGTCCAAATGTTTCATCAAC 480
DB 421 GAAAAAATATTAAGAATTTTTCAGAGATTTTGTACATATTGTCCAAATGTTTCATCAAC 480
QY 481 ACTTCTTGA 489
DB 481 ACTTCTTGA 489

RESULT 4
AR085740
LOCUS AR085740 489 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1 from patent US 5985262.
ACCESSION AR085740
VERSION AR085740.1 GI:10012506
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 489)
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE Method of treatment with epithelium derived T-cell factor
JOURNAL Patent: US 5985262-A 1 16-NOV-1999;
FEATURES
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        /organism="unknown"
BASE COUNT 159 a 79 c 95 g 156 t
ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 2.6e-236;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACCAACATTTGAGAAGTATTTCCATCCAGTGCCTCATTTTGGGCTGTTTCAGT 60
DB 1 ATGAGAAATTCGAAACCAACATTTGAGAAGTATTTCCATCCAGTGCCTCATTTTGGGCTGTTTCAGT 60
QY 61 CTAACAGTCATTTCTAACTGAAGCTGGCATTCTATGCTCTTCATTTTGGGCTGTTTCAGT 120
DB 61 CTAACAGTCATTTCTAACTGAAGCTGGCATTCTATGCTCTTCATTTTGGGCTGTTTCAGT 120
QY 121 GCAGGGCTTCTAAACAGAGCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAAATT 180
DB 121 GCAGGGCTTCTAAACAGAGCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAAATT 180
QY 181 GAAGATCTTATTCATCTATGCATATTGATGCTACTTTATATACGGAAGTGATGTTTCAC 240
DB 181 GAAGATCTTATTCATCTATGCATATTGATGCTACTTTATATACGGAAGTGATGTTTCAC 240
QY 241 CCCAGTTGCAAAAGTAACAGCAATGAAGTGCTTCTCTGGAGTTACAAAGTTATTTCACTT 300
DB 241 CCCAGTTGCAAAAGTAACAGCAATGAAGTGCTTCTCTGGAGTTACAAAGTTATTTCACTT 300
QY 301 GAGTCCCGAGATGCAAGTATTCATCATACAGTAGAGAAATCTGATCATCTCTAGCAAAAC 360
DB 301 GAGTCCCGAGATGCAAGTATTCATCATACAGTAGAGAAATCTGATCATCTCTAGCAAAAC 360
QY 361 AGTTTGCTTCTTAATGGGAATGTAACAGAATCTGGATGCAAGAATCTGAGGAACCTGGAG 420
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Db 361 AGTTGCTCTTAATGGGAATGTAACAGAACTGGATGCAAGAATGTGAGGAACCTGGAG 420
Qy 421 GAAAAAATATTAAGAAATTTTTCGACAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480
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Db 421 GAAAAAATATTAAGAAATTTTTCGACAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480
Qy 481 ACTTCTTGA 489
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Db 481 ACTTCTTGA 489

RESULT 5
AR122046
LOCUS AR122046 489 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 2 from patent US 6165466.
ACCESSION AR122046
VERSION AR122046.1 GI:14106363
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 489)
AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.
TITLE Antagonists of interleukin-15
JOURNAL Patent: US 6165466-A 2 26-DEC-2000;
FEATURES
source Location/Qualifiers
BASE COUNT 159 a 79 c 95 g 156 t
ORIGIN
Query Match 100.0%; Score 489; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 2.6e-236;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAATTTTCGAACACACATTTGAGAAGTATTTCATCCAGTGCTACTTGTGTTTACTT 60
Db 1 ATGAGAATTTTCGAACACACATTTGAGAAGTATTTCATCCAGTGCTACTTGTGTTTACTT 60
Qy 61 CTAACAGTCATTTCTTAACCTGAAGCTGGCATTCATGCTCTTCAATTTTGGGCTGTTTCAGT 120
Db 61 CTAACAGTCATTTCTTAACCTGAAGCTGGCATTCATGCTCTTCAATTTTGGGCTGTTTCAGT 120
Qy 121 GCAGGGCTTCTTAACACAGAGCAACTGGTGAATGTAATGAATGATTAAGTGAATTTGAAAAAAT 180
Db 121 GCAGGGCTTCTTAACACAGAGCAACTGGTGAATGTAATGAATGATTAAGTGAATTTGAAAAAAT 180
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Db 181 GAAGATCTTATTCATCTATGCATATTGATGCTACTTTATATACGGAAGTGAATGTTTCAC 240
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Db 241 CCCAGTTGCAAAAGTAACAGCAATGAAGTCTTCTCTTGGAGTTACAAGTTATTTCAC 300
Qy 301 GAGTCCGGAGATGCAAGTATTTCATGATACAGTAGAAAAATCTGATCATCTAGCAAAACAAC 360
Db 301 GAGTCCGGAGATGCAAGTATTTCATGATACAGTAGAAAAATCTGATCATCTAGCAAAACAAC 360
Qy 361 AGTTTGTCTTCTTAATGGGAATGTAACAGATCTGGATGCAAGAATGTGAGGAACCTGGAG 420
Db 361 AGTTTGTCTTCTTAATGGGAATGTAACAGATCTGGATGCAAGAATGTGAGGAACCTGGAG 420
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Db 421 GAAAAAATATTAAGAAATTTTTCGACAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480
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Db 481 ACTTCTTGA 489

RESULT 7
AR125105
LOCUS AR125105 489 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 2 from patent US 6177079.
ACCESSION AR125105
VERSION AR125105.1 GI:14111167
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 489)
AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.
TITLE Antagonists of interleukin-15
JOURNAL Patent: US 6168783-A 2 02-JAN-2001;
FEATURES
source Location/Qualifiers
BASE COUNT 159 a 79 c 95 g 156 t
ORIGIN
Query Match 100.0%; Score 489; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 2.6e-236;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAATTTTCGAACACACATTTGAGAAGTATTTCATCCAGTGCTACTTGTGTTTACTT 60
Db 1 ATGAGAATTTTCGAACACACATTTGAGAAGTATTTCATCCAGTGCTACTTGTGTTTACTT 60
Qy 61 CTAACAGTCATTTCTTAACCTGAAGCTGGCATTCATGCTCTTCAATTTTGGGCTGTTTCAGT 120
Db 61 CTAACAGTCATTTCTTAACCTGAAGCTGGCATTCATGCTCTTCAATTTTGGGCTGTTTCAGT 120
Qy 121 GCAGGGCTTCTTAACACAGAGCAACTGGTGAATGTAATGAATGATTAAGTGAATTTGAAAAAAT 180
Db 121 GCAGGGCTTCTTAACACAGAGCAACTGGTGAATGTAATGAATGATTAAGTGAATTTGAAAAAAT 180
Qy 181 GAAGATCTTATTCATCTATGCATATTGATGCTACTTTATATACGGAAGTGAATGTTTCAC 240
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Qy 361 AGTTTGTCTTCTTAATGGGAATGTAACAGATCTGGATGCAAGAATGTGAGGAACCTGGAG 420
Db 361 AGTTTGTCTTCTTAATGGGAATGTAACAGATCTGGATGCAAGAATGTGAGGAACCTGGAG 420
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Db 421 GAAAAAATATTAAGAAATTTTTCGACAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480
Qy 481 ACTTCTTGA 489
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Db 481 ACTTCTTGA 489

RESULT 6
AR122868
LOCUS AR122868 489 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 2 from patent US 6168783.
ACCESSION AR122868
VERSION AR122868.1 GI:14107834
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 489)
AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.
TITLE Antagonists of interleukin-15
JOURNAL Patent: US 6168783-A 2 02-JAN-2001;
FEATURES
source Location/Qualifiers
BASE COUNT 159 a 79 c 95 g 156 t
ORIGIN
Query Match 100.0%; Score 489; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 2.6e-236;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 GCAGGGCTTCTTAACACAGAGCAACTGGTGAATGTAATGAATGATTAAGTGAATTTGAAAAAAT 180
Qy 181 GAAGATCTTATTCATCTATGCATATTGATGCTACTTTATATACGGAAGTGAATGTTTCAC 240
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Qy 481 ACTTCTTGA 489
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Db 481 ACTTCTTGA 489

RESULT 7
AR125105
LOCUS AR125105 489 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 2 from patent US 6177079.
ACCESSION AR125105
VERSION AR125105.1 GI:14111167
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 489)
AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.
TITLE Antagonists of interleukin-15
JOURNAL Patent: US 6168783-A 2 02-JAN-2001;
FEATURES
source Location/Qualifiers
BASE COUNT 159 a 79 c 95 g 156 t
ORIGIN
Query Match 100.0%; Score 489; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 2.6e-236;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAATTTTCGAACACACATTTGAGAAGTATTTCATCCAGTGCTACTTGTGTTTACTT 60
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Db 121 GCAGGGCTTCTTAACACAGAGCAACTGGTGAATGTAATGAATGATTAAGTGAATTTGAAAAAAT 180
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Db 421 GAAAAAATATTAAGAAATTTTTCGACAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480
Qy 481 ACTTCTTGA 489
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Db 481 ACTTCTTGA 489
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REFERENCE 1 (bases 1 to 489)  
AUTHORS Grabstein, K.H., Pettit, D.K. and Paxton, R.J.  
TITLE Antagonists of interleukin-15  
JOURNAL Patent: US 6177079-A 2 23-JAN-2001;  
FEATURES Location/Qualifiers

Source  
1. .489  
BASE COUNT 159 a 79 c 95 g 156 t  
ORIGIN /organism="unknown"

Query Match 100.0%; Score 489; DB 6; Length 489;  
Best Local Similarity 100.0%; Pred. No. 2.6e-236;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAATTCGAAACACACATTGAGAAGTATTTCATCCAGTGCCTACTGTGTTTACTT 60  
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Db 481 ACTTCTTGA 489

RESULT 8  
AX006786  
LOCUS AX006786  
DEFINITION Sequence 4 from Patent WO0002582.  
ACCESSION AX006786  
VERSION AX006786.1 GI:9994822  
KEYWORDS  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 489)  
AUTHORS Londei, M., Quarantino, S. and Maiuri, L.  
TITLE Treatment of celiac disease with interleukin-15 antagonists  
JOURNAL Patent: WO 0002582-A 4 20-JAN-2000;  
LONDEI MARCO (GB); QUARANTINO SONIA (GB); MATHILDA AND TERENCE  
KENNEDY I (GB); MAIURI LUIGI (IT)

FEATURES  
source  
1. .489  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"

BASE COUNT 159 a 79 c 95 g 156 t  
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Query Match 100.0%; Score 489; DB 6; Length 489;  
Best Local Similarity 100.0%; Pred. No. 2.6e-236;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 481 ACTTCTTGA 489

RESULT 9  
AX320244  
LOCUS AX320244  
DEFINITION Sequence 3 from Patent WO0187330.  
ACCESSION AX320244  
VERSION AX320244.1 GI:17901652  
KEYWORDS  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (sites)  
AUTHORS Strom, T.B. and Maslinski, W.  
TITLE Compositions and methods for achieving immune suppression  
JOURNAL Patent: WO 0187330-A 3 22-NOV-2001;  
Beth Israel Deaconess Medical Center, Inc. (US)

FEATURES  
source  
1. .489  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"

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RESULT 12
LOCUS I62692
DEFINITION Sequence 1 from patent US 5660824.
ACCESSION I62692
VERSION I62692.1 GI:2480400
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 489)
AUTHORS Grabstein,K.H., Quinlan,L.S. and Troutt,A.B.
TITLE Muscle trophic factor
JOURNAL Patent: US 5660824-A 1 26-AUG-1997;
FEATURES
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BASE COUNT 159 a 79 c 95 g 156 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.6e-236;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACCAACATTTGAGAGATTTCCATCCAGTGTCTACTTGGCTGTTTACTT 60
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QY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489
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Db 421 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTGTCCAAATGTTCAATCAAC 480
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Db 481 ACTTCTTGA 489

RESULT 13
LOCUS I79219
DEFINITION Sequence 1 from patent US 5707616.
ACCESSION I79219
VERSION I79219.1 GI:3207509
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 489)
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE Method for treating or preventing gastrointestinal disease with
epithelium-derived T-cell factor
JOURNAL Patent: US 5707616-A 1 13-JAN-1998;
FEATURES
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BASE COUNT 159 a 79 c 95 g 156 t
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Query Match 100.0%; Score 489; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 2.6e-236;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 481 ACTTCTTGA 489
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Db 481 ACTTCTTGA 489

RESULT 14  
LOCUS ARI03280 1202 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 11 from patent US 6087172.  
ACCESSION ARI03280  
VERSION ARI03280.1 GI:12814868  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1202)  
AUTHORS Veerapaneni,D., Hamanaka,S. and Nozawa,I.  
TITLE Ribozymes targeted to human IL-15 mRNA  
JOURNAL Patent: US 6087172-A 11 JUL-2000;  
FEATURES Location/Qualifiers  
Source 1..1202  
/organism="unknown"  
BASE COUNT 355 a 219 c 249 g 379 t  
ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 1202;  
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Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 421 GAAAAAATATTAAGAATTTTTCAGAGTTTGTACATATTTGTCCAAATGTTTCATCAAC 480  
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Db 737 GAAAAAATATTAAGAATTTTTCAGAGTTTGTACATATTTGTCCAAATGTTTCATCAAC 796  
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QY 481 ACTTCTTGA 489  
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Db 797 ACTTCTTGA 805  
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RESULT 15  
LOCUS AX024715 1202 bp DNA linear PAT 15-SEP-2000  
DEFINITION Sequence 1 from Patent WO0028019.  
ACCESSION AX024715  
VERSION AX024715.1 GI:10184794  
KEYWORDS  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1202)  
AUTHORS Doudevani,A. and Chaimovitz,C.  
TITLE Antisense oligomer  
JOURNAL Patent: WO 0028019-A 1 18-MAY-2000;  
MOR RESEARCH APPLIC LTD (IL); DOUDEVANI AMOS (IL); UNIV BEN  
GURION (IL); CHAIMOVITZ CIDIO (IL)  
FEATURES Location/Qualifiers  
Source 1..1202  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 355 a 219 c 249 g 379 t  
ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 1202;  
Best Local Similarity 100.0%; Pred. No. 2.2e-236;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAATTCGAACCCACATTTGAGAAGTATTTCCATCCAGTGTCTACTTGTGTTTACTT 60  
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Db 317 ATGAGAATTCGAACCCACATTTGAGAAGTATTTCCATCCAGTGTCTACTTGTGTTTACTT 376  
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QY 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTTCTTCTTGGGCTGTTTCAAGT 120  
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Db 377 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTTCTTCTTGGGCTGTTTCAAGT 436  
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QY 121 GCAGGGCTTCCCTAAACAGAACCCCAACTGGGTGAATGTAATGAATGATTTGAAAAAAATT 180  
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Db 437 GCAGGGCTTCCCTAAACAGAACCCCAACTGGGTGAATGTAATGAATGATTTGAAAAAAATT 496  
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Db 557 CCCAGTTGCAAGTAACAGCAATGAAGTCTTCTCTTGGAGTTACAAGTTATTTTCACTT 616  
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QY 421 GAAAAAATATTAAGAATTTTTCAGAGTTTGTACATATTTGTCCAAATGTTTCATCAAC 480  
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Db 737 GAAAAAATATTAAGAATTTTTCAGAGTTTGTACATATTTGTCCAAATGTTTCATCAAC 796  
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QY 481 ACTTCTTGA 489  
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Db 797 ACTTCTTGA 805  
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RESULT 16  
LOCUS AX301227 1202 bp DNA linear PAT 30-NOV-2001  
DEFINITION Sequence 1 from Patent WO0185920.  
ACCESSION AX301227  
VERSION AX301227.1 GI:17382318  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (sites)  
AUTHORS Bancheureau,J.F., Mohamadzadeh,M. and Palucka,A.K.  
TITLE Compositions and methods for producing antigen-presenting cells  
JOURNAL Patent: WO 0185920-A 1 15-NOV-2001;

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BASE COUNT   355 a 219 c 249 g 379 t
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317 ATGAGAATTTTCGAACACCATTTGAGAAGTATTTCCATCCAGTGTCTACTTGTGTTTACTT 376
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377 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTTTCATTTTGGGCTGTTTCACT 436
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437 GCAGGGCTTCTAAACAGAGCCCACTGGGTGAATGTAATAGTGAATTTGAAAAAATT 496
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481 ACTTCTTGA 489
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797 ACTTCTTGA 805

RESULT 17
HSU14407
LOCUS      HSU14407          1202 bp      mRNA      linear      PRI 21-SEP-1994
DEFINITION Human Interleukin 15 (IL15) mRNA, complete cds.
ACCESSION U14407
VERSION   U14407.1
KEYWORDS  GI:540098
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1202)
AUTHORS   Grabstein,K.K., Eisenman,J., Sheanebeck,K., Rauch,C.,
           Srinivasan,S., Fung,V., Beers,C., Richardson,J., Schoenborn,M.A.,
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Abdieleh,M., Johnson,L., Alderson,M.R., Watson,J.D., Anderson,D.M.
and Giri,J.G.
Cloning of a T cell growth factor that interacts with the beta
chain of the interleukin-2 receptor
Science 264 (5161), 965-968 (1994)
94233380
REFERENCE 2 (bases 1 to 1202)
AUTHORS   Anderson,D.M.
TITLE     Direct Submision
JOURNAL   Submitted (06-SEP-1994) Dirk M. Anderson, Immunex Research and
Development Corp., 51, University St., Seattle, WA 98101, USA
FEATURES
  source      Location/Qualifiers
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                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /cell_line="IMTLH"
                /cell_type="stromal"
                /tissue_type="Bone marrow"
                1..1202
                /gene="IL15"
                314..460
                /gene="IL15"
                /evidence="experimental"
                317..805
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                /note="cytokine; T cell growth factor; secreted protein"
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                /product="Interleukin 15"
                /protein_id="AAA21551.1"
                /db_xref="GI:540099"
                /translation="MRISKPHLRSISIQCYLCLLNSHFLTEAGIHVFLGCFSGALP
                KTEANWNVISDLKKIEDLIQSMHIDATLYTESDVHPCKVTAMKCFLELLEQVLSLES
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                TS"
BASE COUNT   355 a 219 c 249 g 379 t
ORIGIN
1  ATGAGAATTTTCGAACACCATTTGAGAAGTATTTCCATCCAGTGTCTACTTGTGTTTACTT 60
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317 ATGAGAATTTTCGAACACCATTTGAGAAGTATTTCCATCCAGTGTCTACTTGTGTTTACTT 376
   |||||
61  CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTTTCATTTTGGGCTGTTTCACT 120
   |||||
377 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTTTCATTTTGGGCTGTTTCACT 436
   |||||
121 GCAGGGCTTCTAAACAGAGCCCACTGGGTGAATGTAATAGTGAATTTGAAAAAATT 180
   |||||
437 GCAGGGCTTCTAAACAGAGCCCACTGGGTGAATGTAATAGTGAATTTGAAAAAATT 496
   |||||
181 GAAGATCTTATTAATCTATGCATATTCATGCTTTCATGCTTTCATTTGGGCTGTTTCACT 240
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497 GAAGATCTTATTAATCTATGCATATTCATGCTTTCATGCTTTCATTTGGGCTGTTTCACT 556
   |||||
241 CCCAGTTGCAAGTAACAGCAATGAAGTCTTCTCTTGGAGTTACAAAGTATTTTCACTT 300
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Query Match      100.0%; Score 489; DB 9; Length 1202;
Best Local Similarity 100.0%; Pred. No. 2.2e-236;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1  ATGAGAATTTTCGAACACCATTTGAGAAGTATTTCCATCCAGTGTCTACTTGTGTTTACTT 60
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Db 317 ATGAGAATTTTCGAACACCATTTGAGAAGTATTTCCATCCAGTGTCTACTTGTGTTTACTT 376
   |||||
QY 61  CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTTTCATTTTGGGCTGTTTCACT 120
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Db 377 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTTTCATTTTGGGCTGTTTCACT 436
   |||||
QY 121 GCAGGGCTTCTAAACAGAGCCCACTGGGTGAATGTAATAGTGAATTTGAAAAAATT 180
   |||||
Db 437 GCAGGGCTTCTAAACAGAGCCCACTGGGTGAATGTAATAGTGAATTTGAAAAAATT 496
   |||||
QY 181 GAAGATCTTATTAATCTATGCATATTCATGCTTTCATGCTTTCATTTGGGCTGTTTCACT 240
   |||||
Db 497 GAAGATCTTATTAATCTATGCATATTCATGCTTTCATGCTTTCATTTGGGCTGTTTCACT 556
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QY 241 CCCAGTTGCAAGTAACAGCAATGAAGTCTTCTCTTGGAGTTACAAAGTATTTTCACTT 300
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Db 557 CCCAGTTGCAAAAGTAACAGCAATGAAGTGTCTTCTTTGGAGTTACAAAGTTATTTCACTT 616
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Db 617 GAGTCCGGAGATGCAAGTATTTCATGATACAGTACAAAATCTGATCATCTAGCAAAACAAC 676
Qy 361 AGTTTGTCTTCTTAATGGGAATGTAAAGAAATCTGGATGCAAAAGAAATGTGAGGAACACTGGAG 420
Db 677 AGTTTGTCTTCTTAATGGGAATGTAAAGAAATCTGGATGCAAAAGAAATGTGAGGAACACTGGAG 736
Qy 421 GAAAAAATATTAAGAAATTTTTCAGAGTTTTTGTACATATTGTCCAAATGTTTCATCAAC 480
Db 737 GAAAAAATATTAAGAAATTTTTCAGAGTTTTTGTACATATTGTCCAAATGTTTCATCAAC 796
Qy 481 ACTTCTTGA 489
Db 797 ACTTCTTGA 805

RESULT 18
AX320242
LOCUS AX320242 489 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 1 from Patent WO0187330.
ACCESSION AX320242
VERSION AX320242.1 GI:17901650
KEYWORDS
SOURCE
ORGANISM human.
REFERENCE
AUTHORS Strom,T.B. and Maslinski,W.
TITLE Compositions and methods for achieving immune suppression
JOURNAL Patent: WO 0187330-A 1 22-NOV-2001;
Beth Israel Deaconess Medical Center, Inc. (US)
FEATURES
source
1..489
/organism="Homo sapiens"
/db_xref="taxon:9606"
CDS
1..489
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD19389.1"
/db_xref="gi:17901651"
/translation="MRISKPHLRISIQCYLCILLNSHFLTEAGIHVILGCFSGAGLP
KTEANWNVISDLKKIEDLIQSMHIDATLVESDVHPSCVKVTAMKCFLELLEQLVISLES
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TS"
BASE COUNT 158 a 79 c 96 g 156 t
ORIGIN

Query Match 90.8%; Score 444; DB 6; Length 489;
Best Local Similarity 100.08; Pred. No. 1.5e-213; Indels 0; Gaps 0;
Matches 444; Conservative 0; Mismatches 0;

Qy 1 ATGAGAATTTTCAAAACCACTTTGAGAAGTATTTCCATCCAGTGTCTTGTGTTTACTT 60
Db 1 ATGAGAATTTTCAAAACCACTTTGAGAAGTATTTCCATCCAGTGTCTTGTGTTTACTT 60
Qy 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTTCAATTTTGGGCTGTTTCAGT 120
Db 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTTCAATTTTGGGCTGTTTCAGT 120
Qy 121 GCAGGGCTTCTAAACACAGACCACTGGGTGAATGTAATAGTGATTTGAAAAAAT 180
Db 121 GCAGGGCTTCTAAACACAGACCACTGGGTGAATGTAATAGTGATTTGAAAAAAT 180
Qy 181 GAAGATCTTATTCATCTATGCTATTTGATGCTACTTTATACGGAAGTATGTTTCAAC 240
Db 181 GAAGATCTTATTCATCTATGCTATTTGATGCTACTTTATACGGAAGTATGTTTCAAC 240
Qy 241 CCCAGTTTCAAAACCACTTTGAGAAGTATTTCCATCCAGTGTCTTGTGTTTACTT 60
Db 241 CCCAGTTTCAAAACCACTTTGAGAAGTATTTCCATCCAGTGTCTTGTGTTTACTT 60
Qy 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTTCAATTTTGGGCTGTTTCAGT 120
Db 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTTCAATTTTGGGCTGTTTCAGT 120
Qy 121 GCAGGGCTTCTAAACACAGACCACTGGGTGAATGTAATAGTGATTTGAAAAAAT 180
Db 121 GCAGGGCTTCTAAACACAGACCACTGGGTGAATGTAATAGTGATTTGAAAAAAT 180
Qy 181 GAAGATCTTATTCATCTATGCTATTTGATGCTACTTTATACGGAAGTATGTTTCAAC 240
Db 181 GAAGATCTTATTCATCTATGCTATTTGATGCTACTTTATACGGAAGTATGTTTCAAC 240
Qy 241 CCCAGTTTCAAAACCACTTTGAGAAGTATTTCCATCCAGTGTCTTGTGTTTACTT 300
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Db 241 CCCAGTTTCAAAAGTAACAGCAATGAAGTGTCTTCTTTGGAGTTACAAAGTTATTTCACTT 300
Qy 301 GAGTCCGGAGATGCAAGTATTTCATGATACAGTACAAAATCTGATCATCTAGCAAAACAAC 360
Db 301 GAGTCCGGAGATGCAAGTATTTCATGATACAGTACAAAATCTGATCATCTAGCAAAACAAC 360
Qy 361 AGTTTGTCTTCTTAATGGGAATGTAAAGAAATCTGGATGCAAAAGAAATGTGAGGAACACTGGAG 420
Db 361 AGTTTGTCTTCTTAATGGGAATGTAAAGAAATCTGGATGCAAAAGAAATGTGAGGAACACTGGAG 420
Qy 421 GAAAAAATATTAAGAAATTTTTCG 444
Db 421 GAAAAAATATTAAGAAATTTTTCG 444

RESULT 19
AR094649
LOCUS AR094649 489 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 5 from patent US 6001973.
ACCESSION AR094649
VERSION AR094649.1 GI:10021763
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 489)
AUTHORS Strom,T.B. and Maslinski,W.
TITLE Antagonists of interleukin-15
JOURNAL Patent: US 6001973-A 5 14-DEC-1999;
FEATURES
source
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/organism="unknown"
BASE COUNT 159 a 80 c 95 g 155 t
ORIGIN

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Best Local Similarity 99.8%; Pred. No. 1.6e-210;
Matches 488; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGAGAATTTTCAAAACCACTTTGAGAAGTATTTCCATCCAGTGTCTTGTGTTTACTT 60
Db 1 ATGAGAATTTTCAAAACCACTTTGAGAAGTATTTCCATCCAGTGTCTTGTGTTTACTT 60
Qy 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTTCAATTTTGGGCTGTTTCAGT 120
Db 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTTCAATTTTGGGCTGTTTCAGT 120
Qy 121 GCAGGGCTTCTAAACACAGACCACTGGGTGAATGTAATAGTGATTTGAAAAAAT 180
Db 121 GCAGGGCTTCTAAACACAGACCACTGGGTGAATGTAATAGTGATTTGAAAAAAT 180
Qy 181 GAAGATCTTATTCATCTATGCTATTTGATGCTACTTTATACGGAAGTATGTTTCAAC 240
Db 181 GAAGATCTTATTCATCTATGCTATTTGATGCTACTTTATACGGAAGTATGTTTCAAC 240
Qy 241 CCCAGTTTCAAAAGTAACAGCAATGAAGTGTCTTCTTTGGAGTTACAAAGTTATTTCAC 300
Db 241 CCCAGTTTCAAAAGTAACAGCAATGAAGTGTCTTCTTTGGAGTTACAAAGTTATTTCAC 300
Qy 301 GAGTCCGGAGATGCAAGTATTTCATGATACAGTACAAAATCTGATCATCTAGCAAAACAAC 360
Db 301 GAGTCCGGAGATGCAAGTATTTCATGATACAGTACAAAATCTGATCATCTAGCAAAACAAC 360
Qy 361 AGTTTGTCTTCTTAATGGGAATGTAAAGAAATCTGGATGCAAAAGAAATGTGAGGAACACTGGAG 420
Db 361 AGTTTGTCTTCTTAATGGGAATGTAAAGAAATCTGGATGCAAAAGAAATGTGAGGAACACTGGAG 420
Qy 421 GAAAAAATATTAAGAAATTTTTCGAGAGTTTTTGTACATATTGTCCAAATGTTTCATCAAC 480
Db 421 GAAAAAATATTAAGAAATTTTTCGAGAGTTTTTGTACATATTGTCCAAATGTTTCATCAAC 480
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QY 481 ACTTCTTGA 489
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Db 481 ACTTCTTGA 489

RESULT 20
BD008811
LOCUS Antagonists of interleukin-15. 489 bp DNA linear PAT 31-JAN-2002
DEFINITION BD008811
ACCESSION BD008811
VERSION BD008811.1 GI:18637184
KEYWORDS JP 2001502521-A/4.
SOURCE unclassified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 489)
AUTHORS Strom, T. and Maslinski, W.
TITLE Antagonists of interleukin-15
JOURNAL Patent: JP 2001502521-A 4 27-FEB-2001;
COMMENT BETH ISRAEL DEACONESS MEDICAL CENTER
OS Unidentified
PN JP 2001502521-A/4
PD 27-FEB-2001
PP 25-APR-1997 JP 1997539046
PR 26-APR-1996 US 60/016634
PI TERRY STROM, WLODZIMIERZ MASLINSKI
PC C12N15/24, C07K14/54, A61K38/20, C12N15/62, G01N33/68 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..489
FT /organism='Unidentified'.
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1..489
/organism='unidentified'
/db_xref='taxon:32644'
BASE COUNT 159 a 80 c 95 g 155 t
ORIGIN

Query Match 89.6%; Score 438; DB 6; Length 489;
Best Local Similarity 99.8%; Pred. No. 1.6e-210;
Matches 488; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACACACATTGAGAAGTATTTCATCCAGTCGCTACTTGTTTACTT 60
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Db 1 ATGAGAAATTCGAAACACACATTGAGAAGTATTTCATCCAGTCGCTACTTGTTTACTT 60
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QY 61 CTAACAGTCATTTCTAACTGAAGCTGGCATTCATGCTCTTCAATTTGGGCTGTTTCAGT 120
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Db 61 CTAAACAGTCATTTCTAACTGAAGCTGGCATTCATGCTCTTCAATTTGGGCTGTTTCAGT 120
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QY 121 GCAGGCTTCCTAAAACAGAACCAACTGGGTAATGTAATAGTCAATTTGAAAAAAAT 180
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QY 181 GAAGATCTTATTCATCTATGATATTTGATGCTACTTTATATACGGAAGTGTTCAC 240
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Db 181 GAAGATCTTATTCATCTATGATATTTGATGCTACTTTATATACGGAAGTGTTCAC 240
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QY 241 CCCAGTTGCAAAAGTACAGCAATGAAGTCTTCTCTTGGAGTTACAAGTATTTCAC 300
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Db 241 CCCAGTTGCAAAAGTACAGCAATGAAGTCTTCTCTTGGAGTTACAAGTATTTCAC 300
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QY 301 GAGTCGGAGATGCAAGTATTTCATGATACAGTAGAAAAATCTGATCATCTAGCAACAAC 360
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Db 301 GAGTCGGAGATGCAAGTATTTCATGATACAGTAGAAAAATCTGATCATCTAGCAACAAC 360
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QY 361 AGTTTGTCTTCTAATGGGAATGTACAGAAATCTGGATGCAAAAGATGTGAGGAAC 420
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QY 421 GAAAAAATATTAAAGAAATTTTTCAGAGAGTTTGTGTACATATTGTCCAAATGTTTCATCAAC 480
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Db 421 GAAAAAATATTAAAGAAATTTTTCAGAGAGTTTGTGTACATATTGTCCAAATGTTTCATCAAC 480
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QY 481 ACTTCTTGA 489
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Db 481 ACTTCTTGA 489

RESULT 21
HSIL15MR
LOCUS H sapiens mRNA for interleukin 15 (partial). 453 bp mRNA linear PRI 26-SEP-1995
DEFINITION H sapiens mRNA for interleukin 15 (partial).
ACCESSION Z38000
VERSION Z38000.1 GI:995656
KEYWORDS interleukin; interleukin-15.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 111 to 452)
AUTHORS SOREL, M.A. and Jacques, Y.
TITLE IL15 expression in human keratinocytes
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 453)
AUTHORS SOREL, M.A.
TITLE Direct Submission
JOURNAL Submitted (03-OCT-1994) Michel A Sorel, Institut de biologie,
INSERM U 211, 9 Quai de Moncousu, Nantes, 44035, FRANCE
FEATURES
Location/Qualifiers
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/isolate='INDIVIDUAL'
/db_xref='taxon:9606'
/sex='Male'
/cell_type='HUMAN KERATINOCYTES FROM FORESKIN'
/tissue_type='EPIDERMAL TISSUE'
111..452
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<111..>452
/codon_start=1
/product='interleukin-15'
/protein_id='CAA86100.1'
/db_xref='GI:995657'
/translation='NWNVISDLKIEDLIQSMHIDATLYTESDVHPKSVKVTAMKCFLL
LEQVISLESQDASIHDTVENLIILANSLSSNGNVNTESGKECELEBKNIKEFLQS
FVHIQVFINTS'
BASE COUNT 146 a 75 c 87 g 145 t
ORIGIN

Query Match 82.2%; Score 402; DB 9; Length 453;
Best Local Similarity 99.8%; Pred. No. 2.7e-192;
Matches 452; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 35 CCATCCAGTGCTACTTGTTTACTTCTAAACAGTCATTTTCTAACTGAAGCTGGCATTC 94
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Db 1 CCATCCAGTGCTACTTGTTTACTTCTAAACAGTCATTTTCTAACTGAAGCTGGCATTC 94
|||||
QY 95 ATGTCTTCAATTTTGGGCTGTTTTCAGTGCAGGGCTTCTCTAAACAGAGCAACTGGGTGA 154
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Db 61 ATGTCTTCAATTTTGGGCTGTTTTCAGTGCAGGGCTTCTCTAAACAGAGCAACTGGGTGA 120
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QY 155 ATGTAATAAGTATTTGAAAAAATTTGAAGATCTTATTCATCTATGATGCTA 214
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Db 121 ATGTAATAAGTATTTGAAAAAATTTGAAGATCTTATTCATCTATGATGCTA 180
|||||
QY 215 CTTTATATACGAAAGTATGTTTCCACCCAGTTGCAAGTAAACAGCAACTGGCTTC 274
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Db 181 CTTTATATACGAAAGTATGTTTCCACCCAGTTGCAAGTAAACAGCAACTGGCTTC 240
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QY 275 TCTTGAGTTTACAAGTATTTTTCACCTTGGAGATGCAAGTATTCATGATACAGTAG 334
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Db 241 TCTTGGAGTTACAAAGTTATTTTACATTGAGTCGGAGATGCAAGTATTCATGATACAGTAG 300  
QY 335 AAAATCTGATCATCTTAGCAACACACAGTTTCTCTTAATCGGAATGTAACAGAACTCG 394  
Db 301 AAAATCTGATCATCTTAGCAACACACAGTTTCTCTTAATCGGAATGTAACAGAACTCG 360  
QY 395 GATGCAAAAGATGTGAGGAACCTGGAGGAAAAAATATTAAAGAAATTTTTCAGAGTTTTG 454  
Db 361 GATGCAAAAGATGTGAGGAACCTAGAGGAAAAAATATTAAAGAAATTTTTCAGAGTTTTG 420  
QY 455 TACATATTTGCCAAATGTTTCATCAACACTCTT 487  
Db 421 TACATATTTGCCAAATGTTTCATCAACACTCTT 453  
RESULT 22  
AR094650  
LOCUS AR094650 489 bp DNA linear PAT 08-SEP-2000  
DEFINITION Sequence 7 from patent US 6001973.  
ACCESSION AR094650  
VERSION AR094650.1 GI:10021765  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 489)  
AUTHORS Strom, T. B. and Maslinski, W.  
TITLE Antagonists of Interleukin-15  
JOURNAL Patent: US 6001973-A 7 14-DEC-1999;  
FEATURES  
Location/Qualifiers  
source 1..489  
BASE COUNT 158 a 80 c 96 g 155 t  
ORIGIN

Query Match 80.4%; Score 393; DB 6; Length 489;  
Best Local Similarity 99.8%; Pred. No. 9.5e-188;  
Matches 443; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATGAGAATTTTCGAACACACATTTGAGAAGTATTTCCATCCAGTCTACTTGTGTTACTT 60  
Db 1 ATGAGAATTTTCGAACACACATTTGAGAAGTATTTCCATCCAGTCTACTTGTGTTACTT 60  
QY 61 CTAACAGTCATTTTCTTAAGTGAAGTGGCATTCTCTTCAATTTTGGCTGTTTCAGT 120  
Db 61 CTAACAGTCATTTTCTTAAGTGAAGTGGCATTCTCTTCAATTTTGGCTGTTTCAGT 120  
QY 121 GCAGGGCTTCTTAAACAGAGCCAACTGGGTGAATGTAATAGTGATTTGAAAAAAT 180  
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QY 241 CCCAGTTGCAAGTAAACAGCAATGAAGTGGTCTTCTCTTGGAGTTTACAAATTTTTCAC 300  
Db 241 CCCAGTTGCAAGTAAACAGCAATGAAGTGGTCTTCTCTTGGAGTTTACAAATTTTTCAC 300  
QY 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAGAATACTGATCATCTCTAGCAACAAC 360  
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QY 361 AGTTTGTCTTCTAATGGGAATGAACAGATCTGGATGCAAGAAATGTGAGGAACCTGGAG 420  
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QY 421 GAAAAAATATTAAAGAAATTTTTC 444  
Db 421 GAAAAAATATTAAAGAAATTTTTC 444

RESULT 24

RESULT 23  
BD008812  
LOCUS Antagonists of Interleukin-15.  
DEFINITION BD008812  
ACCESSION BD008812  
VERSION BD008812.1 GI:18637185  
KEYWORDS JP 2001502521-A/5.  
SOURCE unidentified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 489)  
AUTHORS Strom, T. and Maslinski, W.  
TITLE Antagonists of Interleukin-15  
JOURNAL Patent: JP 2001502521-A 5 27-FEB-2001;  
BETH ISRAEL DEACONESS MEDICAL CENTER  
COMMENT OS Unidentified  
PN JP 2001502521-A/5  
PD 27-FEB-2001  
PF 25-APR-1997 JP 1997539046  
PR 26-APR-1996 US 60/016634  
PI TERRY STROM, WLODZIMIERZ MASLINSKI  
PC C12N15/24, C07K14/54, A61K38/20, C12N15/62, G01N33/68 CC  
KEYWORDS Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers  
FT source 1..489  
FT /organism='Unidentified'.  
FEATURES  
Location/Qualifiers  
source 1..489  
/organism='unidentified'  
/db\_xref='taxon:32644'  
BASE COUNT 158 a 80 c 96 g 155 t  
ORIGIN

Query Match 80.4%; Score 393; DB 6; Length 489;  
Best Local Similarity 99.8%; Pred. No. 9.5e-188;  
Matches 443; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATGAGAATTTTCGAACACACATTTGAGAAGTATTTCCATCCAGTCTACTTGTGTTACTT 60  
Db 1 ATGAGAATTTTCGAACACACATTTGAGAAGTATTTCCATCCAGTCTACTTGTGTTACTT 60  
QY 61 CTAACAGTCATTTTCTTAAGTGAAGTGGCATTCTCTTCAATTTTGGCTGTTTCAGT 120  
Db 61 CTAACAGTCATTTTCTTAAGTGAAGTGGCATTCTCTTCAATTTTGGCTGTTTCAGT 120  
QY 121 GCAGGGCTTCTTAAACAGAGCCAACTGGGTGAATGTAATAGTGATTTGAAAAAAT 180  
Db 121 GCAGGGCTTCTTAAACAGAGCCAACTGGGTGAATGTAATAGTGATTTGAAAAAAT 180  
QY 181 GAAGATCTTATTCATCTATGATATTTGATGCTACTTTATATACGGAAGTGATGTTTCA 240  
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QY 241 CCCAGTTGCAAGTAAACAGCAATGAAGTGGTCTTCTCTTGGAGTTTACAAATTTTTCAC 300  
Db 241 CCCAGTTGCAAGTAAACAGCAATGAAGTGGTCTTCTCTTGGAGTTTACAAATTTTTCAC 300  
QY 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAGAATACTGATCATCTCTAGCAACAAC 360  
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QY 361 AGTTTGTCTTCTAATGGGAATGAACAGATCTGGATGCAAGAAATGTGAGGAACCTGGAG 420  
Db 361 AGTTTGTCTTCTAATGGGAATGAACAGATCTGGATGCAAGAAATGTGAGGAACCTGGAG 420  
QY 421 GAAAAAATATTAAAGAAATTTTTC 444  
Db 421 GAAAAAATATTAAAGAAATTTTTC 444

RESULT 24

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HSIL15MR1
LOCUS          HSIL15MR1          643 bp      mRNA      linear      PRI 27-SEP-1996
DEFINITION    H.sapiens mRNA for interleukin-15 (cell line NCIH69).
ACCESSION     X94222
VERSION       X94222.1 GI:1495459
KEYWORDS      interleukin-15.
SOURCE        human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1 (bases 1 to 643)
AUTHORS      Meazza,R., Verdiani,S., Biassoni,R., Coppolecchia,M., Gaggero,A.,
               Orengo,A.M., Colombo,M.P., Azzarone,B. and Ferrini,S.
               Identification of a novel interleukin-15 (IL-15) transcript isoform
               generated by alternative splicing in human small cell lung cancer
               cell lines
JOURNAL       Oncogene 12 (10), 2187-2192 (1996)
MEDLINE       96218668
REFERENCE     2 (bases 1 to 643)
AUTHORS      Ferrini,S.
TITLE        Direct Submission
JOURNAL       Submitted (12-DEC-1995) S. Ferrini, Istituto Nazionale Ricerca
               Cancro, Pharmacology, Largo R. Benzi 10, Genova, 16132, Italy
FEATURES      Location/Qualifiers
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               /isolate="H69/1"
               /db_xref="taxon:9606"
               /clone="1"
               /cell_line="NCIH69"
               /tissue_type="SCLC"
               /clone_lib="H69"
               /dev_stage="adult"
               223..630
               /codon_start=1
               /product="interleukin-15 (IL-15)"
               /protein_id="CAA63913.1"
               /db_xref="GI:1495460"
               /db_xref="SWISS-PROT:P40933"
               /translation="MVLGTIDLCSCFSAGLPRKTEANWNVISDLKKIEDLIQSMHIDA
               TLYTESDVHPCKVTKMCFLELQVISLESGDASIHDTVENLIILANNSLSSNGNVT
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BASE COUNT    201 a 111 c 123 g 208 t
ORIGIN
Query Match    77.7%; Score 380; DB 9; Length 643;
Best Local Similarity 100.0%; Pred. No. 3.4e-181;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 110 GCTGTTTCAGTCAGGGCTTCCTAAACAGAGCCAACTGGGTGAATGTAAGTGATT 169
DB 251 GCTGTTTCAGTCAGGGCTTCCTAAACAGAGCCAACTGGGTGAATGTAAGTGATT 310
QY 170 TGAATAAATTTGAAGATCTTATTCATCTATGCATATTCATGCTACTTATATACGGAAA 229
DB 311 TGAATAAATTTGAAGATCTTATTCATCTATGCATATTCATGCTACTTATATACGGAAA 370
QY 230 GTGATGTTTCAACCCAGTTCGAAGTAACAGCAATGAAGTGCTTTCTCTTGGAGTTACAAG 289
DB 371 GTGATGTTTCAACCCAGTTCGAAGTAACAGCAATGAAGTGCTTTCTCTTGGAGTTACAAG 430
QY 290 TTATTTTCACTTGAAGTCCGGAGATGCAAGTATTCATGATACAGTACAGAAATCTGATCATCC 349
DB 431 TTATTTTCACTTGAAGTCCGGAGATGCAAGTATTCATGATACAGTACAGAAATCTGATCATCC 490
QY 350 TAGCAAAACACAGTTTGTCTTCTTAATGGGAATGTAACAGAAATCTGGATGCAAGAAATGTG 409
DB 491 TAGCAAAACACAGTTTGTCTTCTTAATGGGAATGTAACAGAAATCTGGATGCAAGAAATGTG 550
QY 410 AGGAACACAGAAATTTTGAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAA 469
DB 551 AGGAACACAGAAATTTTGAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAA 610
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QY 470 TGTTCATCAACACTTCTTGA 489
DB 611 TGTTCATCAACACTTCTTGA 630

RESULT 25
HSIL15MR2
LOCUS          HSIL15MR2          643 bp      mRNA      linear      PRI 27-SEP-1996
DEFINITION    H.sapiens mRNA for interleukin-15 (cell line NCIH82).
ACCESSION     X94223
VERSION       X94223.1 GI:1495461
KEYWORDS      interleukin-15.
SOURCE        human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1 (bases 1 to 643)
AUTHORS      Meazza,R., Verdiani,S., Biassoni,R., Coppolecchia,M., Gaggero,A.,
               Orengo,A.M., Colombo,M.P., Azzarone,B. and Ferrini,S.
               Identification of a novel interleukin-15 (IL-15) transcript isoform
               generated by alternative splicing in human small cell lung cancer
               cell lines
JOURNAL       Oncogene 12 (10), 2187-2192 (1996)
MEDLINE       96218668
REFERENCE     2 (bases 1 to 643)
AUTHORS      Ferrini,S.
TITLE        Direct Submission
JOURNAL       Submitted (12-DEC-1995) S. Ferrini, Istituto Nazionale Ricerca
               Cancro, Pharmacology, Largo R. Benzi 10, Genova, 16132, Italy
FEATURES      Location/Qualifiers
               source
               1..643
               /organism="Homo sapiens"
               /isolate="H82/1"
               /db_xref="taxon:9606"
               /cell_line="NCIH82"
               /tissue_type="SCLC"
               /clone_lib="H82-1,-2"
               /dev_stage="adult"
               223..630
               /codon_start=1
               /product="interleukin-15 (IL-15)"
               /protein_id="CAA63914.1"
               /db_xref="GI:1495462"
               /db_xref="SWISS-PROT:P40933"
               /translation="MVLGTIDLCSCFSAGLPRKTEANWNVISDLKKIEDLIQSMHIDA
               TLYTESDVHPCKVTKMCFLELQVISLESGDASIHDTVENLIILANNSLSSNGNVT
               ESGKECELEBKIKFELQSFVHVQMFINTS"
BASE COUNT    200 a 111 c 124 g 208 t
ORIGIN
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Query Match    77.7%; Score 380; DB 9; Length 643;
Best Local Similarity 100.0%; Pred. No. 3.4e-181;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 110 GCTGTTTCAGTCAGGGCTTCCTAAACAGAGCCAACTGGGTGAATGTAAGTGATT 169
DB 251 GCTGTTTCAGTCAGGGCTTCCTAAACAGAGCCAACTGGGTGAATGTAAGTGATT 310
QY 170 TGAATAAATTTGAAGATCTTATTCATCTATGCATATTCATGCTACTTATATACGGAAA 229
DB 311 TGAATAAATTTGAAGATCTTATTCATCTATGCATATTCATGCTACTTATATACGGAAA 370
QY 230 GTGATGTTTCAACCCAGTTCGAAGTAACAGCAATGAAGTGCTTTCTCTTGGAGTTACAAG 289
DB 371 GTGATGTTTCAACCCAGTTCGAAGTAACAGCAATGAAGTGCTTTCTCTTGGAGTTACAAG 430
QY 290 TTATTTTCACTTGAAGTCCGGAGATGCAAGTATTCATGATACAGTACAGAAATCTGATCATCC 349
DB 431 TTATTTTCACTTGAAGTCCGGAGATGCAAGTATTCATGATACAGTACAGAAATCTGATCATCC 490
QY 350 TAGCAAAACACAGTTTGTCTTCTTAATGGGAATGTAACAGAAATCTGGATGCAAGAAATGTG 409
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Db 491 TAGCAACACAGTTTGCTTCTAATGGAATGTAACAGATCTCGATGCAAGAATGTG 550  
Qy 410 AGGAACTGGAGGAAAAAATAATTAAGAATTTTTCAGAGTTTGTACATATTGTCCAAA 469  
Db 551 AGGAACTGGAGGAAAAAATAATTAAGAATTTTTCAGAGTTTGTACATATTGTCCAAA 610  
Qy 470 TGTTCATCAACACTTCTTGA 489  
Db 611 TGTTCATCAACACTTCTTGA 630  
RESULT 26  
HSIL15  
LOCUS HSI15 486 bp mRNA linear PRI 30-MAY-1997  
DEFINITION H.sapiens mRNA for interleukin-15.  
ACCESSION Y09908  
VERSION Y09908.1 GI:2143255  
KEYWORDS Igkv signal peptide; IL-15 gene; interleukin-15.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS 1 (bases 1 to 486)  
TITLE Meazza,R. and Ferrini,S.  
JOURNAL Expression of two IL-15 mRNA isoforms in human tumors does not  
correlate with secretion: role of different signal peptides  
REFERENCE Unpublished  
AUTHORS 2 (bases 1 to 486)  
TITLE Direct Submission  
JOURNAL Submitted (08-APR-1997) S. Ferrini, IST, Immunopharmacology, Largo  
R. Benzi 10, Genova, 16132, ITALY  
REMARK revised by author  
FEATURES  
source Location/Qualifiers  
1..486  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
gene 57..467  
CDS /gene="IL-15"  
/gene="IL-15"  
/codon\_start=1  
/product="interleukin-15"  
/protein\_id="CAA71044.1"  
/db\_xref="GI:2143256"  
/db\_xref="SPTREMBL:O00440"  
/translation="MDQVQIFSLISASVMSRANVNVISDLKKIEDLIQSMHID  
ATLYTSDVHPKSVKVTAMKCFLELQVLSLGDASIHDTVENLIILANNSSNGNV  
TESGCKECEELEEKIKEFLQSFVHVQMFINTS"  
BASE COUNT 154 a 81 c 100 g 151 t  
ORIGIN  
Query Match 71.4%; Score 349; DB 9; Length 486;  
Best Local Similarity 100.0%; Pred. No. 1.7e-165;  
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 141 AGCCAACTGGGTGAATGTAATAGTGTGTAAGGATTTGAAAAAATTCAGACATCTTATTCATCTAT 200  
Db 119 AGCCAACTGGGTGAATGTAATAGTGTGTAAGGATTTGAAAAAATTCAGACATCTTATTCATCTAT 178  
Qy 201 GCATATTGATGCTACTTCTTATATACGGAAGTGATGTTACCCCGAGTTGCAAAAGTAACAGC 260  
Db 179 GCATATTGATGCTACTTCTTATATACGGAAGTGATGTTACCCCGAGTTGCAAAAGTAACAGC 238  
Qy 261 AATGAAGTCTTCTCTTGGAGTTTACAAGTTATTTCACCTTCAGTCCCGAGATGCAAGTAT 320  
Db 239 AATGAAGTCTTCTCTTGGAGTTTACAAGTTATTTCACCTTCAGTCCCGAGATGCAAGTAT 298  
Qy 321 TCATCATACAGTAGAAAAATCTGATCATCTCCTAGCAACACAGTTTGTCTTCTTAATGGGAA 380  
Db 299 TCATCATACAGTAGAAAAATCTGATCATCTCCTAGCAACACAGTTTGTCTTCTTAATGGGAA 358

Qy 381 TGTAAACAGATCTCGATGCAAGAATGTGAGAACTGGAGGAAAAAATAATTAAGAATTT 440  
Db 359 TGTAAACAGATCTCGATGCAAGAATGTGAGAACTGGAGGAAAAAATAATTAAGAATTT 418  
Qy 441 TTTGCAGAGTTTGTACATATTGTCCAAATGTTTCATCAACACTTCTTGA 489  
Db 419 TTTGCAGAGTTTGTACATATTGTCCAAATGTTTCATCAACACTTCTTGA 467  
RESULT 27  
AR070288  
LOCUS AR070288 345 bp DNA linear PAT 18-FEB-2000  
DEFINITION Sequence 12 from patent US 5892001.  
ACCESSION AR070288  
VERSION AR070288.1 GI:7221176  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 345)  
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.  
TITLE Epithelium-derived T-cell factor antibodies  
JOURNAL Patent: US 5892001-A 12 06-APR-1999;  
FEATURES Location/Qualifiers  
source 1..345  
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BASE COUNT 121 a 49 c 68 g 107 t  
ORIGIN  
Query Match 70.6%; Score 345; DB 6; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1.9e-163;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 145 AACTGGGTGAATCTAATAAGTGAATTTGAAAAAATTTGAAGATCTTATTCATCTATGCAAT 204  
Db 1 AACTGGGTGAATCTAATAAGTGAATTTGAAAAAATTTGAAGATCTTATTCATCTATGCAAT 60  
Qy 205 ATTGATGCTACTTTATATACGGAAGTGTGTCACCCAGTTGCAACAGCAATG 264  
Db 61 ATTGATGCTACTTTATATACGGAAGTGTGTCACCCAGTTGCAACAGCAATG 120  
Qy 265 AAGTGTCTTCTCTGGAGTTACAAGTTATTTCACCTTCAGTCCGGAGATCAAGTATTCAT 324  
Db 121 AAGTGTCTTCTCTGGAGTTACAAGTTATTTCACCTTCAGTCCGGAGATCAAGTATTCAT 180  
Qy 325 GATACAGTAGAAAAATCTGATCATCTCTAGCAACACACAGTTTGTCTTCTTAATGGGAATGA 384  
Db 181 GATACAGTAGAAAAATCTGATCATCTCTAGCAACACACAGTTTGTCTTCTTAATGGGAATGA 240  
Qy 385 ACAGAATCTGGATGCAAGAATGTGAGGAAGTGTGAGGAACTGGAGGAAAAAATAATTAAGAATTTTG 444  
Db 241 ACAGAATCTGGATGCAAGAATGTGAGGAAGTGTGAGGAACTGGAGGAAAAAATAATTAAGAATTTTG 300  
Qy 445 CAGAGTTTGTACATATTGTCCAAATGTTTCATCAACACTTCTTGA 489  
Db 301 CAGAGTTTGTACATATTGTCCAAATGTTTCATCAACACTTCTTGA 345

RESULT 28  
AR05747  
LOCUS AR05747 345 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 12 from patent US 5985262.  
ACCESSION AR05747  
VERSION AR05747.1 GI:10012513  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 345)  
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.  
TITLE Method of treatment with epithelium derived T-cell factor

JOURNAL Patent: US 5985262-A 12 16-NOV-1999;  
FEATURES Location/Qualifiers  
source 1. 345  
BASE COUNT 121 a 49 c 68 g 107 t  
ORIGIN

Query Match 70.6%; Score 345; DB 6; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1.9e-163;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTTGAAGATCTTATTTCAATCTATGCAT 204  
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Db 1 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTTGAAGATCTTATTTCAATCTATGCAT 60  
QY 205 ATTGATGCTACTTTATATACGGAAGTGATGTTTCACCCCGAGTTGCAAGTAACAGCAATG 264  
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Db 61 ATTGATGCTACTTTATATACGGAAGTGATGTTTCACCCCGAGTTGCAAGTAACAGCAATG 120  
QY 265 AAGTGCCTTTCTCTGGAGTTACAAGTTATTTCACTTGAGTCCGGAGATGCAAGTATTTCAAT 324  
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Db 121 AAGTGCCTTTCTCTGGAGTTACAAGTTATTTCACTTGAGTCCGGAGATGCAAGTATTTCAAT 180  
QY 325 GATACAGTAGAATAATCTGATCATCTAGCAAAACAACAGATTTTCTTCTAATGGGAATGTA 384  
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Db 181 GATACAGTAGAATAATCTGATCATCTAGCAAAACAACAGATTTTCTTCTAATGGGAATGTA 240  
QY 385 ACAGAACTCTGGATGCAAAAGAAATGTGAGGAACGTGGAGGAAAAAATATTAAAGAAATTTTG 444  
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Db 241 ACAGAACTCTGGATGCAAAAGAAATGTGAGGAACGTGGAGGAAAAAATATTAAAGAAATTTTG 300  
QY 445 CAGAGTTTGTACATATTTGTCACAAATGTTTCATCAACACTTCTTGA 489  
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Db 301 CAGAGTTTGTACATATTTGTCACAAATGTTTCATCAACACTTCTTGA 345

RESULT 29  
LOCUS 128856  
DEFINITION Sequence 12 from patent US 5574138. linear PAT 06-FEB-1997  
ACCESSION I28856  
VERSION I28856.1 GI:1819640  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 345)  
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.  
TITLE Epithelium-derived T-cell factor  
JOURNAL Patent: US 5574138-A 12 12-NOV-1996;  
FEATURES Location/Qualifiers  
source 1. .345  
BASE COUNT 121 a 49 c 68 g 107 t  
ORIGIN

Query Match 70.6%; Score 345; DB 6; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1.9e-163;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTTGAAGATCTTATTTCAATCTATGCAT 204  
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Db 1 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTTGAAGATCTTATTTCAATCTATGCAT 60  
QY 205 ATTGATGCTACTTTATATACGGAAGTGATGTTTCACCCCGAGTTGCAAGTAACAGCAATG 264  
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Db 61 ATTGATGCTACTTTATATACGGAAGTGATGTTTCACCCCGAGTTGCAAGTAACAGCAATG 120  
QY 265 AAGTGCCTTTCTCTGGAGTTACAAGTTATTTCACTTGAGTCCGGAGATGCAAGTATTTCAAT 324  
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Db 121 AAGTGCCTTTCTCTGGAGTTACAAGTTATTTCACTTGAGTCCGGAGATGCAAGTATTTCAAT 180

QY 325 GATACAGTAGAATAATCTGATCATCTAGCAAAACAACAGATTTTCTTCTAATGGGAATGTA 384  
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Db 181 GATACAGTAGAATAATCTGATCATCTAGCAAAACAACAGATTTTCTTCTAATGGGAATGTA 240  
QY 385 ACAGAACTCTGGATGCAAAAGAAATGTGAGGAACGTGGAGGAAAAAATATTAAAGAAATTTTG 444  
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Db 241 ACAGAACTCTGGATGCAAAAGAAATGTGAGGAACGTGGAGGAAAAAATATTAAAGAAATTTTG 300  
QY 445 CAGAGTTTGTACATATTTGTCACAAATGTTTCATCAACACTTCTTGA 489  
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Db 301 CAGAGTTTGTACATATTTGTCACAAATGTTTCATCAACACTTCTTGA 345

RESULT 30  
LOCUS 179226  
DEFINITION Sequence 12 from patent US 5707616. linear PAT 10-JUN-1998  
ACCESSION I79226  
VERSION I79226.1 GI:3207516  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 345)  
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.  
TITLE Method for treating or preventing gastrointestinal disease with  
epithelium-derived T-cell factor  
JOURNAL Patent: US 5707616-A 12 13-JAN-1998;  
FEATURES Location/Qualifiers  
source 1. 345  
BASE COUNT 121 a 49 c 68 g 107 t  
ORIGIN

Query Match 70.6%; Score 345; DB 6; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1.9e-163;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTTGAAGATCTTATTTCAATCTATGCAT 204  
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Db 1 AACTGGGTGAATGTAATAAGTGAATTTGAAAAAATTTGAAGATCTTATTTCAATCTATGCAT 60  
QY 205 ATTGATGCTACTTTATATACGGAAGTGATGTTTCACCCCGAGTTGCAAGTAACAGCAATG 264  
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Db 61 ATTGATGCTACTTTATATACGGAAGTGATGTTTCACCCCGAGTTGCAAGTAACAGCAATG 120  
QY 265 AAGTGCCTTTCTCTGGAGTTACAAGTTATTTCACTTGAGTCCGGAGATGCAAGTATTTCAAT 324  
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Db 121 AAGTGCCTTTCTCTGGAGTTACAAGTTATTTCACTTGAGTCCGGAGATGCAAGTATTTCAAT 180  
QY 325 GATACAGTAGAATAATCTGATCATCTAGCAAAACAACAGATTTTCTTCTAATGGGAATGTA 384  
|||||  
Db 181 GATACAGTAGAATAATCTGATCATCTAGCAAAACAACAGATTTTCTTCTAATGGGAATGTA 240  
QY 385 ACAGAACTCTGGATGCAAAAGAAATGTGAGGAACGTGGAGGAAAAAATATTAAAGAAATTTTG 444  
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Db 241 ACAGAACTCTGGATGCAAAAGAAATGTGAGGAACGTGGAGGAAAAAATATTAAAGAAATTTTG 300  
QY 445 CAGAGTTTGTACATATTTGTCACAAATGTTTCATCAACACTTCTTGA 489  
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Db 301 CAGAGTTTGTACATATTTGTCACAAATGTTTCATCAACACTTCTTGA 345

RESULT 31  
LOCUS AR087004  
DEFINITION Sequence 1 from patent US 5985663. linear PAT 07-SEP-2000  
ACCESSION AR087004  
VERSION AR087004.1 GI:10013770  
KEYWORDS  
SOURCE Unknown.

ORGANISM	Unknown.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
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ORGANISM Macaca fascicularis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
Cercopithecinae; Macaca.  
REFERENCE 1 (bases 1 to 492)  
AUTHORS Tatsumi, M.  
TITLE Direct Submission  
JOURNAL Submitted (20-JAN-1997) Masashi Tatsumi, National Institute of  
Health, Department of Veterinary Science, Toyama-23-1,  
Shiojuku-ku, Tokyo 162, Japan (E-mail: tatsumi@nih.go.jp,  
Tel:81-3-5285-1111, Fax:81-3-5285-1179)  
REFERENCE 2 (bases 1 to 492)  
AUTHORS Tatsumi, M.  
TITLE Molecular cloning and expression of cynomolgus monkey  
interleukin-15  
JOURNAL Unpublished (1997)  
FEATURES  
source Location/Qualifiers  
1..492  
/organism="Macaca fascicularis"  
/db\_xref="taxon:9541"  
/cell\_type="peripheral blood mononuclear cells"  
sig\_peptide 1..144  
CDS 1..489  
/codon\_start=1  
/product="interleukin-15 precursor"  
/protein\_id="BAAL19149.1"  
/db\_xref="GI:1799530"  
/translation="MRISKPHLRVSIOCYLCLLLNSHFLTEAGIHVFLGCFSGALP  
KTEANWNVISDLKIEDLIQSMHIDATLYTESDVHPCKVTAMKCFLELQVISHES  
GDTDHDVTENLIILANNILSSNGNITESGCKECEELEEKNIKEFLOSFVHVQMFN  
TS"  
mat\_peptide 145..486  
BASE COUNT 161 a 81 c 93 g 157 t  
ORIGIN  
Query Match 29.0%; Score 142; DB 9; Length 492;  
Best Local Similarity 99.5%; Pred. No. 8.6e-61;  
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 32 TTTCATCCAGTCTACTGTGTTTACTTCTAAACAGTCATTTCTAACTGAAGCTGGCA 91  
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DB 32 TTTCATCCAGTCTACTGTGTTTACTTCTAAACAGTCATTTCTAACTGAAGCTGGCA 91  
QY 92 TTCATGCTTCTCATTTTGGGCTGTTTTCAGTCGAGGCTTCTTAAACAGCAAGCAACTGGG 151  
|||||  
DB 92 TTCATGCTTCTCATTTTGGGCTGTTTTCAGTCGAGGCTTCTTAAACAGCAAGCAACTGGG 151  
QY 152 TGAATGTAATAAGTCATTTGAAAAAATTGAAGATCTTATTCATCTATGCATATTGATG 211  
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DB 152 TGAATGTAATAAGTCATTTGAAAAAATTGAAGATCTTATTCATCTATGCATATTGATG 211  
QY 212 CTACTTTATATAC 224  
|||||  
DB 212 CTACTTTATATAC 224  
RESULT 34  
MMU19843  
LOCUS 559 bp mRNA linear PRI 03-FEB-1996  
DEFINITION Macaca mulatta interleukin-15 (IL-15) mRNA, complete cds.  
ACCESSION U19843  
VERSION U19843.1 GI:644803  
KEYWORDS  
SOURCE rhesus monkey.  
ORGANISM Macaca mulatta  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
Cercopithecinae; Macaca.  
REFERENCE 1 (bases 1 to 559)  
AUTHORS Villinger, F., Brar, S.S., Mayne, A., Chikkala, N. and Ansari, A.A.

TITLE Comparative sequence analysis of cytokine genes from human and  
nonhuman primates  
JOURNAL J. Immunol. 155 (8), 3946-3954 (1995)  
MEDLINE 96003435  
REFERENCE 2 (bases 1 to 559)  
AUTHORS Villinger, F.J.  
TITLE Direct Submission  
JOURNAL Submitted (13-JAN-1995) Francois J. Villinger, Emory University,  
Pathology, 1327 Clifton Rd. Atlanta, GA 30322, USA  
FEATURES  
source Location/Qualifiers  
1..559  
/organism="Macaca mulatta"  
/db\_xref="taxon:9541"  
/clone="Rm1 IL-15 clone 3"  
/cell\_type="peripheral blood mononuclear cells"  
/tissue\_type="blood"  
1..559  
/gene="IL-15"  
28..516  
/gene="IL-15"  
/codon\_start=1  
/product="interleukin-15"  
/protein\_id="AAB60398.1"  
/db\_xref="GI:644804"  
/translation="MRISKPHLRVSIOCYLCLLLNSHFLTEAGIHVFLGCFSGALP  
KTEANWNVISDLKIEDLIQSMHIDATLYTESDVHPCKVTAMKCFLELQVISHES  
GDTDHDVTENLIILANNILSSNGNITESGCKECEELEEKNIKEFLOSFVHVQMFN  
TS"  
variation 41  
/gene="IL-15"  
/replace="c"  
119  
variation  
/gene="IL-15"  
/replace="c"  
BASE COUNT 179 a 93 c 105 g 182 t  
ORIGIN  
Query Match 29.0%; Score 142; DB 9; Length 559;  
Best Local Similarity 99.5%; Pred. No. 8.4e-61;  
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 32 TTTCATCCAGTCTACTGTGTTTACTTCTAAACAGTCATTTCTAACTGAAGCTGGCA 91  
|||||  
DB 59 TTTCATCCAGTCTACTGTGTTTACTTCTAAACAGTCATTTCTAACTGAAGCTGGCA 118  
QY 92 TTCATGCTTCTCATTTTGGGCTGTTTTCAGTCGAGGCTTCTTAAACAGCAAGCAACTGGG 151  
|||||  
DB 119 TTCATGCTTCTCATTTTGGGCTGTTTTCAGTCGAGGCTTCTTAAACAGCAAGCAACTGGG 178  
QY 152 TGAATGTAATAAGTCATTTGAAAAAATTGAAGATCTTATTCATCTATGCATATTGATG 211  
|||||  
DB 179 TGAATGTAATAAGTCATTTGAAAAAATTGAAGATCTTATTCATCTATGCATATTGATG 238  
QY 212 CTACTTTATATAC 224  
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DB 239 CTACTTTATATAC 251  
RESULT 35  
HSDNAIL15  
LOCUS 14968 bp DNA linear PRI 20-DEC-1996  
DEFINITION H. sapiens IL15 gene.  
ACCESSION X91233  
VERSION X91233.1 GI:992997  
KEYWORDS IL15 gene; interleukin-15.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 14968)  
AUTHORS Krause, H., Jandrig, B., Wernicke, C., Bultone-Paus, S., Pohl, T. and  
Diamantstein, T.

Genomic structure and chromosomal localization of the human interleukin 15 gene (IL-15)  
Cytokine 8 (9), 667-674 (1996)  
97086948  
REFERENCE 2 (bases 1 to 14968)  
Krause, H.G.  
Direct Submission  
Submitted (09-SEP-1995) H.G. Krause, Univ. Klinik, Benjamin Franklin, Inst. f. Immunologie, Hindenburgdamm 27, D-12203 Berlin, FRG

Overlaps with U14407 & U03099.  
Location/Qualifiers

1. .14968  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="4"  
/map="q25-35"  
/clone="11/4"  
/clone\_lib="Stratagene Cat.#945203"  
1. .247  
/number=1  
/evidence=experimental

248. .357  
/number=2  
join(<248. .357,1351. .1448,2807. .2892,8696. .8740,10603. .10739,13493. .14001)

join(347. .357,1351. .1448,2807. .2892,8696. .8740,10603. .10739,13493. .13604)

/gene="IL15"  
join(347. .357,1351. .1448,2807. .2892,8696. .8740,10603. .10739,13493. .13604)

/gene="IL15"  
/codon\_start=1  
/product="interleukin-15"  
/protein\_id="CAA62616.1"

/db\_xref="GI:992998"  
/translation="MRISKPHLSISIQVLCILNLSHFLTEAGHVFILGCFSGALP  
KTEANWVSDLKIEDLIQSMHIDATLVESDHPSCVKVTAMKCFLEQLQVISLES  
GDASITHDIVENLIILIANLSLSNGVTSKGCKEELEEKNIKEFLOSFVHIVQMFN  
TS"

358. .1350  
/gene="IL15"  
/number=2  
/evidence=experimental

1351. .1448  
/gene="IL15"  
/number=3  
1449. .2806  
/gene="IL15"

/number=3  
/evidence=experimental  
2807. .2892  
/gene="IL15"

/number=4  
2893. .8695  
/gene="IL15"  
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8696. .8740  
/gene="IL15"

/number=5  
8741. .10602  
/gene="IL15"  
/number=5  
/evidence=experimental

10603. .10739  
/gene="IL15"  
/number=6  
10740. .13492  
/gene="IL15"

/number=6  
/evidence=experimental

exon  
BASE COUNT 5108 a 2436 c 2758 g 4666 t  
ORIGIN

Query Match 28.2%; Score 138; DB 9; Length 14968;  
Best Local Similarity 100.0%; Pred. No. 4.7e-59;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 CCCAGTTGCAAGTAACAGCAATGAAGTCTTCTCTTGGAGTTACAAGTTATTTCACTT 300  
|||||  
Db 10603 CCCAGTTGCAAGTAACAGCAATGAAGTCTTCTCTTGGAGTTACAAGTTATTTCACTT 10662  
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QY 301 GAGTCCGAGATCAAGTATTCATGATACAGTAGAAATCTGATCATCTCCTAGCAACAAC 360  
|||||  
Db 10663 GAGTCCGAGATCAAGTATTCATGATACAGTAGAAATCTGATCATCTCCTAGCAACAAC 10722  
|||||

QY 361 AGTTTGTCTTCTTAATGGG 378  
|||||  
Db 10723 AGTTTGTCTTCTTAATGGG 10740  
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RESULT 36  
AC096774 178438 bp DNA linear PRI 26-SEP-2001  
LOCUS Homo sapiens chromosome 4 clone RP11-286D5, complete sequence.  
DEFINITION AC096774 AC025061  
ACCESSION AC096774.1 GI:15778749  
VERSION HTG.  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 178438)  
AUTHORS Waterston,R.H.  
TITLE The sequence of Homo sapiens clone  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178438)  
AUTHORS Waterston,R.H.  
TITLE Direct Submission  
JOURNAL Submitted (26-SEP-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

COMMENT On Sep 26, 2001 this sequence version replaced gi:7387373.  
----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: http://genome.wustl.edu/gsc/index.shtml  
Contact: submissions@watson.wustl.edu  
----- Project Information -----  
Center project name: H\_NH0286D05  
Drafting center: WIBR  
----- Location/Qualifiers -----  
1. .178438  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="4"  
/clone="RP11-286D5"  
BASE COUNT 57172 a 32631 c 33072 g 55563 t  
ORIGIN

Query Match 28.2%; Score 138; DB 9; Length 178438;  
Best Local Similarity 100.0%; Pred. No. 2.9e-59;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 CCCAGTTGCAAGTAACAGCAATGAAGTCTTCTCTTGGAGTTACAAGTTATTTCACTT 300  
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Db 42078 CCCAGTTGCAAGTAACAGCAATGAAGTCTTCTCTTGGAGTTACAAGTTATTTCACTT 42137  
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Qy 301 GAGTCCGAGATGCAAGTATTTCATGATACAGTAGAGAAATCTGATCCTAGCAACAAC 360  
|||||  
Db 42138 GAGTCCGAGATGCAAGTATTTCATGATACAGTAGAGAAATCTGATCCTAGCAACAAC 42197  
|||||  
Qy 361 AGTTTGCTTCTTAATGGG 378  
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Db 42198 AGTTTGCTTCTTAATGGG 42215  
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RESULT 37  
LOCUS AR004267 489 bp DNA linear PAT 04-DEC-1998  
DEFINITION Sequence 1 from patent US 5747024.  
ACCESSION AR004267  
VERSION AR004267.1 GI:3965146  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 489)  
AUTHORS Grabstein,K.H. and Widmer,M.B.  
TITLE Vaccine adjuvant comprising interleukin-15  
JOURNAL Patent: US 5747024-A 1 05-MAY-1998;  
FEATURES Location/Qualifiers  
source 1..489  
BASE COUNT 162 a 81 c 92 g 154 t  
ORIGIN  
Query Match 21.9%; Score 107; DB 6; Length 489;  
Best Local Similarity 99.4%; Pred. No. 4.4e-43;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 67 AGTCATTTTCTAACTGAAGCTGCATTCATCTTCATTTTGGCTGTTTCAGTCGAGG 126  
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Db 67 AGTCATTTTCTAACTGAAGCTGCATTCATCTTCATTTTGGCTGTTTCAGTCGAGG 126  
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Qy 127 CTTCCCTAAACAGACCACTGGGTGAATGTAATAGTGATTTGAAAAAATTGAAGAT 186  
|||||  
Db 127 CTTCCCTAAACAGACCACTGGGTGAATGTAATAGTGATTTGAAAAAATTGAAGAT 186  
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Qy 187 CTTATTCATCTATGCATATTGATGCTACTTTATATAC 224  
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Db 187 CTTATTCATCTATGCATATTGATGCTACTTTATATAC 224  
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RESULT 38  
LOCUS AR024348 489 bp DNA linear PAT 05-DEC-1998  
DEFINITION Sequence 1 from patent US 5795966.  
ACCESSION AR024348  
VERSION AR024348.1 GI:3977642  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 489)  
AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.  
TITLE Antagonists of interleukin-15  
JOURNAL Patent: US 5795966-A 1 18-AUG-1998;  
FEATURES Location/Qualifiers  
source 1..489  
BASE COUNT 162 a 81 c 92 g 154 t  
ORIGIN  
Query Match 21.9%; Score 107; DB 6; Length 489;  
Best Local Similarity 99.4%; Pred. No. 4.4e-43;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 67 AGTCATTTTCTAACTGAAGCTGGCATTCATCTTCATTTTGGCTGTTTCAGTCGAGG 126  
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Db 67 AGTCATTTTCTAACTGAAGCTGGCATTCATCTTCATTTTGGCTGTTTCAGTCGAGG 126  
|||||  
Qy 127 CTTCCCTAAACAGACCACTGGGTGAATGTAATAGTGATTTGAAAAAATTGAAGAT 186  
|||||  
Db 127 CTTCCCTAAACAGACCACTGGGTGAATGTAATAGTGATTTGAAAAAATTGAAGAT 186  
|||||  
Qy 187 CTTATTCATCTATGCATATTGATGCTACTTTATATAC 224  
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Db 187 CTTATTCATCTATGCATATTGATGCTACTTTATATAC 224  
|||||

RESULT 39  
LOCUS AR070282 489 bp DNA linear PAT 18-FEB-2000  
DEFINITION Sequence 4 from patent US 5892001.  
ACCESSION AR070282  
VERSION AR070282.1 GI:7221170  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 489)  
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.  
TITLE Epithelium-derived T-cell factor antibodies  
JOURNAL Patent: US 5892001-A 4 06-APR-1999;  
FEATURES Location/Qualifiers  
source 1..489  
BASE COUNT 162 a 81 c 92 g 154 t  
ORIGIN  
Query Match 21.9%; Score 107; DB 6; Length 489;  
Best Local Similarity 99.4%; Pred. No. 4.4e-43;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 67 AGTCATTTTCTAACTGAAGCTGCATTCATCTTCATTTTGGCTGTTTCAGTCGAGG 126  
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Db 67 AGTCATTTTCTAACTGAAGCTGCATTCATCTTCATTTTGGCTGTTTCAGTCGAGG 126  
|||||  
Qy 127 CTTCCCTAAACAGACCACTGGGTGAATGTAATAGTGATTTGAAAAAATTGAAGAT 186  
|||||  
Db 127 CTTCCCTAAACAGACCACTGGGTGAATGTAATAGTGATTTGAAAAAATTGAAGAT 186  
|||||  
Qy 187 CTTATTCATCTATGCATATTGATGCTACTTTATATAC 224  
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Db 187 CTTATTCATCTATGCATATTGATGCTACTTTATATAC 224  
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RESULT 40  
LOCUS AR085741 489 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 4 from patent US 5985262.  
ACCESSION AR085741  
VERSION AR085741.1 GI:10012507  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 489)  
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.  
TITLE Method of treatment with epithelium derived T-cell factor  
JOURNAL Patent: US 5985262-A 4 16-NOV-1999;  
FEATURES Location/Qualifiers  
source 1..489  
BASE COUNT 162 a 81 c 92 g 154 t  
ORIGIN  
Query Match 21.9%; Score 107; DB 6; Length 489;  
Best Local Similarity 99.4%; Pred. No. 4.4e-43;  
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 67 AGTCATTTTCTAACTGAAGCTGGCATTCATCTTCATTTTGGCTGTTTCAGTCGAGG 126  
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Db 67 AGTCATTTTCTAACTGAAGCTGGCATTCATCTTCATTTTGGCTGTTTCAGTCGAGG 126  
|||||  
Qy 127 CTTCCCTAAACAGACCACTGGGTGAATGTAATAGTGATTTGAAAAAATTGAAGAT 186  
|||||  
Db 127 CTTCCCTAAACAGACCACTGGGTGAATGTAATAGTGATTTGAAAAAATTGAAGAT 186  
|||||  
Qy 187 CTTATTCATCTATGCATATTGATGCTACTTTATATAC 224  
|||||  
Db 187 CTTATTCATCTATGCATATTGATGCTACTTTATATAC 224  
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Query Match 21.9%; Score 107; DB 6; Length 489;  
Best Local Similarity 99.4%; Pred. No. 4.4e-43;

Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
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Db	67	AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGGG	126						
Qy	127	CTTCCTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTGAAGAT	186						
Db	127	CTCCCTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTGAAGAT	186						
Qy	187	CTTATTCAATCTATGCATATTTGATGCTACTTTATATAC	224						
Db	187	CTTATTCAATCTATGCATATTTGATGCTACTTTATATAC	224						
RESULT 41									
LOCUS	AR122045	AR122045	489 bp	DNA	linear	PAT 16-MAY-2001			
DEFINITION	Sequence 1 from patent US 6165466.								
ACCESSION	AR122045								
VERSION	AR122045.1	GI:14106362							
KEYWORDS	Unknown.								
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	1 (bases 1 to 489)								
AUTHORS	Grabstein,K.H., Pettit,D.K. and Paxton,R.J.								
TITLE	Antagonists of Interleukin-15								
JOURNAL	Patent: US 6165466-A 1 26-DEC-2000;								
FEATURES	Location/Qualifiers								
source	1..489								
BASE COUNT	162 a	81 c	92 g	154 t					
ORIGIN	/organism="unknown"								
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Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
Qy	67	AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGGG	126						
Db	67	AGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGGG	126						
Qy	127	CTTCCTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTGAAGAT	186						
Db	127	CTCCCTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAAATTGAAGAT	186						
Qy	187	CTTATTCAATCTATGCATATTTGATGCTACTTTATATAC	224						
Db	187	CTTATTCAATCTATGCATATTTGATGCTACTTTATATAC	224						
RESULT 42									
LOCUS	AR122867	AR122867	489 bp	DNA	linear	PAT 16-MAY-2001			
DEFINITION	Sequence 1 from patent US 6168783.								
ACCESSION	AR122867								
VERSION	AR122867.1	GI:14107833							
KEYWORDS	Unknown.								
SOURCE	Unknown.								
ORGANISM	Unclassified.								
REFERENCE	1 (bases 1 to 489)								
AUTHORS	Grabstein,K.H., Pettit,D.K. and Paxton,R.J.								
TITLE	Antagonists of Interleukin-15								
JOURNAL	Patent: US 6168783-A 1 02-JAN-2001;								
FEATURES	Location/Qualifiers								
source	1..489								
BASE COUNT	162 a	81 c	92 g	154 t					
ORIGIN	/organism="unknown"								

Query Match 21.9%; Score 107; DB 6; Length 489;									
Best Local Similarity 99.4%; Pred. No. 4.4e-43;									
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
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Db	67	AGTCATTTTCTAACTGAAGCTGGCAATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGG	126						
Qy	127	CTTCCTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT	186						
Db	127	CTCCCTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT	186						
Qy	187	CTTATTCAATCTATGCATATTTGATGCTACTTTATATAC	224						
Db	187	CTTATTCAATCTATGCATATTTGATGCTACTTTATATAC	224						
RESULT 43									
LOCUS	AR125104	AR125104	489 bp	DNA	linear	PAT 16-MAY-2001			
DEFINITION	Sequence 1 from patent US 6177079.								
ACCESSION	AR125104								
VERSION	AR125104.1 GI:14111166								
KEYWORDS	Unknown.								
SOURCE	Unknown.								
ORGANISM	Unclassified.								
REFERENCE	1 (bases 1 to 489)								
AUTHORS	Grabstein, K.H., Pettit, D.K. and Paxton, R.J.								
TITLE	Antagonists of interleukin-15								
JOURNAL	Patent: US 6177079-A 1 23-JAN-2001;								
FEATURES	Location/Qualifiers								
source	1..489								
BASE COUNT	162 a	81 c	92 g	154 t					
ORIGIN	/organism="unknown"								
Query Match 21.9%; Score 107; DB 6; Length 489;									
Best Local Similarity 99.4%; Pred. No. 4.4e-43;									
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
Qy	67	AGTCATTTTCTAACTGAAGCTGGCAATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGG	126						
Db	67	AGTCATTTTCTAACTGAAGCTGGCAATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGG	126						
Qy	127	CTTCCTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT	186						
Db	127	CTCCCTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT	186						
Qy	187	CTTATTCAATCTATGCATATTTGATGCTACTTTATATAC	224						
Db	187	CTTATTCAATCTATGCATATTTGATGCTACTTTATATAC	224						
RESULT 44									
LOCUS	AX006785	AX006785	489 bp	DNA	linear	PAT 06-SEP-2000			
DEFINITION	Sequence 3 from Patent WO0002582.								
ACCESSION	AX006785								
VERSION	AX006785.1 GI:9994821								
KEYWORDS	unidentified.								
SOURCE	unidentified.								
ORGANISM	unclassified.								
REFERENCE	1 (bases 1 to 489)								
AUTHORS	Londei, M., Quarantino, S. and Maiuri, L.								
TITLE	Treatment of celiac disease with interleukin-15 antagonists								
JOURNAL	Patent: WO 0002582-A 3 20-JAN-2000;								
FEATURES	Location/Qualifiers								
source	1..489								
BASE COUNT	162 a	81 c	92 g	154 t					
ORIGIN	/organism="unknown"								

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1..489
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BASE COUNT 162 a 81 c 92 g 154 t
ORIGIN

Query Match 21.9%; Score 107; DB 6; Length 489;
Best Local Similarity 99.4%; Pred. No. 4.4e-43;
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 67 AGTCATTTTCTAACGAGAGCTGGCATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126
Db 67 AGTCATTTTCTAACGAGAGCTGGCATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126

Qy 127 CTTCCTAAACAGAGCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186
Db 127 CTCCCTAAACAGAGCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186

Qy 187 CTTATTCATCTATGCATATTGATGCTACTTTATATAC 224
Db 187 CTTATTCATCTATGCATATTGATGCTACTTTATATAC 224

RESULT 45
LOCUS I25782 489 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 1 from patent US 5552303.
ACCESSION I25782
VERSION I25782.1 GI:1605652
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 489)
AUTHORS Grabstein,K., Anderson,D., Eisenman,J., Fung,V. and Rauch,C.
TITLE DNA encoding epithelium-derived T-cell factor
JOURNAL Patent: US 5552303-A 1 03-SEP-1996;
FEATURES
source
BASE COUNT 162 a 81 c 92 g 154 t
ORIGIN

Query Match 21.9%; Score 107; DB 6; Length 489;
Best Local Similarity 99.4%; Pred. No. 4.4e-43;
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 67 AGTCATTTTCTAACGAGAGCTGGCATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126
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Qy 127 CTTCCTAAACAGAGCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186
Db 127 CTCCCTAAACAGAGCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186

Qy 187 CTTATTCATCTATGCATATTGATGCTACTTTATATAC 224
Db 187 CTTATTCATCTATGCATATTGATGCTACTTTATATAC 224

RESULT 46
LOCUS I28850 489 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 4 from patent US 5574138.
ACCESSION I28850
VERSION I28850.1 GI:1819631
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 489)
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AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE Epithelium-derived T-cell factor
JOURNAL Patent: US 5574138-A 4 12-NOV-1996;
FEATURES
source
BASE COUNT 162 a 81 c 92 g 154 t
ORIGIN

Query Match 21.9%; Score 107; DB 6; Length 489;
Best Local Similarity 99.4%; Pred. No. 4.4e-43;
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 67 AGTCATTTTCTAACGAGAGCTGGCATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126
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Qy 127 CTTCCTAAACAGAGCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186
Db 127 CTCCCTAAACAGAGCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186

Qy 187 CTTATTCATCTATGCATATTGATGCTACTTTATATAC 224
Db 187 CTTATTCATCTATGCATATTGATGCTACTTTATATAC 224

RESULT 47
LOCUS I79220 489 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 4 from patent US 5707616.
ACCESSION I79220
VERSION I79220.1 GI:3207510
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 489)
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE Method for treating or preventing gastrointestinal disease with
epithelium-derived T-cell factor
JOURNAL Patent: US 5707616-A 4 13-JAN-1998;
FEATURES
source
BASE COUNT 162 a 81 c 92 g 154 t
ORIGIN

Query Match 21.9%; Score 107; DB 6; Length 489;
Best Local Similarity 99.4%; Pred. No. 4.4e-43;
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 67 AGTCATTTTCTAACGAGAGCTGGCATTCATGCTCTTCATTTTGGGCTGTTTCAGTGCAGGG 126
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Qy 127 CTTCCTAAACAGAGCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTGAAGAT 186
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Qy 187 CTTATTCATCTATGCATATTGATGCTACTTTATATAC 224
Db 187 CTTATTCATCTATGCATATTGATGCTACTTTATATAC 224

RESULT 48
LOCUS CAU03099 1275 bp mRNA linear PRI 25-MAY-1994
DEFINITION Cercopithecus aethiops simian interleukin 15 mRNA, complete cds.
ACCESSION U03099
VERSION U03099.1 GI:493521
KEYWORDS
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SOURCE      African green monkey.
ORGANISM    Cercopithecus aethiops
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
Cercopitheciinae; Cercopithecus.
REFERENCE   1 (bases 1 to 1275)
AUTHORS     Grabstein,K.H., Eisenman,J., Shanebeck,K., Rauch,C., Srinivasan,S.,
            Fung,V., Beers,C., Richardson,J., Schoenborn,M.A., Ahldeh,M.,
            Johnson,L., Alderson,M.R., Watson,J.D., Anderson,D.M. and Giri,J.G.
TITLE       Cloning of a T cell growth factor that interacts with the beta
            chain of the interleukin-2 receptor
JOURNAL     Science 264, 965-968 (1994)
MEDLINE     94233380
REFERENCE   2 (bases 1 to 1275)
AUTHORS     Anderson,D.M.
TITLE       Direct Submission
JOURNAL     Submitted (02-NOV-1993) Dirk M. Anderson, Immunex Research and
            Development Corp., 51 University St., Seattle, WA 98101, USA
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Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 127 CTTCTCTAAACAGAGCCCACTGGTGGAATGTAATGAATGATTTGAAAAAATTTGAAGAT 186
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Db 610 CTTCTCTAAACAGAGCCCACTGGTGGAATGTAATGAATGATTTGAAAAAATTTGAAGAT 669
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Qy 187 CTTATTCAATCATCATATTGATCTACTTTATATAC 224
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Db 670 CTTATTCAATCATCATATTGATCTACTTTATATAC 707
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RESULT 49
AC068518/C AC068518 164469 bp DNA linear HTG 03-MAY-2000
DEFINITION Homo sapiens chromosome 4 clone RP11-393K13 map 4, WORKING DRAFT
SEQUENCE, 13 unordered pieces.
ACCESSION AC068518
VERSION AC068518.1 GI:7684450
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human
ORGANISM Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 164469)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 4, Clone RP11-393K13
Unpublished
2 (bases 1 to 164469)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karacas,A.,
Klein,J., Lacroque,K., Lamazares,R., Landers,T., Lehoczy,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGuck,A., McKernan,K., McPheeters,R.,
Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neil,D., Oliver,T.M., Oliver,J., Peterson,K., Pierle,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tessaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Willson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (03-MAY-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L5542
Center clone name: 393_K13
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 155576 bases at least Q40
Consensus quality: 160252 bases at least Q30
Consensus quality: 162041 bases at least Q20
Insert size: 172000; agarose-fp
Quality coverage: 4.3 in Q20 bases; agarose-fp
Quality coverage: 4.5 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1444: contig of 1444 bp in length
* 1445 1544: gap of 100 bp
* 1545 3513: contig of 1969 bp in length
* 3514 3613: gap of 100 bp
* 3614 6328: contig of 2715 bp in length
* 6329 6428: gap of 100 bp
* 6429 9397: contig of 2969 bp in length
* 9398 9497: gap of 100 bp
* 9498 14140: contig of 4643 bp in length
* 14141 14240: gap of 100 bp
* 14241 20363: contig of 6123 bp in length

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\* 20364 20463: gap of 100 bp  
\* 20464 30637: contig of 10174 bp in length  
\* 30638 30737: gap of 100 bp  
\* 30738 43011: contig of 12274 bp in length  
\* 43012 43111: gap of 100 bp  
\* 43112 57766: contig of 14655 bp in length  
\* 57767 57866: gap of 100 bp  
\* 57867 73189: contig of 15323 bp in length  
\* 73190 73289: gap of 100 bp  
\* 73290 98890: contig of 25601 bp in length  
\* 98891 98990: gap of 100 bp  
\* 98991 125697: contig of 26707 bp in length  
\* 125698 125797: gap of 100 bp  
\* 125798 164469: contig of 38672 bp in length.

FEATURES

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ACCESSION AR070289  
VERSION AR070289.1 GI:7221177  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 345)  
AUTHORS Grabstein, K.H., Anderson, D.M., Eisenman, J.R., Fung, V. and Rauch, C.  
TITLE Epithelium-derived T-cell factor antibodies  
JOURNAL Patent: US 5892001-A 13 06-APR-1999;  
FEATURES  
source  
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Location/Qualifiers  
/organism="unknown"  
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Best Local Similarity 100.0%; Pred. No. 2.1e-29;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 205 ATTGATGCTACTTTATATAC 224  
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Db 61 ATTGATGCTACTTTATATAC 80  
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Search completed: August 6, 2002, 21:32:10  
Job time: 5080 sec

Query Match 20.2%; Score 99; DB 2; Length 164469;  
Best Local Similarity 100.0%; Pred. No. 1.6e-39;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GAACACATTTGAGAGTATTTCCATCCAGTCTACTTGTGTCTTAAACAGTCA 71  
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Db 77622 GAACACATTTGAGAGTATTTCCATCCAGTCTACTTGTGTCTTAAACAGTCA 77563  
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Qy 72 TTTTCTAACTGAAGTGGCATTCTTCATTTGGG 110  
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Db 77562 TTTTCTAACTGAAGTGGCATTCTTCATTTGGG 77524  
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RESULT 50

AR070289

LOCUS

DEFINITION

Sequence 13 from patent US 5892001.

345 bp

DNA

linear

PAT 18-FEB-2000

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